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version 5.1.6
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GenCore (c) 1993
         Copyright
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model
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Run on:

June 21, 2004, 15:41:49; Search time 47.1111 Seconds (without alignments) 1433.395 Million cell updates/sec

1273 1 MVSKGEELFTGVVPILVELD......VLLGFVTAAGITLGMDELYK 239 US-09-887-784-64A Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

1586107

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp2000s:*
3: geneseqp2000s:*
4: geneseqp2001s:* geneseqp20028:* geneseqp2003as:* geneseqp2003bs:* geneseqp20048:* 2 M 4 M 9 L 8

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
	1269	7 66	239		AAE17518	Aael 7518 Enhanced
10	1269	7.66	363	•	ABR40352	0
ım	1269	99.7	893	4	AAG65781	Amino
4	1269	99.7	1132	4	AAG65782	Amino
S	1261	99.1	239	S	AAE17517	7
9	1258	98.8	239	٣	AAB22882	Aab22882 Enhanced
7	1258	98.8	239	m	AAY54349	Aay54349 Amino aci
c c	1258	98.8	239	٣	AAY79584	4
9	1258	98.8	239	4	AAB50804	Aab50804 Jellyfish
10	1258	98.8	239	4	AAB85900	Aab85900 A. victor
11	1258	98.8	239	4	AAB31171	Aab31171 Amino aci
12	1258	98.8	239	2	AAG66198	Aag66198 A. victor
13	1258	98.8	239	Ŋ	ABG94444	Abg94444 Protease
14	1258	98.8	239	S	AAE14599	
15	1258	8.86	239	9	AAE34958	Aae34958 Aequorea
16	1258	98.8	239	9	AAG79829	Aag79829 Green flu
17	1258	98.8	239	9	ABR83616	vo
18	1258	98.8	239	9	ADA38074	Ada38074 Aeguorea
19	1258	98.8	239	7	ABU63204	Abu63204 Aequorea
20	1258	98.8	239	7	ADC18358	Adc18358 EGFP (enh
21	1258	98.8	239	7	ABW00914	Abw00914 Aeguorea
22	1258	98.8	239	7	ADE28570	Ade28570 Enhanced
23	1258	98.8	246	7	ABM79011	н
24	1258	98.8	248	ß	AAG68319	Aag68319 Jellyfish
25	1258	98.8	259	'n	AAU99804	4

265 2 AAW97451 270 5 AAU99803 272 5 AAU99802 273 5 AAU99801 280 3 AAV50142 281 3 AAV50142 281 3 AAV50142 281 3 AAV50142 281 3 AAV50142 281 3 AAV50142 281 7 ADE2856 296 7 ADE2856 297 7 ADE2856 296 7 ADE2856 297 7 ADE2856 298 7 ADE2856 299 7 ADE2856 299 7 ADE2856 290 7 ADE28	Aaw97451 Wild-type Aau99803 Biomembra Aau99802 Biomembra Aau99800 Biomembra			шоощ	Aay42181 EGFP/DRM Abr3050 HUB1-GFP Aay54359 GFP mutan Abr83621 RUB1-GFP
	AAW97451 AAU99803 AAU99802 AAU99800	AAU99801 AAU99807 AAY50142	AAU10888 ADE28562 ADE28564 ADE28568	ADE28566 AAB22860 AAY79638 ABG94422	AAY42181 ABR83620 AAY54359 ABR83621
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	22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	0 1 0 0	1 4 6 6 6 7	33 38 30 40 11	4 4 4 4 0 6 4 0

ALIGNMENTS

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/note= "Wild type Glu substituted with Gly; This corresponds to position 222 in the wild type protein"
                                                                                                                               /note= "Wild type Phe substituted with Leu, This
corresponds to position 64 in the wild type protein"
223
                                                                   Jellyfish, green fluorescent protein, GFP, protein redistribution, cellular function, genetic reporter; mutant; Stoke's shift, mutein.
                                                   Enhanced F64L-E222G jellyfish green fluorescent protein mutant
                                                                                                                       Location/Qualifiers
AAE17518 standard; protein; 239 AA
                                   (first entry)
                                                                                             Aequorea victoria.
                                                                                                                        Key
Misc-difference
                                                                                                                                                        Misc-difference
                                   22-APR-2002
                                                                                                       Synthetic.
                  AAE17518;
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WO200198338-A2 27-DEC-2001.

19-JUN-2000; 2000DK-0000953. 20-JUN-2000; 2000US-02126B1P. 10-MAX-2001; 2001DK-0000739. 10-MAX-2001; 2001US-0290170P. 18-JUN-2001; 2001WO-EP006848.

Thastrup 0; Bjorn SP, Pagliaro L, (BIOI-) BIOIMAGE AS

WPI; 2002-098224/13. N-PSDB; AAD28163.

Novel fluorescent protein in in vitro assay for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution, has a green fluorescent protein with F64L and E222G mutation.

Claim 9; Page 37; 41pp; English.

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CC The invention relates to a fluorescent protein derived from green fluorescent protein (GFP) or its analogue. The GFP containing mutations of at FetL and ES226 has a bigger compared to other GFP's making it very suitable for high throughput screening due to better resolution. The fluorescent protein is useful in invitro assays for measuring protein care activity, or for measuring protein care activity, or for measuring protein care activity, or for measuring protein care activity. The fluorescent protein is useful in studying cellular functions in living cells; as protein tags in transgenic animals, living and fixed cells; organelle tags, secretion marker and genetic reporter. The fluorescent protein is also useful as a cell or organsle integrity marker, a marker for changes in cell morphology, as transfection marker, and as a marker to be used in combination with fluorescence activated cell sorting (FACS). The novel proteins can also be used as reporters to monitor live or dead biomass of organisms, such as fungi. The fluorescent protein are correctly as markers in transcriptional and translational cuseful for screening promoters and for transcrands and chromosomes. The fluorescent protein are cuseful for screening promoters and for tagging plasmids and chromosomes. The fluorescent protein engineered into the genome of a phage is useful care changed and as a mortant colling chasigning diagnostic tool. The present sequence is a DNA encoding channer of for designing diagnostic tool. The present protein (GFP) mutant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.7%; Score 1269; DB 5;
99.6%; Pred. No. 4.3e-124;
iive 0; Mismatches 1;
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11-OCT-2001; 2001US-0328896P.
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les 238; Conservative
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Aeguoría victoria.
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Nielsen SJ;

Terry ER,

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The invention relates to a novel cell, comprising three heterologous conjugates (HC), a first HC (HC1) comprising an anchor protein that specifically binds to an internal structure within the cell conjugated to an interactor protein (IP) of type A, a second HC (HC2) comprising IP of type B conjugated to a first protein of interest conjugated to detectable group. The cell is useful for detecting if a compound disrupts or induces the interaction between two intracellular proteins. The cell is also useful for screening compounds that modulate the interaction between two intracellular group. The cell is also useful intracellular proteins. The proteins. The proteins compounds the interaction between two exemplification of the invention
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                                                                        Novel cell for identifying modulators of protein interaction, contains a first conjugate comprising anchor protein, second conjugate having type B interactor protein and third conjugate with detectable group.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MVSKGEBLFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 99.7%; Score 1269; DB 6; Best Local Similarity 99.6%; Pred. No. 8.1e-124; Matches 238; Conservative 0; Mismatches 1;
                                                                                                                                                  Disclosure; Page 112-113; 118pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG65781 standard; protein; 893 AA.
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29-MAY-2000; 2000DK-00000849.
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                  WPI; 2003-430211/40.
N-PSDB; ACC72604.
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Aequorea victoria.
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25-OCT-2001.

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The invention relates to determining, if a compound, is a dislocator of PDE4. The method comprises testing if the compound removes PDE4 spots, which may optionally be induced by a Rolipram-like reference compound, and testing if it inhibits the catalytic activity of the PDE4, where the compound is a dislocator of PDE4, if it removes PDE spots and if it does not inhibit the catalytic activity of PDE4. The method is useful for identifying compounds useful for the treatment of diseases of the central nervous system such as depression and for the treatment of inflammatory disease such as joint inflammation, Crohn's disease, inflammatory bowel compounds useful for the treatment of inflammatory bowel including asthma, chronic bronchitis, pulmonary disease candotoxic shock, toxic shock syndrome, systemic lupus erthematosis, psoriasis, bone resorption diseases, reperfusion injury, cancer and HIV including asthma affinity for the catalytic site on intracellular distribution of the PDE for the preparation of a medicament. The present carrier can minimize or reverse the effect of catalytic site on intracellular distribution of the PDE for the preparation of a HSPDE4A1-E222G fusion
                                                                                                                                           Determining if a compound is a dislocator of PDE4 for identifying compounds for treating CNS and inflammatory disease comprises identifying compounds which remove PDE4 spots.
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  Bjorn SP, Thastrup O, Almholt DC;
                                                                                                                                                                                                                                         Example 1; Page 156-160; 160pp; English.
Scudder KM,
                                                                      WPI; 2001-611727/70
                                                                                                  N-PSDB; AAI66852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 893 AA;
                      Praestegaard M;
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VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
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Amino acid sequence of HSPDE4A4-E222G fusion protein.
          AAG65782 standard; protein; 1132 AA
                                07-JAN-2002 (first entry)
                      AAG65782;
    RESULT
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rusa; central nervous system, antiinflammatory, cytostatic, nootropic, autoimmune; ischemic, osteopathic, GFP, green fluorescent protein; fusion protein,

Aequorea victoria. WO200179526-A2

Homo sapiens

Enhanced F641 jellyfish green fluorescent protein mutant.

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PDE4. The method comprises testing if the compound removes PDE4 spots, which may optionally be induced by a Rolipram-like reference compound, and testing if it inhibits the catalytic activity of the PDE4, where the compound is a dislocator of PDE4, if it removes PDE spots and if it does not inhibit the catalytic activity of PDE4. The method is useful for identifying compounds useful for the treatment of diseases of the central nervous system such as depression and for the treatment of inflammatory disease such as joint inflammation, Crohn's disease, inflammatory disease, respiratory disease, chronic obstructive pulmonary disease.

(COPD), including astima, chronic bronchtis, pulmonary disease, chock syndrome, systemic lupus erthematosis, psoriasis, bone resorption diseases, reperfusion injury, cancer and HIV infection. The use of a reagent that can mimic or reverse the effect of the compound with affinity for the catalytic site on intracellular distribution of the PDE for the preparation of a medicament. The present sequence represents the amino acid sequence of a HSPDE4A4-E223G fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            954 LVTTLSYGVQCFSRYPDHMKQHDPFKSAMPEGYVQERTIFFKDDGNYKTRAEVKPEGDTL 1013
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                                                                                                                                                                                                                                                                                                      Determining if a compound is a dislocator of PDE4 for identifying compounds for treating CNS and inflammatory disease comprises identifying compounds which remove PDE4 spots.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to determining, if a compound, is a dislocator of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                 Thastrup O, Almholt DC;
                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 162-167; 160pp; English.
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                                                                                                                                                                                 Bjorn SP,
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                                      11-APR-2001; 2001WO-DK000264
                                                                            17-APR-2000; 2000DK-0000651.
29-MAY-2000; 2000DK-00000849.
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                                                                                                                                                                                 Scudder KM,
                                                                                                                                                                                                                                            WPI; 2001-611727/70.
N-PSDB; AAI66853.
                                                                                                                                        (BIOI-) BIOIMAGE AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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Matches
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Novel Eluorescent protein in in vitro assay for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution, has a green fluorescent protein with F64L and E222G
                                                                             /note= "Wild type Phe substituted with Leu; This corresponds to position 64 in the wild type protein"
Jellyfish; green fluorescent protein; GFP; protein redistribution; cellular function; genetic reporter; mutant; Stoke's shift; mutein.
                                                            Location/Qualifiers
                                                                                                                                                                                                                                          Thastrup 0;
                                                                                                                                                                                                                                                                                                                                         Example 1; Page 35; 41pp; English.
                                                                                                                                                                   19-JUN-2000; 2000DK-00000953.
20-JUN-2000; 2000US-02126B1P.
10-MAX-2001; 2001DK-00000739.
10-MAX-2001; 2001US-0290170P.
                                                                                                                                                  18-JUN-2001; 2001WO-EP006848
                                                                                                                                                                                                                                          Bjorn SP, Pagliaro L,
                                                                                                                                                                                                                                                             WPI; 2002-098224/13
                                                                                                                                                                                                                     (BIOI-) BIOIMAGE AS
                               Aequorea victoria.
                                                                                                                                                                                                                                                                       N-PSDB; AAD28162
                                                                     Misc-difference
                                                                                                           WO200198338-A2
                                                                                                                              27-DEC-2001.
                                        Synthetic.
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the inversement protein (GFP) or the analogue. The GFP containing mutations at F64% and E222G has a bigger compared to other GFP's making it very suitable for high throughput screening due to better resolution. The fluorescent protein is useful in invitro assays for measuring protein kinase activity or dephosphorylation activity, or for measuring protein kinase activity or dephosphorylation activity, or for measuring protein cedistribution. The fluorescent protein is useful is studying cellular functions in living cells; as protein tags in transgenic animals, living and fixed cells; organelle tags, secretion marker and genetic reporter. The fluorescent protein is also useful as a cell or organelle integrity marker, a marker for changes in cell morphology, as transfection marker, and as a marker to be used in combination with fluorescence activated cell systing (FACS). The novel proteins can also be used as reporters to monitor live or dead biomass of organisms, such as fungi. The fluorescent protein is also useful as markers in transcriptional and translational correction for screening promoters and for tagging plasmids and chromosomes. The fluorescent protein are construction of the genome of a phage is useful for accepting promoters and for tagging plasmids and chromosomes. The invention relates to a fluorescent protein derived from

Sequence 239 AA;

for designing diagnostic tool. The present sequence is enhanced F64L jellyfish green fluorescent protein (GFP) mutant

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6.1 LVTALSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                            61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                  9
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                                                                                  MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                    1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                         Gaps
                                         ;
0
99.1%; Score 1261; DB 5; Length 239; 99.2%; Pred. No. 3e-123;
                                         2; Indels
                 Pred. No. 3e-123;
0; Mismatches
                                    Matches 237; Conservative
                   Local Similarity
Query Match
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1.31 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180

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The invention relates to systems, methods and reagents for cell-based screening or detection of compounds which affect particular biological functions. The methods of the invention utilise fluorescent biodetector molecules which, when acted on by a compound of interest, cause an ancient, when acted on by a compound of interest, cause an alteration in the cellular distribution of at least the fluorescent codety. In one embodiment, the biosensors comprise hear shock proteins (GFP) to derivatives thereof). Such biosensors are located in protein (GFP), or derivatives thereof). Such biosensors are located in another embodiment biodetector proteins can be used to detect protease activity. Such protease biodetector fusion proteins comprise one or more fluorescent proteins, a recognition signal which is cleaved by the protease; and at least one cellular localisation signal. The latter two components may be from heterologous sources. Due to the components of a single protein which is acted upon by the protease, or may be from heterologous sources. Due to the collocations signal, the biodetector protein is localised to a particular region of the cell. Once acted on by the protease of interest, the codinate to other locations within the cell. The presence of a second localisation signal attached to the fluorescent protein enables the fluorescent protein to be directed to a different cellular compartment after cleavage of the protease recognition sequence. The change in distribution of the fluorescent protein can be detected using imaging methods with a high degree of spatial resolution. The methods and Biodetector protein; fusion protein; recognition site; cellular targetting sequence; cellular localisation; fluorescent protein; protease activity detection; toxin detection; cellular stress detection; 181 DHYQQNTFIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239 181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWVLLEFVTAAGITLGMDELYK 239 cells Automated cell-based characterization of toxin by contacting cellicontaining luminescent reporter molecules with test substance and Enhanced green fluorescent protein (EGFP), SEQ ID NO:46. drug discovery; cell based screening. Example 11; Fig 29A; 336pp; English. A AAB22882 standard; protein; 239 99US-0122152P. 99US-0123399P. 99US-00352171. 25-FEB-2000; 2000WO-US004794. 10-JAN-2001 (first entry) Giuliano KA, Kapur R; (CETT-) CETTOWICS INC analyzing optically. WPI; 2000-594086/56. Aequorea victoria. N-PSDB; AAA93373 WO200050872-A2. 26-FEB-1999; 08-MAR-1999; 12-JUL-1999; 31-AUG-2000. Synthetic. AAB22882; RESULT 6 AAB22882 원 8

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cellular activities and to screen compounds which modulate these activities. Biosensors containing a recognition site for caspase, for example, may be used for the screening of compounds which modulate apoptosis, while biosensors containing other protease recognition sites may be used for the detection of proteolytic toxins (such as anthrax lethal factor). The method provides improved target validation and candidate compound optimisation by combining many cell screening formats with fluorescence-based molecular reagents and computer-based feature extraction, data analysis and automation, resulting in increased quantity and speed of data collection and faster evaluation of drug candidates. Sequences AAB22881-B22885 represent fluorescent proteins which may used as components of biosensor fusion proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                        61 LVTALSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                             VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
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biosensors of the invention can be used to investigate a wide range of
                                                                                                                                                                                                                                                                                                                                                   1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of the mutant green fluorescent protein EGFP.
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                                                                                                                                                                                                                                                                            Length 239;
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                                                                                                                                                                                                                                                                            Score 1258; DB 3;
Pred. No. 6.1e-123;
1; Mismatches 2;
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98US-00172063.
                                                                                                                                                                                                                                                                            sch 98.8%; al Similarity 98.7%; 236; Conservative
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(UYOR-) UNIV OREGON STATE.
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                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 236; Conserv
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                                                                                                                                                                                                                                           Sequence 239 AA;
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61 LVTALSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein based on the Aguarda green fluorescent protein (GFP). The emission intensity changes as pH varies between 5 and 10 of the present protein are novel. The functional engineered fluorescent proteins show reversible changes in fluorescence over physiological pH ranges. They can also be used for determining the pH of samples and cells. The polymucleotides can also be used to produce transpent and cells. The polymucleotides pH sensors can be delivered to cells in the form of polymucleotides encoding the protein sensor fused to a targeting signal. The targeting signal directs the expression of the protein sensors to restricted cell locations. This makes it possible to measure the pH of a precisely defined cellular region or organelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09
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                                                                                                                                                    New functional engineered green fluorescent proteins, used for measuring the pH in biological samples and cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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                                                                                                                                                                                                                                                                                                                sequence represents a functional engineered fluorescent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.8%; Score 1258; DB 3; 98.7%; Pred. No. 6.1e-123; ive 1; Mismatches 2;
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                                                                                                                                                                                                                                                    Disclosure; Page 9; 89pp; English
Wachter RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY79584 standard; peptide; 239
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Matches 236; Conservative
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Tsien RY, Llopis J,
                                                    WPI: 2000-116540/10
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                                                                                         N-PSDB; AAZ45642
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26-MAY-1999;
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AAB50804 standard; protein; 239 AA
                               Claim 14; Fig 29A; 218pp; English
                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                   Jellyfish GFP mutant EGFP.
                                                                                                                                       236; Conservative
                                                                                                                                  Local Similarity
  WPI; 2000-365644/31.
N-PSDB; AAA27573.
                                                                                                                                                                                                                                                                           Aequorea victoria.
                                                                                                                       Sequence 239 AA;
                                                                                                                                                                                                                                                                                   WO200071565-A2
                                                                                                                                                                                                                                           14-MAR-2001
                                                                                                                                                                                                                                                                                          30-NOV-2000
                                                                                                                                                                                                                                   AAB50804;
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                                                                                                                               Query Match
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The present sequence is a fluorescnet protein used in the construction of a fluorescent protein indicator. The indicator comprises a sensor polypeptide that is responsive to a chemical, biological, electrical or physiological parameter, and a fluorescence protein functional group. The sensor polypeptide is operatively inserted into the fluorescent moiety. The fluorescent indicator is useful for detecting the presence of a response indicator and adetecting a change in fluorescence, in which a change is indicator and detecting a change in fluorescence, in which a change is indicative of the effect of the parameter on the sensor polypeptide. The movel fluorescent proteins are advantageous due to their reduced size as compared to the FRET (fluorescence resonance energy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                                                                                                                                                          Novel fluorescent proteins comprising a sensor protein inserted into them, useful for measuring the response of a sensor biological, chemical, electrical or physiological parameter in vivo or in vitro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MYSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPMPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Melanin concentrating hormone receptor; MCHR; MCH; chimeric; fus fluorescent polypeptide; orexigenic; anabolic; food intake; GFP; green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A. victoria green fluorescent protein (GFP) and linker sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 98.8%; Score 1258; DB 4; Length 239; Best Local Similarity 98.7%; Pred. No. 6.1e-123; Matches 236; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 24; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB85900 standard; protein; 239 AA
                                                99US-00316919.
17-MAY-2000; 2000WO-US013684
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                                                                                                                            (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                   Baird GA;
                                                                                                                                                                                                                                   2001-032017/04
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                                                                                                                                                                                                                                                               N-PSDB; AAC90488.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 239 AA;
                                                21-MAY-1999;
21-MAY-1999;
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                                                                                                                                                                                                                                                    The present sequence is that of the EGFP signal domain, which can be included in novel recombinant protease biosensors (PBS) of the invention. The PBS (see AAY7953-8-54) comprise: a first domain (see AAY79579-87) comprising at least 1 detectable polypeptide signal such as the present sequence, a second domain (see AAY79588-622) comprising at least 1 reactant target sequence. A recombinant nucleic comprising at least 1 reactant target sequence. A recombinant nucleic acid (see AAAZ767-43) encoding the PB, an expression vector, and a genetically engineered host cell are also claimed. A claimed method for identifying compounds that modify protease activity in a cell involves contacting a host cell that possesses the recombinant PB with a test compound, and determining the PB distribution in the host cell, where compounds that modify protease activity in a host cell include the protease activity by the test compound. Claimed kits for identifying compounds that modify protease activity in a host cell include the recombinant nucleic acid, or the recombinant PB, or the vector, or the host cell. The PB is useful in high content screens to detect in vivo activation of enzymatic activity, and to identify specific activity based on cleavage of a known recognition motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LVTALSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDŢL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                    Recombinant nucleic acid encoding a protease biosensor useful for fluorescence based cell and molecular biochemical assays for drug discovery comprising three operably linked nucleic acid sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.8%; Score 1258; DB 3;
98.7%; Pred. No. 6.1e-123;
iive 1; Mismatches 2;
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WO200168706-A1

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The specification describes a method for assessing the growth rate and death rate of a micro-organism within a predetermined time period in a desired environment. The method comprises introducing at least two reporter genes encoding luminescent and/or fluorescent products into the micro-organisms, incubating the micro-organism within the desired environment, and detecting luminescence and/or fluorescence after a predetermined time period. Use of two different markers within a micro-organism enables the differentiation between growth and death rates. The method is used to assess the growth rate and death rate of a microorganism within a predetermined time period in a desired environment. The present sequence represents a green fluorescent protein (GFP), and is encoded by a plasmid which encodes luminescent and fluorescent proteins, and is used in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assessing growth and death rates of a micro-organism in a desired environment, by introducing 2 reporter genes encoding luminescent and fluorescent products and detecting luminescent fluorescence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyan-green fluorescent protein; fluorescence; recombinant; GFP; green fluorescent protein; EGFP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 98.8%; Score 1258; DB 4; Length 239; Best Local Similarity 98.7%; Pred. No. 6.1e-123; Matches 236; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A. victoria green fluorescent protein (EGFP).
                                                                                                                                                                                                                                                                                                                             Disclosure; Page 27; 32pp; English
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                          99FI-00001296
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                                                                                                                                                                            2001-061737/07
                                                                                                                               Lilius E, Virta M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aequorea victoria
                                                                   (LILI/) LILIUS E.
                                                                                         VIRTA M.
                                                                                                                                                                                                N-PSDB; AAC86954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 239 AA;
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                          07-JUN-1999;
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                                                                                         (VIRT/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides melanin concentrating hormone (MCH) receptor (MCHR) chimeric and fusion proteins. The MCHR chimeric proteins comprise MCHR polypeptide regions from different species. The MCHR fusion protein comprise MCHR polypeptide region and a fluorescent polypeptide region and applyed of the MCHR polypeptide region and a fluorescent polypeptide region. The MCHR fusion proteins can be expressed by standard recombinant methodology. MCH action promotes feeding (orexigenic) and up regulation of MCH activity stimulates food intake. The present sequence represents a A. victoria green fluorescent protein (GFP) and a linker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LVTALSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                 Fusion proteins comprising melanin concentrating hormone receptor
peptides and fluorescent proteins, useful for identifying appetite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of a green fluorescent protein (GFP).
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Pred. No. 6.1e-123;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ā
                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 14; 71pp; English.
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                                          14-MAR-2001; 2001WO-US008071
                                                                                     15-MAR-2000; 2000US-0189698P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 98.7
Matches 236; Conservative
                                                                                                                           (MERI ) MERCK & CO INC
                                                                                                                                                                                                                WPI; 2001-565791/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aequorea victoria.
                                                                                                                                                                                                                                        N-PSDB; AAH47304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200075367-A1
20-SEP-2001
                                                                                                                                                                                                                                                                                                                           stimulants.
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                                                                                                                                                                       Marsh DJ;
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AAB3117

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Gaps ö 9 9

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17-SEP-1999;
29-OCT-1999;
01-DEC-1999;
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                                                                                                        KAPU/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                                                                                                                            The invention relates to a gene encoding proteins having cyan-green fluorescence characteristic and having a function of showing stable fluorescence characteristic in acid region. A method for the preparation of a cyan-green fluorescent protein is provided which involves a transformant transformed by a recombinant vector comprising the gene, where the transformant is cultured and the protein is collected from the fluorescent protein (EGPP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVTALSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1258; DB 5;
Pred. No. 6.1e-123;
1; Mismatches 2;
                                                                                                                                                                                            A gene encoding cyan-green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protease biosensor signal sequence #6.
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                                                                                                                                                                                                                                         Example; Page 14; 20pp; Japanese
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98US-00031271.
99US-0123152P.
99US-012399P.
99US-00352171.
    04-AUG-2000; 2000JP-00237165
                                              04-AUG-2000; 2000JP-00237165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 98.8%; Local Similarity 98.7%; es 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-00513783
                                                                                      (RIKA ) RIKAGAKU KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                WPI; 2002-299190/34
                                                                                                                                                       N-PSDB; ABL40628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 239 AA;
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12-JUL-1999;
31-AUG-1999;
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The invention describes methods of automated detection, classification
and identification comprising treating cells containing luminoscent
contained to the contain transport of locations with a test substance, where
contain the contain luminescent signals and converting optical information
control location to obtain luminescent signals and converting optical information
control digital data to interpret presence of toxins in the test substance.
The method are useful for detection of toxins into the test substance.
The method are useful for detection of toxins chosen from proteases, ADP-
ribosylating toxins, cytotoxic phospholipases, and exfoliative toxins.

Control of toxic threat agents. The first two levels of
chectors of toxic threat agents. The first two levels of
characterisation ensure a rapid readout of toxin class without
characterisation ensure a rapid readout of toxin class without
control of a protease biosensor related signal sequence used in the cell-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGGEGDATYGKLTLKFICTTGKLPVPWPT
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                                                                                                                                                                                                                                                                                                                                                                                          Automated cell-based toxin detection, classification, and/or identification by treating cells involves use of three classes of luminescent reporter molecules such as detectors, classifiers or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1258; DB 5;
Pred. No. 6.1e-123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 10; Fig 29A; 214pp; English
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99US-00398965.
99US-00430656.
99US-0168408P.
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98.7%;
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Best Local Similarity 98.7
Matches 236; Conservative
                                                                                                                                                                                                                                       Kapur R;
                                                                                                                                                                                                                                                                                                     WPI: 2002-634730/68.
                                                                                                                                        GIULIANO K.
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                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABS71491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 239 AA;
                                                                                                                                                                   KAPUR R
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The invention relates to a method for mutagenesis that comprises synthesising a mutated strand and a complementary strand by use of synthesising a mutated strand and a complementary strand by use of comparimers. The method basically comprises a DNA synthesis in which one or more primers that have a nucleotide sequence containing at least one can take the prosphorylated 5'-terminus are annealed to a template DNA condition then subjected to an elongation reaction using a thermostable high-can didelity DNA polymerase, after which the phosphorylated 5'-terminus and then subjected to an elongation reaction using a thermostable DNA ligase to synthesise a circular DNA containing the primers; a digestion in which the stop of DNA synthesis is repeated several fines to amplify the DNA containing the primers and then, at least DNAs other than the amplified circular DNA are digested into several fragments obtained in the step of DNA synthesis in which, with the several fragments obtained in the step of digestion as megaprimers, the megaprimers are annealed to the circular DNA synthesised above, followed by an elongation reaction performed using the thermostable high-fidelity DNA polymerase. The method is useful for mutagenesis, particularly for introducing candom mutations at certain sites of the nucleotide sequence. The present method is simple, speedy, economical and widely applicable. The present method is simple, appear a victoria enhanced green fluorescent protein (GFP) used for mitagenesis in an exemplification of the invention. The EGFP is derived the contain the green fluorescent protein (GFP) sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Method for mutagenesis, e.g. for introducing certain or random mutations at certain sites of the nucleotide sequence, comprises synthesizing a mutated strand and a complementary strand by use of megaprimers.
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                                           . .3
note= "Wild-type GFP Met-Ser are replaced with Met-Val-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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                                                                                                                                                               /note= "GFP Ser65 is replaced by Thr"
                                                                                                                        "GFP Phe64 is replaced by Leu"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 13-14; 31pp; English.
                     Location/Qualifiers
                                                                                                                                                                                                                                                                                            03-AUG-2001; 2001EP-00306650
                                                                                                                                                                                                                                                                                                                                   04-AUG-2000; 2000JP-00237166
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                                                                                                                            note=
                                                                                                                                                                                                                                                                                                                                                                                                                        Miyawaki A, Sawano A;
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                                                                                                                                                                                                                                                                                                                                                                             (RIKE ) RIKEN KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAD27910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 239 AA;
                                       Misc-difference
                                                                                                                                           Misc-difference
                                                                                                    Misc-difference
                                                                                                                                                                                                         EP1178109-A1
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Matches
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comprising a phosphorylation polypeptide and a fluorescent procein or in operative linkage, a donor molecule, a phosphorylatable domain, a phosphorylation bindicators of the invention and an acceptor molecule. The phosphorylation indicators of the invention are useful for detecting kinases or phosphatases in a biological sample. They are also useful in this throughput analysis e.g. for detecting a kinase inhibitor or phosphatase inhibitor. The present sequence is Aequorea victoria enhanced green fluorescent protein (EGFP) used in the invention
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               181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 239
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                                                                                                                                                                                                                                                 Phosphorylation indicator; fluorescent protein; detection; phosphatase; kinase; enhanced green fluorescent protein; EGFP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel chimeric phosphorylation indicators, useful for detecting kinase/phosphatase in samples, has donor molecule, phosphorylatable domain, phosphoaminoacid binding domain, and acceptor molecule, in
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                                                                                                                                                                                                                  Aequorea victoria enhanced green fluorescent protein (EGFP).
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Pred. No. 6.1e-123;
1; Mismatches 2;
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                                                                                                                  AAE34958 standard; protein; 239
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Best Local Similarity 98.7%;
Matches 236; Conservative
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Search completed: June 21, 2004, 15:54:09 Job time: 48:1111 secs

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Sequence 46, Appli
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Sequence 6, Appli
Sequence 129, Appli
Sequence 129, Appli
Sequence 127, Appli
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1 MVSKGEELFTGVVPILVELD......VLLGFVTAAGITLGMDELYK 239
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-417-197-113

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                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 75, Appli Sequence 71, Appl Sequence 11, Appl Sequence 119, Appl Sequence 116, Appl Sequence 176, Appl Sequence 177, Appl Sequence 178, Appl Sequence 53, Appl Sequence 61, Appl	SAMPLE	Length 239; Indels 0; Gaps 0;	GKLTLKFICTTGKLPVPWPT 60 	FKDDGNYKTRAEVKFEGDTL 120 	IKVNFKIRHNIEDGSVQLA 180 IKVNFKIRHNIEDGSVQLA 180	LGFVTAAGITLGMDELYK 239 LEFVTAAGITLGMDELYK 239
US-08-818-252-2 US-08-818-252-6 US-08-818-253-4 US-08-818-253-4 US-09-417-197-75 US-09-417-197-13 US-09-417-197-139 US-09-417-197-141 US-09-417-197-141 US-09-417-197-143 US-09-417-197-17 US-09-417-197-77 US-09-417-197-53 US-09-417-197-53 US-09-417-197-53 US-09-417-197-53 US-09-417-197-53 US-09-417-197-53 US-09-417-197-63 US-09-417-197-63	ALIGNMENTS 172063 M. Hes GITHE PHOF A BIOLOGICAL US/09/172,063 09/094,359 09/094,359 19 Version 4.0	; Score 1258; DB 3; Le ; Pred. No. 2.7e-127; 1; Mismatches 2; 1	LDGDVNGHKFSVSGEGEGDATY LDGDVNGHKFSVSGEGEGDATY	LVTALSYGVQCFSRYPDHMKQHDFFKSAMPBGYVQBRTIFFKDDGNYKTRABVKFBGDT -	VNRIELKGIDFKEDGNILGHKLEYNYNSHNYYIMADKORNGIKVNFKIRHNIEDGSVOLA 	DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNBKRDHMVLLGFVTAAGITLGMDELYK
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	ULT 1 G09-172-063-3 equence 3, Application US/0 atent No. 6150176 APPLICANT: Tsien, Roger Y. APPLICANT: Tsien, Roger Y. APPLICANT: Machter, Rebekka APPLICANT: Machter, Rebekka APPLICANT: Wachter, Rebekka APPLICANT: Wachter, Rebekka APPLICANT: Wachter, Rebekka APPLICANT: Wachter, Rebekka APPLICANT: Baching Juan APPLICANT: Baching Juan TITLE OF INVENTION: FLUORES TITLE OF INVENTION: FLUORES TITLE OF INVENTION: Baching FILE REFERENCE: 0725-7/0710 CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: EARLIER PILING DATE: 1998-0 CURMENT PRING DATE: 1998-0 MUMBER OF SEQ ID NOS: 38 LENGTH: 239 LENGTH: SERVING: COLINIAN LOCATION: (0)(0)		MVSKGEELI MVSKGEELI	LVTALSYGVQCF : LVTTLTYGVQCF	VNRIELKG VNRIELKG	DHYQQNTP DHYQQNTP
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 239;
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US-09-513-733A-46
                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                        APPLICANT: Giuliano, Kenneth A.
APPLICANT: Kapur, Ravi
TITLE OF INVENTION: A System for Cell Based Screening
FILE REFERENCE: 97-022-L1
CURRENT APPLICATION NUMBER: US/09/513,783A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 180
SOFTWARE: PatentIn Ver. 2.0
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| Patent No. 6469154
| GENERAL INFORMATION:
| APPLICANT: Taien, Roger Y. |
| TITLE OF INVENTION: FLOORESCENT PROTEIN INDICATORS |
| FILE REFIRENCE: 07257/073001|
| CURRENT APPLICATION NUMBER: US/09/316,919 |
| CURRENT FILING DATE: 1999-05-21 |
| NUMBER: OF SEQ ID NOS: 63 |
| SOFTWARE: FastsEQ for Windows Version 4.0 |
| SEQ ID NO 4 |
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98.8%; Score 1258; DB 4;
Best Local Similarity 98.7%; Pred. No. 2.7e-127;
Matches 236; Conservative 1; Mismatches 2;
                    ; Sequence 46, Application US/09513783A; Patent No. 6416959; GENERAL INFORMATION:
                                                                                                                                                                                                                                        SEQ ID NO 46
LENGTH: 239
TYBE: PAT
ORGANISM: Artificial Sequence
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ORGANISM: Aequorea victoria
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Best Local Similarity 98.7'
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-09-513-733A-46
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APPLICANT: Miyawaki, Atsushi
APPLICANT: Miyawaki, Atsushi
APPLICANT: Mochter, Bebeka
APPLICANT: Machter, Bebeka
APPLICANT: Machter, Bancher, Bennarion: Fire Reference: 07257/071001
CURRENT APPLICATION NUMBER: US/09/602,641
CURRENT APPLICATION NUMBER: 09/172,063
PRIOR FILING DATE: 1998-10-13
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 239
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Pred. No. 2.7e-127;
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Facent No. 6673610
GENERAL INFORMATION:
APPLICANT: Miyawaki, Atsushi
APPLICANT: Sawano, Asako
TITLE OF INVENTION: METHOD FOR MUTAGENESIS
FILE REFRENCE: 11283-012001
CURRENT APPLICATION NUMBER: US/09/920, 922
CURRENT FILING DATE: 2001-08-02
PRIOR FILING DATE: 2000-04
NUMBER OF SEQ ID NOS: 9
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Patent No. 6608189
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ORGANISM: Aequorea victoria
FEATURE:
LOCATION: (0)...(0)
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Best Local Similarity 98.7
Matches 236; Conservative
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US-09-602-641-3
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US-09-920-922-2
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Patent No. 6306600
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APPLICANT: Kain, Steve
APPLICANT: Li, Xianqiang
TITLE OF INVENTION: Rapidly Degrading GFP-Fusion Proteins and Methods
TITLE OF INVENTION: 0.f Use
FILE REPERENCE: D6100
CURRENT APPLICATION NUMBER: US/09/062,102
CURRENT FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: US 60/060,855
EARLIER PILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) OTHER INFORMATION: Sequence of the EGFP-MODC422-461 fusion protein.; Patent No. 6130313
US-062-102-1
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Pred. No. 3.4e-127;
1; Mismatches 2;
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Pred. No. 2.7e-127;
1; Mismatches 2;
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2 LENGTH: 239 TYPE: PRT
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Patent No. 6130313
GENERAL INFORMATION:
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                                                                                                                                                          Query Match 98.8%;
Best Local Similarity 98.7%;
Matches 236; Conservative
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                                                                                        ; ORGANISM: Aequorea victoria
US-09-920-922-2
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Best Local Similarity 98.7
Matches 236; Conservative
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US-09-062-102-1
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Sequence 1, Application US/09364946
; Sequence 1, Application US/09364946
; Patent No. 6306600
; GENERAL INFORMATION:
    APPLICANT: Kain, Steve
    APPLICANT: Li, Xiangiang
; TITLE OF INVENTION: Rapidly Degrading GFP-Fusion Proteins and Methods
; TITLE OF INVENTION: of Use
; TITLE OF INVENTION: of Use
; TITLE OF INVENTION of Use
; TILE REFERENCE: D6100CIF/D2
; CURRENT APPLICATION NUMBER: US 09/364,946
; CURRENT FILING DATE: 1999-07-30
; EARLIER FILING DATE: 1999-11-13
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO: 14
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Patent No. 6416559

GENERAL INFORMATION:
APPLICANT: Giuliano, Kenneth A.
APPLICANT: Giuliano, Kenneth A.
TITLE OF INVENTION: A System for Cell Based Screening
FILE REFERENCE: 97-02-L1

FURBUR APPLICATION NUMBER: US/09/513,783A

CURRENT FILING DATE: 2000-02-25

NUMBER OF SEQ ID NOS: 180

SEQ ID NO 2

LENGTH: 294
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Pred. No. 3.4e-127;
1; Mismatches 2;
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Best Local Similarity 98.7%;
Matches 236; Conservative
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Best Local Similarity
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Wachter, Rebekka M.

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                                         51 LVTALSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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Fatent No. 6150176
Fatent No. 6150176
GENERAL INFORMATION:
APPLICANT: Taien, Roger Y.
APPLICANT: Miyawaki, Ateushi
APPLICANT: Miyawaki, Ateushi
APPLICANT: Miyawaki, Juan Rebekka M.
APPLICANT: Machter, Rebekka M.
APPLICANT: Machter, Sumes
ITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
ITLE OF INVENTION: PLUORESCENT PROTEIN SENSORS FOR
ITLE OF INVENTION: PLUORESCENT PROTEIN SENSORS
ITLE REFERENCE: 07257/071001
CURRENT APPLICATION NUMBER: US/09/172,063
CURRENT FILME DATE: 1998-10-13
EARLIER APPLICATION NUMBER: 09/094,359
BARLIER FILME DATE: 1998-06-09
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
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OTHER INFORMATION: GT-EGFP
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Matches 236; Conservative
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US-09-172-053-21
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US-09-602-641-21
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LENGTH: 323
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Sequence 21, Application US/09602641; Patent No. 6608189; GENERAL INFORMATION:

APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
APPLICANT: Llopis, Juan

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85 MYSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LVTALSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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APPLICANT: Lovett, David H.
APPLICANT: Lovett, David H.
APPLICANT: Turck, Johanna
TITLE OF INVENTION: Selective Induction of Apoptosis in
TITLE OF INVENTION: Malignant Cancer Cells by Delivery of N-Terminal
TITLE OF INVENTION: Inherleukin-1-Alpha Pro-Piece Polypeptide
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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APPLICANT: Remington, S. James
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MASSURING THE PH OF A BIOLOGICAL SAMPLE
FILE REPERENCE: 0257/071001
CURRENT APPLICATION NUMBER: US/09/602,641
CURRENT RILING DATE: 1908-10-13
NUMBER OF SED ID NOS: 38
SOFTWARE: FESSESQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1258; DB 4;
Pred. No. 4.2e-127;
1; Mismatches 2;
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APPLICATION NUMBER: US/09/085,305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
CITY: Palo Alto
STATE: CA
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29-MAY-1998
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Best Local Similarity 98.7%;
Matches 236; Conservative
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Aequorea victoria
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: VARIANT
LOCATION: (0)...(0)
OTHER INFORMATION: GT-EGFP
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MEDIUM TYPE: Diskett
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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US-09-085-305-6
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Sequence 127, Application US/09417197

Sequence 127, Application US/09417197

Sequence 127, Application US/09417197

Batefit No. 651801

GENERAL INFORMATION:

APPLICANT: Ole THASTRUP, et al.

TITLE OF INVENTION: On A Cellular Response

FILE REFERENCE: 3759-0110P

CURRENT APPLICATION NUMBER: US/09/417,197

CURRENT APPLICATION NUMBER: US/09/417,197

NUMBER OF SEQ ID NOS: 143

SOFTWARE: Patentin version 3.0

SEQ ID NO 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LVTALSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                  321 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 379
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                      181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
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                                                                                                                                                                               Sequence 48, Application US/09800170
Patent No. 6481667
GENERAL INFORMATION:
APPLICANT: Kinsella, Todd
TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES
FILE REFERENCE: A-68614-1/DJB/MS/RMK
CURRENT APPLICATION NUMBER: US/09/800,170
CURRENT PILING DATE: 2001-08-28
PRIOR PILING DATE: 2000-03-06
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin version 3.1
SEQ ID NO 48
LENGTH: 434
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Pred. No. 6.6e-127;
1; Mismatches 2;
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98.7%; Pred. No. 6.8e-127;
tive 1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Synechocystis PCC6803
US-09-800-170-48
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Best Local Similarity 98.7%;
Matches 236; Conservative
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Best Local Similarity 98.7%
Matches 236; Conservative
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Sequence 129, Application US/09417197
Patent No. 6518021
GENERAL INFORMATION:
APPLICANT: Ole THASTRUP, et al.
TITLE OF INVENTION: On A Cellular Response
FILE OF INVENTION: On A Cellular Response
FILE REFERENCE: 3759-0110P
CURRENT PILITION NUMBER: US/09/417,197
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 LVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 305
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98.8%; Score 1258; DB 4; Length 379;
Best Local Similarity 98.7%; Pred. No. 5.4e-127;
Matches 236; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Length 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                     Score 1258; DB 3;
Pred. No. 5.1e-127;
1; Mismatches 2;
                                             36,513
ER: 6510/102US1
                    NAME: Francis, Carol L
REGISTRATION NUMBER: 36,513
REFERENCE/DOCKET NUMBER: 6510
TELECOMMULTATION INFORMATION:
TELEPHONE: 650-327-3400
TELEFAX: 650-327-331
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 98.7%;
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: amino acid
STRANDEDNESS: single
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-09-085-305-6
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US-09-417-197-129
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LENGTH: 379
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21 VNRIBLKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                             LVTALSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                  61 LVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Sequence 170, Application US/09513783A |
| Sequence 170, Application US/09513783A |
| Patent NC. 6416959 |
| GENERAL INFORMATION |
| APPLICANT: Giuliano, Kenneth A. |
| APPLICANT: Kapur, Ravi |
| TITLE OF INVENTION: A System for Cell Based Screening |
| FILE REFERENCE: 97-022-11 |
| CURRENT APPLICATION NUMBER: US/09/513,783A |
| CURRENT FILING DATE: 2000-02-25 |
| NUMBER OF SEQ ID NOS: 180 |
| SOFTWARE: PatentIN Ver. 2.0 |
| SEQ ID NO 170 |
| LENGTH: 459 |
| LENGTH: 459 |
| LENGTH: 459 |
| SEQ ID NO 170 |
| LENGTH: 459 |
| CONTROL OF SET OF
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ORGANISM: Artificial Sequence
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Best Local Similarity 98.7
Matches 236; Conservative
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US-09-513-783A-170
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Search completed: June 21, 2004, 16:04:01 Job time: 13.7778 secs

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1940.117 Million cell updates/sec
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1 MVSKGEELFTGVVPILVELD......VLLGFVTAAGITLGMDELYK 239
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1163542 segs, 282313646 residues
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                                                                                                                             - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES		
Result No.	Score	* Query Match	* Query Match Length DB	DB	ID	Description	
1	1269	99.7	239	. 6	US-09-887-784-4	Sequence 4, Appli	
7	1269	99.7	239	12	US-10-296-953-4	Sequence 4, Appli	
٣	1269	7.66	363	14	US-10-270-223-6	Sequence 6, Appli	
4	1269	7.66	893	14	US-10-257-909A-30	Sequence 30, Appl	
S	1269	7.66	٦	14	US-10-257-909A-32	Sequence 32, Appl	
9	1261	99.1		σ	US-09-887-784-2	Sequence 2, Appli	
7	1261	99.1		12	US-10-296-953-2	Sequence 2, Appli	
80	1258	98.8		σ	US-09-920-922-2	Sequence 2, Appli	
σ	1258	98.8		δ	US-09-999-745-4	Sequence 4, Appli	
10	1258	98.8		10	US-09-866-538-4	Sequence 4, Appli	
11	1258	98.8		10	US-09-797-496B-2	Sequence 2, Appli	
12	1258	98.8		10	US-09-794-308-4	4	
13	1258	98.8		10	US-09-865-291-4	4	
14	1258	98.8	239	12	US-10-457-982-3	Sequence 3, Appli	
15	1258	98.8		14	US-10-121-258-13		

Sequence 7, Appli	46	ď	'n	4,		11	٦,	37	35	Sequence 2, Appli	39	33	31	35	29	11	1	21	Sequence 7, Appli	13	7,	Sequence 13, Appl	16	•	Seguence 5, Appli	o,		Sequence 33, Appl	Sequence 34, Appl
US-10-221-461-7	-10-100-9	10-177-390-	-10-338-411	-10 - 370 -	10-389-	US-10-314-861-11	19-931-	-10-	-10-314-861-3	-01	10-314-861-3	10 - 314	10-314-	-10 - 033 - 71	10-314-861	-41	10-389-	10-457-98	-10-338-	US-10-338-411-13	-10-389-	10-389-	-10-314-	-10-338-411	389-640	-10 - 338	10-389-64	-10-033-717-	US-10-033-717-34
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ALIGNMENTS

ö 61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120 61 LVTALSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120 121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180 9 -1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT 60 181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239 181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239 1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT Gape ö Length 239; Indels Score 1269; DB 9; Pred. No. 5.8e-124; 0; Mismatches 1; Sequence 4, Application US/09887784;
Patent No. US20020177189A1;
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICATIONT: BJONN, Sara et al.
TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS;
FILE REPERENCE: 3759-0115P;
CURRENT APPLICATION NUMBER: US/09/887,784;
CURRENT FILING DATE: 2001-06-19;
NUMBER OF SEQ ID NOS: 24 SOFTWARE: PatentIn version 3.0 Query Match
Best Local Similarity 99.6%;
Matches 238; Conservative SEQ ID NO 4 LENGTH: 239 TYPE: PRT ORGANIOM: Aequoria Victoria US-09-887-784-4 US-09-887-784-4 셤 g ద qq ò ò ò ò

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Sequence 30, Application US/10257909A

Publication No. US20030187056A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: distribution of phosphodiesterase (PDE) enzymes
CURRENT APPLICATION NUMBER: US/10/257,909A
CURRENT FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 30
ILENGTH: 893
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TITLE OF INVENTION: Live cell procedures to identify compounds modulating intracellula
TITLE OF INVENTION: distribution of phosphodiesterase (PDE) enzymes
FILE REPERENCE: 3759-0125P
CURRENT APPLICATION NUMBER: US/10/257,909A
CURRENT FILING DATE: 2002-10-17
NUMBER OF SEO ID NOS: 36
SOFTWARE: PastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 99.7%; Score 1269; DB 14; Best Local Similarity 99.6%; Pred. No. 3.8e-123; Matches 238; Conservative 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-257-909A-30
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TITLE OF INVENTION: AN IMPROVED METHOD TO DETECT INTERACTIONS BETWEEN CELLULAR COMPON
TITLE OF INVENTION: INTERACTIONS OF ELLS, AND TO EXTRACT QUANTITATIVE INFORMA-TION RE
TITLE OF INVENTION: INTERACTIONS BY FLUORESCENCE REDISTRIBUTION.
FILE REFERENCE: 3759-0126P
CURRENT APPLICATION UNDER: US/10/270,223
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 363
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Pred. No. 5.8e-124;
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Best Local Similarity 99.6%; Pred. No. 1.1e-123;
Matches 238; Conservative 0; Mismatches 1;
                                                                                                                    APPLICANT: BJORN, SARA P.
APPLICANT: BJORN, SARA P.
APPLICANT: BJORN, SARA P.
TAPLICANT: THASTRUP, OLE
TITLE GAIT: THASTRUP, OLE
TITLE REPRENCE: PL0095
CURRENT APPLICATION NUMBER: US/10/296,953
CURRENT PILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: 60/212,681
PRIOR FILING DATE: 2000-06-19
PRIOR FILING DATE: 2000-06-19
PRIOR FILING DATE: 2001-05-10
PRIOR FILING DATE: 2001-05-10
PRIOR FILING DATE: 2001-05-10
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/290,170
PRIOR FILING DATE: 2001-05-10
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; ORGANISM: Aequoria Victoria and Human
US-10-270-223-6
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                                                  ; Sequence 4, Application US/10296953; Publication No. US20040072995A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.78;
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ORGANISM: Aequorea victoria
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Matches 238; Conservative
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US-10-270-223-6
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RESULT 8
US-09-920-922-2
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                                                                       FEATURE:
// OTHER INFORMATION: Fusion between Aequorea victoria and human US-10-257-909A-32
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Pred. No. 4e-123;
0; Mismatches 2; Indels (
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Fatent No. US20020177189A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BJODEN, Sara et al
TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS
FILE REFERENCE: 3759-0115P
CURRENT APPLICATION NUMBER: US/09/887,784
CURRENT FILING DATE: 2001-06-19
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 239
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                                      TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 99.2%;
Matches 237; Conservative
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; ORGANISM: Aequoria Victoria
US-09-887-784-2
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US-09-887-784-2
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US-10-296-953-2
SEQ ID NO 32
LENGTH: 11
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99.2%; Pred. No. 4e-123;
tive 0; Mismatches 2;
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Best Local Similarity 98.7%; Pred. No. 8.1e-123;
Matches 236; Conservative 1; Mismatches 2;
APPLICANT: BJORN, SARA P.
APPLICANT: BAGILARO, LEN
APPLICANT: THASTRUP, OLE
TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS
TITLE REFERENCE: PLO095
CURRENT APPLICATION NUMBER: US/10/296,953
CURRENT FILING DATE: 2002-11-26
PRICA APPLICATION NUMBER: PA 2000 00953
PRICA APPLICATION NUMBER: 60/212,681
PRICA PAPLICATION NUMBER: 60/212,681
PRICA PELLING DATE: 2000-06-19
PRICA FILING DATE: 2000-06-19
PRICA FILING DATE: 2010-05-10
PRICA APPLICATION NUMBER: 60/290,170
PRICA APPLICATION NUMBER: PA 2001 00739
PRICA PRICA SEQ ID NOS: 24
SOSTWARR: PALENTING DATE: 2010-05-10
PRICA PRICA PRICA DATE: 2010-05-10
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| Sequence 2, Application US/09920922
| Patent No. US2002008348841
| GENERAL INFORMATION:
| APPLICANT: Miyawaki, Atsushi
| APPLICANT: Myawaki, Atsushi
| TITLE OF INVENTION: METHOD FOR MUTAGENESIS
| FILE REFERENCE: 11283-01201
| CURRENT APPLICATION NUMBER: US/09/920, 922
| CURRENT FILING DATE: 2000-08-04
| NUMBER OF SEQ ID NOS: 9
| SEQ ID NO 2
| LENGTH: 239
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; ORGANISM: Aequorea victoria
US-09-920-922-2
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US-10-296-953-2
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Best Local Similarity 99.2
Matches 237; Conservative
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us-09-887-784-64a.rapb

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; ORGANISM: Aequorea victoria
US-09-866-538-4
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Best Local S:
Matches 236
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              61 LVTTLTYGVQCFSRYPDHMKQHDFPKSAMPEGYVQBRTIFFKDDGNYKTRAEVKFEGDTL 120
                                                     VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                                                                                             Sequence 4, Application US/0999745

Patent No. US20020157120A1

GENERAL INFORMATION:

APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

APPLICANT: Tsien, Roger Y.

APPLICANT: Baird, Geoffrey

TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS

FILE REFERENCE: REGENT-10-1

CURRENT APPLICATION NUMBER: US/09/999,745
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Pred. No. 8.1e-123;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/316,920
PRIOR FILING DATE: 1999-05-21
                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 98.7%;
Matches 236; Conservative
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US-09-999-745-4
                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 4
LENGTH: 239
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US-09-999-745-4
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US-09-866-538-4
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OTHER INFORMATION: Aequorea victoria green fluorescent protein modified as described OTHER INFORMATION: in specification
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Publication No. US20030049597A1
Publication No. US20030049597A1
GENERAL INFORMATION:
APPLICANT: Simon, Sanford M.
APPLICANT: Chen, Yu
TITLE OF INVENTION: Chimeric Fluorescent Enzymes and Uses Thereof File Reference: 600-1-267
CURRENT APPLICATION NUMBER: US/09/797,496B
CURRENT APPLICATION NUMBER: 2002-05-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO
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Publication No. US20030170911A1
GENERAL INFORMATION:
APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1258; DB 10;
Pred. No. 8.1e-123;
1; Mismatches 2;
Score 1258; DB 10;
Pred. No. 8.1e-123;
1; Mismatches 2;
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ORGANISM: Artificial Sequence
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al Similarity 98.7%;
236; Conservative
Query Match

Best Local Similarity 98.7%;
Matches 236; Conservative
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US-09-794-308-4
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61 LVTALSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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APPLICANT: TSIEN, ROGER
APPLICANT: Campbell, Robert
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: MONOMERIC AND METHODS FOR MAKING SAME
FILE REFERENCE: UC083.1CP2CP1
CURRENT APPLICATION NUMBER: US/10/121,258
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-02-26
PRIOR FILING DATE: 2001-05-24
                                                                                                                                                                                                                                                                                 Sequence 3, Application US/10457982

Publication No. US20030212265A1

GENERAL INFORMATION:

APPLICANT: Miyawaki, Ateushi
APPLICANT: Miyawaki, Ateushi
APPLICANT: Hopis, Juan
APPLICANT: Hopis, Juan
APPLICANT: Hopis, Juan
APPLICANT: Wachter, Rebeka M.
APPLICANT: Wachter, Rebeka M.
APPLICANT: Wachter, Remington, S. James
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/071001
CURRENT APPLICATION NUMBER: US/10/457,982
CURRENT APPLICATION NUMBER: US/09/602,641

PRIOR APPLICATION NUMBER: US/09/602,641

PRIOR PILING DATE: 2000-06-22

PRIOR FILING DATE: 2000-06-22

SOFTWARE FULL SAMPLE 1398-10-13

NUMBER OF SEQ ID NOS: 38

SOFTWARE FACENCY FOR Windows Version 4.0

SEQ ID NO 3

LENGTH: 239
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98.7%; Pred. No. 8.1e-123;
live 1; Mismatches 2;
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Publication No. US20030059835A1
GENERAL INFORMATION:
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ORGANISM: Aequorea victoria
FEATURE:
NAME/KEY: VARIANT
LOCATION: (0)...(0)
OTHER INFORMATION: EGFP
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Matches 236; Conservative
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US-10-457-982-3
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Sublication No. US2003018622941

SUBJICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA

APPLICANT: TSIEN, ROGET

APPLICANT: TING, Alice

APPLICANT: ZHANG, Jin

TITLE OF INVENTION: EMISSION RATIOMETRIC INDICATORS OF PHOSPHORYLATION

FILE REFERENCE: REGEN1550

CURRENT APPLICATION NUMBER: US/09/865,291

CURRENT PILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 42

SSOTWARE: Patentin version 3.0

SSOTWARE: Patentin version 3.0

LENGTH: 239
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APPLICANT: TSIEN, ROGER

APPLICANT: ZACHARIAS, David

APPLICANT: BAIRD, Geoffrey

TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS

FILE REPERENCE: REGENIS30

CURRENT APPLICATION NUMBER: 2001-02-26

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin var-

SEQ ID NO 4

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Pred. No. 8.1e-123;
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ORGANISM: Aequorea victoria
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ORGANISM: Aequorea victoria
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Best Local Similarity 98.7
Matches 236; Conservative
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Matches 236; Conservative
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Search completed: June 21, 2004, 16:09:26 Job time : 35.7778 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 21, 2004, 15:46:00 ; Search time 10.3333 Seconds

(without alignments)
2224.817 Million cell updates/sec

US-09-887-784-64A 1273 1 WVSKGEBLFTGVVPILVBLD......VLLGFVTAAGITLGMDELYK 239 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	green-fluorescent	hypothetical prote	DNA topoisomerase	iron-sulfur cofact	leucine-tRNA ligas	leucyl-tRNA synthe	synaptogamin o-p65	leucyl-tRNA synthe	hypothetical prote	dihydrolipoamide d		protective surface	cellulase (EC 3.2.	tRNA (uracil-5-)-m	DNA-directed DNA p	inter-alpha-trypsi	hypothetical prote	DNA-binding protei	hypothetical prote	oligoendopeptidase	neuraminidase, pro	DNA-directed DNA p	IgA Fc receptor pr	IgA Fc receptor pr	photosystem II chl	hypothetical prote	alpha-amylase homo	DNA-directed DNA p	imidazoleglycerol-
SUMMARIES	ΩΙ	JQ1514	H72228	D83917	E70390	H64102	E82590	JH0414	AC0582	D71614	I40794	JC4078	F64102	S29043	G81355	JDVLHH	JC5576	AD2052	T06586	C97354	A99552	G95153	JDVLD	A60234	FCSOAG	T06936	T27856	T39539	A36028	E84941
	DB	٦	N	~	~	7	~	N	N	N	-	~	N	~	N	Н	~	N	~	~	N	~	Н	~	-	~	~	N	Н	7
	Query Match Length	238	785	655	370	861	887	439	860	2573	578	797	808	941	357	788	889	281	632	425	613	740	836	1134	1164	461	471	774	2222	353
d	Query Match	7	8.2	7.3	7.2	7.2	7.0	7.0	6.9	6.9					6.8	6.7	6.7	6.7	6.7									6.5		6.4
	Score	1236	105	92.5	91.5	91.5	89.5	89	87.5	87.5	, 87	86.5	86.5	86.5	98	85.5	85.5	85	85	84.5	84.5	84.5	83.5	83.5	83.5	83	83	83	82.5	82
	Result No.		7	m	4	ß	9	7	60	o,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	carboxy-terminal p proprotein convert protein F10B6.14 (lipoxygenase (EC 1 S-layer protein pr	enkephalin precurs synergohymenotropi	polyketide synthas hypothetical prote hypothetical prote	hypothetical prote hypothetical prote coatomer complex a
D90946 H85794	A41798 KXRTC1 F86281	T11852 JC4930	553466 B35678 S68225	AI2140 C64468 S76940	T13674 T13673 ERHUAH
000	2 14 24	000	0 00	0 0 0	1001
682	682 752 760	865	269 310	2518 336 355	734 743 1224
6.4	6 6 6 4. 4. 4.	4.4.	. 4 4.	4.4.4	444
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82	8 8 8 8 7 7 8	882	81.5 81.5	81.5 81 81	81 81 81
30	8 8 8 2 8 4 4	3 9 2	, 89 6 9 8 8 9 8 9 9	4 4 4 0 L 0	. 4 4 4 E 4 6

ALIGNMENTS

RESULT 1 JQ1514 green-fluorescent protein [validated] - hydromedusa (Aequorea victoria)	
C;Species: Aequorea Victoria C;Date: 03-Dec-1999 #sequence revision 03-Dec-1999 #text_change 23-Mar-2001	
R.Presher, D.C.; Eckenrode, V.K.; Ward, W.W.; Prendergast, F.G.; Cormier, M.J.	
Gene III, 229-235, 1992 A;Title: Primary structure of the Aeguorea victoria green-fluorescent protein.	
A; Reference number: JQ1514; MUID:92175527; PMID:1347277	
A; Molecule type: DNA	
A; Residues: 1-107,'S',109-238 <pra1></pra1>	
A;Cross-references: GB:M62654; NID:g155662; PIDN:AAA27722.1; PID:g155663	
A;Accession: UQ1514	
A:Residues: 1-99. fv. 101-140. Lv. 142-218. Vv. 220-238 <pra2></pra2>	
A;Cross-references: GB:M62653; NID:g155660; PIDN:AAA27721.1; PID:g155661	
A, Accession: PQ0335	
A;Molecule type: protein	
A; Residues: 46-64; 74-122; 132-151; 154-183; 185-200 < PRA3>	
R;Inouye, S.; Tsuji, F.I.	
FEBS Lett. 351, 211-214, 1994	
A;Title: Evidence for redox forms of the Aequorea green fluorescent protein.	
A; Reference number: S48693; MUID: 94364470; PMID: 8082767	
A; Accession: S48693	
A STACKUS: DEFINITION AND A STACKUS: DEFINITION AS A STACKUS: DEFINITION AND A STACKUS AS A STAC	
A.Residues: 1-24, O'.26-156, P'.158-171, K', 173-238 <ino></ino>	
A; Cross-references: GB: L29345; NID: 9606383; PIDN: AAAS8246.1; PID: 9606384	
R; Watkins, J.N.; Campbell, A.K.	
submitted to the EMBL Data Library, January 1995	
A; Reference number: S51330	
A;Accession: S51330	
A; Molecule type: mRNA	
A; Residues: 1-13, 'V', 15-24, 'Q', 26-44, 'N', 46-153, 'G', 155-156, 'P', 158-171, 'K', 173-22	~
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17, 'R', 2 A;Cross_references: EMBL:X8359; NID:g634008; PIDN:CAA58789.1; FID:G511, N. 17.2.7; N. 17

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7.2%; Score 91.5; DE 25.9%; Pred. No. 4.4;
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Contents: annotation; X-ray crystallography, 1.9 angstroms; Comment: This protein is excited by the photoprotein aequorin (see PIR:AQJFNV) emittin; Comment: The chromophore of this protein is formed by modification of Ser-dehydro-Tyr-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.M.
Mature 399, 323-329, 1999
A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A/Reference number: A72200; MUID:99287316; PMID:10360571
A/Accession: H72228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hickey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein TM1624 - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: H7228
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hiogarrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VITESYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERIIFYKDDGNYKTRAEVKFEGDILV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 TALSYGVOCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVN 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 60
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0
A, Contents: annotation; X-ray crystallography, 1.9 angstroms C, Comment: This protein is excited by the photoprotein aequorin (se C, Comment: The chromophore of this protein is formed by modification C, Genetics:
A, Gene: GFP
A, Introns: is)2; 167/3
A, Introns: is)2; 167/3
C, Superfamily: green-fluorescent protein
C, Keywords: chromoprotein; luminescence
F, Keywords: chromoprotein; luminescence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
8.2%; Score 105; DB 2; Length 785;
Best Local Similarity 19.7%; Pred. No. 0.86;
Matches 46; Conservative 32; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1236; DB 1;
Pred. No. 2.1e-96;
4; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.1%;
96.6%;
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Best Local Similarity 96.6
Matches 230, Conservative
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C.Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: D83917
R;Takami, H:, Nakasone, K.; Takaki, Y:; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and §
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: D83917
A;Accession: prellminary
A;Molecule type: DNA
A;Residues: 1-655 <270>
A;Residues: C55 <270>
A;Coss-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB05859.1; GSPDB:GN001
A;Experimental source: strain C-125
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A;Tille: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Aceference number: A70300; MUID:98196666; PMID:9537320
A;Accession: E70390
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-370 <AQF>
A;Acoss-references: GB:AE000720; NID:g2983529; PIDN:AAC07111.1; PID:g2983536; GB:AE00065.
A;Experimental source: strain VF5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 SVVNALSEWLIVEIKRDGWVYEQRFENGGKPSTTLEKKGKTROTGTTIHFKPDPTVFSTT 182
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C;Keywords: phosphoprotein; pyridoxal phosphate; sulfurtransferase
F;195/Binding site: pyridoxal phosphate (Liys) (covalent) #status predicted
F;318/Active site: Cys (cysteine persulfide intermediate) #status predicted
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C.Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 07-Dec-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 TLVTALSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQER------TIFFKDDG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 --NYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 ----QKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            iron-sulfur cofactor synthesis protein nifs - Aquifex aeolicus N;Contains: L-cysteine sulfurtransferase (EC 2.8.1.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
A;Gene: BH2140
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 DVNGHK---FSVSGEGEGDAT----YGKLTLKFI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
7.3%; Score 92.5; Di
Best Local Similarity 22.3%; Pred. No. 7.6;
Matches 54; Conservative 37; Mismatches
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DB 2; Length 370;

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A; Reference number: A82515; MUID: 20365717; PMID: 10910347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         483 VAFSGTGSPIKTDPEWRK 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Gene: XF2176
C,Superfamily: leucine-tRNA ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: A59328
A;Contents: annotation
                                                                                 A;Status: preliminary
                                                                                                      A; Molecule type: DNA
                                                    A, Accession: E82590
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Matches
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: E82590
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Willernate names: leucyl-tRNA synthetase
C;Species: Haemophilus influenzae
C;Species: Hat102
C;Accession: H64102
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, P. Gcayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kirkness, B.F.; Kerlavage, P. Grayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.; Frince, L.D.; Fritchman, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Authors: Mole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :Cross-references: GB:U32774; GB:L42023; NID:g1573942; PIDN:AAC22581.1; PID:g1573943;
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                                                                                 224 NGKRSGTENVVGILSLAKALEIIVSNFSRYQEQLKKIRDLFENLLLEA-LPDAQIVGKDA 282
                                                                                                                                                                                                                                                                                  314 TGDKLPI-WVANFVLMHYGTGAVMAVPAH-DQRDF-----EFAQKYSLPIKQVIAPLA 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---KVNFKIRH-------NIEDGSVQLADHYQQNTPIGDGPVLLPDNHYL- 202
                                                                                                                                                                                                                                                      105 GNYKTRAEV---KFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 TGKLP-----VPWPTLVTALSYGVQCFSRYPDHMKQ-HDFFKSAMPEGYVQERTIFFKDD
                                                 KGEELFTGVV----PILVELD-----GDVNGHKF-SVSGEG-----EGDATYGKLTLKFICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 TIGKLPVPWPTLVTALSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKD----
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     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leucine-tRNA ligase (EC 6.1.1.4) - Haemophilus influenzae (strain Rd KW20)
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23;
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C;Superfamily: leucine-tRNA ligase 
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
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  90; Indels
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  30; Mismatches
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24.1%; Pred. No. 13;
ive 26; Mismatches
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                                                                                                                                                                                                                                                                                                                                                       162 IKVNFKIRHNIED 174
                                                                                                                                                                                                                                                                                                                                                                                      343 VRFSFGLLNKEEE 355
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  Conservative
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A; Residues: 1-861 <TIGR>
  50;
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A;Rosidues: 1-887 <AIN>
A;Cross-references: GB:AE004031; GB:AE003849; NID:g9107309; PIDN:AAF84975.1; GSPDB:GN001
A;Cross-references: GB:AE00404; F.; Arruda, P.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H as.Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreixa, A.J.S.

a.Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, E.; Kiramae, E.E.; Laigr-Chado, M.A.; Madeira, A.M.E.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Ollveira, M.A.; de Ollveira, M.C.; de Ollveira, M.Y.; Soatelli, R.V.; Sawasak, A;Authors: da Silva, A.G.; R.; Ada Silva, A.M.; Ada Silva, A.M.; Ada Silva, A.M.; Ala Silva, A.M.; Ala Silva, A.M.; Ala Silva, A.L.; Z.

M; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: MLV', 26-34; XX', 194-199, X', 201-206; X', 322-332, 'D', 334-337 <WEN1>
C; Superfamily: synaptotagmin; protein kinase C C2 region homology
C; Keywords: glycoprotein; membrane protein; synaptic vesicle
F; 75-101/Domain: hydrophobic <HXD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329 TNEQLPV-WVANFVLMAYGTGAVMAVPGHDQRDQEF--ANKYGLPIRQVIALKEPKNQDE 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 ------KTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synabtogamin o-p65-B - electric ray (Discopyge ommata)
N;Alternate names: synaptic vesicle protein o-p65-B
C;Species: Discopyge ommata
C;Spacies: 15-Jan.1993 #sequence_revision 15-Jan.1993 #text_change 13-Aug-1999
C;Accession: JH0414; PS023
R;Wendland, B.; Miler, K.G.; Schilling, J.; Scheller, R.H.
A;Title: Differential expression of the p65 gene family.
A;Reference number: JH0413; MUID:91273991; PMID:2054189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              386 STWEPDVWRDWYADKTR---EPE---LINSAEFDGLDYQDAFEVLAERFE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57; Gaps
A; Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: mRNA
A,Residues: 1-439 <WEN>
A;Cross-references: GB:M64276; NID:g213110; PIDN:AAA49228.1; PID:g213111
A;Experimental source: electric organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F:153-266/Domain: protein kinase C C2 region homology <KC2A>F:284-399/Domain: protein kinase C C2 region homology <KC2B>F:6,46/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 887;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68;
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Local Similarity 22.2%; Pred. No. 20;
les 44; Conservative 29; Mismatches
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A,Gene: PFB0460c
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ACO582
leucyl-tRNA synthetase [imported] - Salmonella enterica subsp. enterica serovar Typhi
leucyl-tRNA synthetase [imported] - Salmonella enterica serovar Typhi
C;Species: i3almonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: ACO582
R;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D; Wain, J; Churcher,
th, T; Connerton, P; Cronin, A; Davis, P; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S; Moule. S; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Atile: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Residues: 1-860 APAR>
A;Genetics:
A;Gene
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D71614
hypothetical protein PFB0460c - malaria parasite (Plasmodium falciparum)
C;Species: Blasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Accession: D71614
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
:; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
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                                                                                          12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.10 RAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                371 SEQALTEKGVLFNSGEFDGLAFBAAFNAIADKL------AEKGVGERKVNYRLR 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.99 VKVFLLPDKKKKYETKVQKKTLNPTFNESFVFKVPYQELGGKTLMMAVYDFDRFSKHDCI 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                471
                                                                                                                                                                                                                                                         117
                                                                                                                                                                                                                                                                                                              -----KNDINMK---DVKGSGGNQDDD 138
                                                                                                                                                                                                                                                                                                                                                                                                                         1.19 DAETGLTEGEDKEEEAKEEEKLGKIQFSLDYDFQANQLTVGIIQAAELPALDMGGTSDPY 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----FKIRHNIEDGSVQLA-----DHYQQNTPI 189
                                                                                                                                                                                            96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 MMPIDTGDNSTEAGVPGEGKND-VFEKLKEKFMNELQKIPDPPWALIAIAIVSGLLLLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----NIEDGSVQLADHYQQNTPIGDGPVLLPDNHYL-STQSALSKDP
                                                                                                                                                                                                                                                         ----OCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEG-----
                                                                                                                                           .. 6 LVELDGDVNGHKFSVSGEGEGDATYCKLTLKFICTTCKLPV-PWPTLVTALSYGV----
                                                                                          Gaps
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                                  DB 2; Length 439
                                                                                       93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 GDGPVLLPD-----NHYLSTQSALSKDPNEKRDHMVLLGFVTAAG
                                                                                                                                                                                                                                                                                                                                                                        --DILVNRIELKGIDFKEDGNI--LGHKLEYNYNSH------
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                                                          8.9;
                             ; Score 89; DB
; Pred. No. 8.9;
46; Mismatches
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23.3%; Pred. No. 29;
tive 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 -NVYIMADKQKN-GIKVN----
                                                                                                                                                                                                                                                                                                           97 CLCICKKCCKKKKNKKEKGKGK-
                             7.0%;
Query Match
Best Local Similarity 19,2-1-1
Thes 56; Conservative
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Matches 42; Conserva
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dihydrolipoamide dehydrogenase (EC 1.8.1.4) [validated] - Clostridium magnum N.Alternate names: 2-oxoglutarate dehydrogenase complex chain E3; acetoin dehydrogenase complex chain E3; S-complex 50K chain C5pecies: Clostridium magnum C5pecies: Clostridium magnum C5pecies: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000 C; Accession: I40794 R.Kruger, N.; Oppermann, F.B.; Lorenzl, H.; Steinbuchel, A. A; Ditle: Biochemical and molecular characterization of the Clostridium magnum acetoin de} A; Reference number: 140789; MUID:94266715; PMID:8206840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Description: catalyzes the oxidation of dihydrolipoamide to lipoamide using NAD A, Description: dehydrogenase enzyme system C; Superfamily: Alcaligenes dihydrolipoamide dehydrogenase; dihydrolipoamide dehydrogenase; c; Keywords: FAD; flavoprotein; lipoamide, NAD; oxidoreductase; redox-active disulfide F; 5-77/Domain: lipoyl/biotin-binding homology <LPB.
F;117-145/Region: beta-alpha-beta FAD nucleotide-binding fold F;119-561/Domain: dihydrolipoamide dehydrogenase homology <DLD>
F;287-315/Region: beta-alpha-beta NAD nucleotide-binding fold F;153-158/Disulfide bonds: redox-active #status predicted
                                                                                                                                                                                                                                                                                                         GB:AE001362; NID:g3845188; PIDN:AAC71881.1; PID:g384519(
Science 282, 1126-1132, 1998
A,Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A,Reference number: A1600; MUID:99021743; PMID:9804551
A,Accession: D71614
A,Accession: D71614
A,Molecule type: DNA
A,Residues: 1-2573 <GAR>
A,COSS-references: GB.AE001396; GB:AE001362; NID:g3845188; PIDN:AAC71881.1. DTN.~~A,Experimental source: clone 3D7
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 ALSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----AKAKLIRDGININNN 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 NVYIMADKOKNGIKVNFKIRHNIEDGSVOLADHYQQNTPIGDGPVLLPDNHYLSTQSALS
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A; Cross-references: GB:L31844; NID:g472324; PIDN:AAA21748.1; PID:g472330
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.9%; Score 87.5; DB 2;
Best Local Similarity 26.2%; Pred. No. 1.2e+02;
Matches 34; Conservative 30; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: 140794
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.8%; Score 87; DB 23.5%; Pred. No. 19; tive 40; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 TYLKRERDYM 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 KDPNEKRDHM
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Matches 54; Conserv
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Qy 179 LADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDH 218 :	
RESULT 11 C1607078 Protective surface antigen D-15 precursor - Haemophilus influenzae (type b) C;Spectise: Haemophilus influenzae A;Variety: type b C;Accesion: JC4078 R;Flack, FS.; Loosmore, S.; Chong, P.; Thomas, W.R. Gene 156, 37-39, 1953 A;Title: The sequencing of the 80-kDa D15 protective surface antigen of Haemophilus infl A;Reference number: JC4078; MUID:9525576; PMID:773723 A;Reference number: JC4078; MUID:9525576; PMID:773723 A;Reference contact type b A;Accession: JC4078 A;Residues: L797 cFLA A;Residues: L797 cFLA A;Residues: L797 cFLA A;Residues: L797 cFLA A;Residues: B;A;Accesser (B:U3361; NID:9537447; PIDN:AAA85645.1; PID:9537448 A;Residues: L797 cFLA A;Residues: B;A;Accesser (B:U3361; NID:9537447; PIDN:AAA85645.1; PID:9537448 A;Residues: L997 cFLA A;Residues: L996 C;Superfamily: protective surface antigen D-15 C;Superfamily: protective surfac	Db 500 FFBYDNSKADTSSNYKRTYGSNYTL-GFPVNENNSYYGLGHTYKISNFALEYN 555 Qy 149 HNYYIMADKOK-NGIKVNFKIRHNIEDGSVQLADHYQQNTPIGGEPVLL 196 Db 556 RNLYIQSMKFKGNGIKTNDFDFSFGWNYNSLNRGYFPTKGVKASLG-GRVTI 606 Qy 197 PDNHYLSTGSALSKDPNEKRDHWVLGFVTAAGTTLG 233 Callilase (EC 3.2.1.4) - Bacillus sp. NAALternate names: endo-1,4-beta-glucanase C,5geoies: Bacillus sp. C,5decesion: 529043 C,5decesion: 529043 C,5decesion: 529043 A,Accession: 529043 A,Accession: 529043 A,Reference number: 529043 A,Reference series: EMBL:MA7420; NID:91037937; PMID:2230718 A,Rolecule type: DNA A,Reference series: EMBL:MA7420; NID:910399367 A,Title: Crystallization and preliminary X-ray analysis of a truncated family A alkaline A,Reference number: PC4404; MUID:98060488; PMID:9399567 A,Rocession: PC4044 A,Rocession: PC4042 A,Rocession: PC4044 A,Rocession: PC4044 A,Rocession: PC4044
149 HNVYIMADKQK-NGIKNNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLL 196	A; Residues: 228-584 <shi> A; Residues: 228-584 <shi> A; Experimental source: strain KSM-635 C; Function: A; Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as cell a; Pathway: cellulose degradation C; Superfamily: Bacillus sp. KSM-635 alkaline cellulase; S-layer repeat homology; Thermotc C; Keywords: glycosidase; hydrolase; polysaccharide degradation F;41-95/Domain: S-layer repeat homology <slr1> F;101-153/Domain: S-layer repeat homology <slr2> F;164-219/Domain: S-layer repeat homology <slr3> F;164-219/Domain: Thermotoga xylanase A amino-terminal repeat homology <txa></txa></slr3></slr2></slr1></shi></shi>
rain Rd KW20) ange 18-Sep-1998 Kirkness, E.F.; Kerlavage, A A.; Kelley, J.M.; Weidman, J	Query Match 6.8%; Score 86.5; DB 2; Length 941; Best Local Similarity 19.8%; Pred. No. 39; Matches 48; Conservative 34; Mismatches 61; Indels 99; Gaps 11; Qy 16_LVBLDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTALS-YGVQCFSR 74
en, N.S.M. .O.; Venter, zae Rd.	Db 240 LVELNGQLTLAGEDGT
C;Superfamily: protective surface antigen D-15 C;Keywords: surface antigen Query Match Query Match Best Local Similarity 21.9%; Pred. No. 32; Matches 48; Conservative 30; Mismatches 78; Indels 63; Gaps 11; Qy 65 LSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTI 99	Qy 191 DGPVJ.PDNHYLSTQSALSKDPN

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A; Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyperference number: A81250; MUD:20150912; PMID:10688204

A; Reference number: A81250; MUD:20150912; PMID:10688204

A; Status: p:eliminary

A; Status: p:e
                                                                                                                     tRNA (uraci..-5-)-methyltransferase (EC 2.1.1.35) Cj0831c (imported) - Campylobacter jeju
C,Species: Campylobacter jejuni
C,Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-directed DNA polymerase (EC 2.7.7.7) - heron hepatitis virus C; Species: heron hepatitis virus, HHBV C; Species: heron hepatitis virus, HHBV A; Note: host Ardea cincrea (gray heron) C; Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 11-Jun-1999 C; Accession: A30082 B; Will, H. C; Accession: A3082 B; Will, H. A; Kaleta, E.F.; Will, H. A; Kille: Isolation and characterization of a hepatitis B virus endemic in herons. A; Reference number: A93037; MUID:88333160; PMID:3418788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 T-------RAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIM 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 ADKQKNGIKVNFKIRHNIEDGSVQLADHYQ-----QNTPIGDGPVLL-PDNHYL 202
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A;Residues: 1-788 <SPR>
A;Cross-references: GB:M22056; NID:G325452; PIDN:AAA45738.1; PID:G325454
C;Superfamily: hepatitis virus DNA-directed DNA polymerase
C;Keywords: DNA biosynthesis; nucleotidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34;
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19.7%; Pred. No. 38;
tive 32; Mismatches 66; Indels 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 24.8%; Pred. No. 12;
Matches 30; Conservative 18; Mismatches 39; Indels
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Best Local Similarity 19.78
Matches 40; Conservative
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203 STQ-----SALSKDPNEKR 216
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298 DRRRRQKGQGVLQAIGREPSETR 320
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Search completed: June 21, 2004, 16:01:55 Job time: 11.3333 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model protein

June 21, 2004, 15:42:24; Search time 6.44444 Seconds (without alignments) 1931.085 Million cell updates/sec Run on:

US-09-887-784-64A

1273 1 MVSKGEELFTGVVPILVELD......VLLGFVTAAGITLGMDELYK score: Sequence: Perfect

239

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt 42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P42212 aeduorea vi	haemophi]			P18947 caenorhabdi		salmone]		haemophi	haemoph			Q9pp92 campylobact			-	-	-				O00116 homo sapien		_	_	P21951 saccharomyc	_		Q9nubl homo sapien	_	P49052 bacillus li		Q7vnf0 haemophilus
SUMMARIES	ΩI	GFP AEOVI	SYL HAEIN	SYL_XYLFA	SY62 DISOM	VIT4 CABEL	SYL SALTI	SYL SALTY	CP51 CANGA	D152 HAEIN	D151 HAEIN	SYL XYLFT	GUN_BACS6	TRMA CAMJE	DPOL_HPBHE	D153_HAEIN	ITH3_MESAU	AMPA_WIGBR	PEPF MYCPU	SYL SHEON	YCO3 KLEPN	GRBE_RAT	ADAS_HUMAN	BAG_STRAG	PSBC_CYAPA	AMY2_SCHPO	DPOE_YEAST	HIS7_BUCAI	PRC_ECOLI	AC2L HUMAN		SLAP BACLI	PENK_MOUSE	SYD_HAEDU
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d	Query Match	97.6	7.2	7.0	7.0		6.9	6.9		•		•	6.8	•	6.7	•	6.7	•	•	•	•	9.9	•	•		•	•	6.4	6.4	6.4	6.4	6.4	6.4	6.4
	Score	1242	91.5	89.5	89	88.5	87.5	87.5	86.5	86.5	86.5	86.5	86.5	86	85.5	85.5	85.5		84.5	84.5	84	83.5	83.5	83.5	83	83	82.5	82	82	82	82	82	81.5	81.5
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D58743 methanococc D53621 homo sapien D55443 helicobacte P97275 cavia porce D8xbn8 escherichia O8fjy9 escherichia P97401 simian foam P91679 drosophila P93882 erwinia car Q9pkt7 chlamydia m P94126 azorhizobiu	
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
YD48 METJA COPA HUMAN TRMB HELPY ADAS CAVPO SYL ECOS 7 SYL ECOLI POL SY 31 OPTI DROME EXPI ERWCA TRXB CHMU GLNA AZOCA	1
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# ALIGNMENTS

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MEDLINE=97299832; PubMed=9154981;
Rouwendal G.J.A., Mendes O., Wolbert E.J.H., de Boer A.D.;
"Enhanced expression in tobacco of the gene encoding green fluorescent
protein by modification of its codon usage.";
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Chemical structure of the hexapeptide chromophore of the Aequorea
                                                                                                                          Aeguorea victoria (Jellyfish).
Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aeguoreidae, Aeguorea.
NCBI_TaxID=6100;
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"Aequoraea green fluorescent protein. Expression of the gene and fluorescence characteristics of the recombinant protein.";
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                                                                                                                                                                                                                                                                         Cormier M.J.;
"Primary structure of the Aequorea victoria green-fluorescent
brotein.":
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96355665; PubMed=8703075;
Ormoe M., Cubitt A.B., Kallio K., Gross L.A., Tsien R.Y.,
Remington S.J.;
                                                                                                                                                                                                                      SEGUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=92175527; PubMed=1347277;
Prasher D.C., Eckenrode V.K., Ward W.W., Prendergast F.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDLINE-98294543; PubMed-9631087;
Yang F., Moss D.G., Phillips G.N. Jr.;
"The molecular structure of green fluorescent protein.";
Nat. Bioeconnol. 14:1246-1251(1996).
                                           P42212; Q17104; Q27903; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)
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                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              green-fluorescent protein.";
Biochemistry 32:1212-1218(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 273:1392-1395(1996).
                                                                                                           Green fluorescent protein.
                                                                                                                                                                                                                                                                                                                        Gene 111:229-233(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHROMOPHORE
                                 GFP AEQVI
                                                                                                                                                                                                                                                                                                         protein.
RESULT 1
GFP_AEOVI
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of modified amino acid residues The chromophore, which is composed of modified amino acid residues The chromophore is formed upon of modified amino acid residues The chromophore is formed upon cyclication of the residues Ser-debydroTyy-Gly.

-!- BIOTECHNOLOGY: Has become a useful and ubiquitous tool for making chimeric proteins of GFP linked to other proteins where it functions as a fluorescent protein tag. GFP tolerates N-and C-terminal fusion to a broad variety of proteins. It has been expressed in bacteria, yeast, slime mold, plants, Drosophila, zebrafish, and in mammalian cells. As a noninvasive fluorescent marker in living cells, it allows for a wide range of applications where it may function as a cell lineage tracer, reporter of gene expression, or as a measure of protein-protein interactions.

-!- DATABASE: NAME=Protein Spotlight;
WWW="http://www.expasy.org/spotlight/articles/sptllthtml".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                MEDINE-99238303; FubMed-10220315;
Elsliger M.A., Wachter R.M., Hanson G.T., Kallio K., Remington S.J.;
Elsliger M.A., Wachter R.M., Hanson G.T., Kallio K., Remington S.J.;
Structural and spectral response of green fluorescent protein
Structural and spectral response of green fluorescent protein
Biochemistry 38:5296-5301(1999).

-!- FUNCTION: Energy-transfer acceptor. Its role is to transduce the
blue chemiluminescence of the protein aequorin into green
fluorescent light by energy transfer. Fluoresces in vivo upon
receiving energy from the Ca(2+)-activated photoprotein aequorin.
Abjorbs light maximally at 395 nm and exhibits a smaller
abjorbance peak at 470 nm. The fluorescence emission spectrum
peaks at 509 nm with a shoulder at 540 nm.
                 CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF MUTANT WITH YELLOW EMMISSION
[7]
X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF MUTANT WITH YELLOW EMMISSION MEDLINE=99455509; PubMed=9782051;
Wachte: R.M., Elsliger M.A., Kallio K., Hanson G.T., Remington S.J.;
"Structural basis of spectral shifts in the yellow-emission variants structure 6:1267-1277(1998).
                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M62654; AAA27722.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M62653; AAA27721.1; -. EMBL; %29345; AAA58246.1; -. EMBL; %96418; CAA65278.1; -.
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1C4F; 14-JUN-00.
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28-AUG-02.
10-APR-02.
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13MB;
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13MF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 VTALSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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Pred. No. 3.5e-96;
1; Mismatches 4; Indels
                                                                                                                                                                                             5-imidazolinone (Ser-Gly).
2,3-DIDEHYDROTYROSINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26886 MW; EASAGF21FBFB6E05 CRC64;
                                                                                                                                                                                                                                                                                                    88888
       PDB; IXX; 10-ARP-02.
PDB; IYFP; 28-OCT-98.
PDB; ZEMD; 20-AUG-97.
PDB; ZEMO; 20-AUG-97.
InterPro; IPR009017; GFP_like.
InterPro; IPR00786; Green_fl_protein.
                                                                                                                                                                                                                                 PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl protein;
Luminescence; 3D-structure.
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Best Local Similarity 97.9°
Matches 233; Conservative
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66
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                                                                                                                              Pfam; PF01353; GFP; 1.
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217
238 AA;
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SEQUENCE
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104 DGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADK-QKNGI 162
                                                                                                                        -----NIEDGSVQLADHYQQNTPIGDGPVLLPDNHYL- 202
                                                                                                                                                           RA Simpson A.J.G., Reinacar 191044; Arruda P., Abreu F.A., Acencio M., Asimpson A.J.G., Reinacd F.C., Arruda P., Baia G.S., Baptista C.S., Radrose M.H., Bonacocorsi B.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camarcoo L.B.A., Carraro D.M., Carrer H., Radeno M.R.P., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Radeno M.R.P., Ferreira W.D., Ferreira W.C.R., Costa-Neto C.M., Radeniani A.P., Ferreira A.J.S., Ferreira W.C.A., Ferro J.A., Radeniani A.P., Ferreira A.J.S., Ferreira W.C.A., Ferro J.A., Radeniani A.P., Goldman M.H.S., Gomes S.L., Gruber A., Radeniani G.B., Lunges S.L., Gruber B.L., Lomos E.G.M., Lemos M.V., Martins E.B., Lopes C.R., Machado J.A., Mardins B.M.P., Mardins E.M.P., Martins E.M.P., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diphosphate + L-leucyl-tRNA(Leu).
-!- SUBCELLUTAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bācteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
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                                                            365 DEEIDLTKOAFVEHGKLVNSDEFDGKNF--DGAFNG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                              879 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
                                                                                                                        163 ---KVNFKIRH-----
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462 GVKSPINADPN 472
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                                                                                                                                                                                                                                             203 STQSALSKDPN 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00133; tRNA-synt_1; 1. PR14NYS; PR00985; TRNASYNTHLEU.
TIGRPAMS; TIGR00396; leug. Back; 1. PR051TE; PS00178; AA TRNA_LIGASE 1; 1. Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diphosphate + L-leucyl-tRNA(Leu).
--- SUBUNT: Monomer (By similarity).
--- SUBCHILL: MOTOMER LOCATION: Cytoplasmic.
--- SUBCELLULAR LOCATION: Cytoplasmic.
--- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95350630; PubMed=7542800;
Ploistochmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.E., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Wienerback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
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                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
NCBL_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP
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619 623 "KMONSKS" REGION.
622 622 ATP (BY SIMILARITY).
861 AA, 97750 MW, EB93304F684C8FB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90;
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24.1%; Pred. No. 6.2;
:ive 26; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIGR: H10921; -. H10921; -. HAWAP; MF_00049; -; I. HAWAP; MF_00049; -; I. InterPro; IPR002300; tRNA-synt_Ia. InterPro; IPR001412; tRNA-synt_I. InterPro; IPR009008; ValRS_IIERS_edit.
                                                                                                                                                                                                             (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U32774; AAC22581.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 269:496-512(1995)
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                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae.
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28-FEB-2003
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P43827;
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SEQUENCE
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                                                                                     RESULT 2
SYL HABLN
DT 01-NO
DT 01-NO
DT 01-NO
DT 28-FE
GN HAGMO
OC PRECE
OC PRECE
OC PRECE
OC RECE
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OC STRAI
RA FEBEE
RA F
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SEQUENCE OF 1-71 FROM N.A.
                                                  JH0414; JH0414.
                                                                                                                                                                                                                                                   6
46
439 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
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                                                                                                                                                                          DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                    DOMAIN
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VIT4 CAEEL
                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                        321 TNEOLPV-WVANFVLMAYGTGAVMAVPGHDQRDQEF--ANKYGLPIRQVIALKEPKNQDE 377
                                                                                                                                                                                                                                                                                                                                         154 MADKQKNG-IKVNFKIRHNIEDGSVQLADHYQQNTPI-------GDGPVLLPDN 199
                                                                                                                                                                                                                                                                                                                                                        -----KTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91273991; PubMed=2054189; MEDLINE=91273991; PubMed=2054189; Mendland B., Miller K.G., Schilling J., Scheller R.H.; Miller K.G., Schilling J., Scheller R.H.; Differential expression of the p65 gene family."; Neuron 6:993-1007(1991).

-I-FUNCTION: May have a regulatory role in the membrane interactions during trafficking of synaptic vesicles at the active zone of the synapse. It binds acidic phospholipids with a specificity that requires the presence of both an acidic head group and a diacyl
                                                                                                                                                                                                                                        TIGKL PVPWPTLVTALSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         backbone.
SUBUNIT: Homodimer or homotrimer (possible).
SUBCELLULAR LOCATION: Synaptic vesicles in neurons.
TISSUE SPECIFICITY: Spinal cord, brainstem, midbrain and electric
                                                                                                                                                                                                                                                                                                         InterPro; IPR002302; Leu-trNAsyntla.
InterPro; IPR004300; tRNA-synt_1a.
InterPro; IPR004191; tRNA-synt_1.
InterPro; IPR0040908; VARS ILES edit.
Pfam; PP00133; tRNA-synt_1; 1.
PRINTS; PR00985; TRNASYNTHIBU.
TIGRFAMS; TIGR00396; leus.
PROSITS; PS00178; AA TRNA_LIGASE[1; 1.
Aminoacyl-tRNA_synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes,
Elasmobranchii, Squalea, Hypnosqualea, Pristiorajea, Batoidea,
Torpediniformes, Narcinoidei, Narcinidae, Discopyge.
                                                                                                                                                                                                                57;
                                                                                                                                                                                         DB 1; Length 879;
                                                                                                                                                                                                                 68; Indels
                                                                                                                                        "KMSKS" REGION.
ATP (BY SIMILARITY).
9FDCCB992092919E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to the synaptotagmin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Synaptotagmin B (Synaptic vesicle protein O-p65-B)
                                                                                                                                                                                         7.0%; Score 89.5; DE 22.2%; Pred. No. 9.4; tive 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                439 AA
                                                                                                                              "HIGH" REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Contains 2 C2 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Discopyge ommata (Electric ray).
                                                                                                                                                                                                                                                                                                                                                                                            200 -HYLSTQSALSKDPNEKR 216
                                                                                                                                                                                                                                                                                                                                                                                                          99796 MW;
                                                                                                                                                                             Query Match
Best Local Similarity 22...
Best Local 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                              55
641
640
                                                                                                                                                    640 6
879 AA;
                                                                                                                 Complete proteome.
SITE 45
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                                                                                                                                                    BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                             108
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 CLCICKKCCCKKKKNKKEKGKGK--------KNDINMK---DVKGSGGNQDDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 LVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPV-PWPTLVTALSYGV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 MMPIDTGDNSTEAGVPGEGKND-VFEKLKEKFMNELOKIPLPPWALIAIAIVSGLLLLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 VKVFLLPDKKKKYETKVQKKTLNPTFNESFVFKVPYQELGGKTLMMAVYDFDRFSKHDCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 -----QCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 -NVYIMADKQKN-GIKVN------PKIRHNIEDGSVQLA-----DHYQQNTPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
CYTOPLASMIC (POTENTIAL).
PHOSPHOLIPID BINDING (PROBABLE).
C2 DOMAIN 1.
C2 DOMAIN 1.
C2 DOMAIN 2.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane, Repeat, Synapse, Multigene family, Glycoprotein.
1 74 VESICULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 GDGPVLLPD-----NHYLSTQSALSKDPNEKRDHMVLLGFVTAAG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 89; DB 1; Length 439;
Pred: No. 4.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 POTENTIAL.
439 CYTOPLASMIC (POTENTIAL).
399 PHOSPHOLIPID BINDING (PROBAB 262 C2 DOWAIN 1.
395 C2 DOWAIN 2.
505 C2 DOWAIN 2.
6 N-LINKED (GLCNAC. ..) (POTE 46 N-LINKED (GLCNAC. ...) (POTE 46 N-LINKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 --DTLVNRIELKGIDFKEDGNI--LGHKLEYNYNSH-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46; Mismatches
                                                                                                                                                                                                                                                          HSSP; P21707; IBYN.
InterPro; IPR000008; C2.
InterPro; IPR00008973; C2 CallB.
InterPro; IPR002149; LRI.
Pfam; PP00168; C2; 2.
SWART; SW00239; C2; 2.
PROSITE; PS00499; C2 DOMAIN_1; 2.
PROSITE; PS50004; C2 DOMAIN_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.0%;
                                                                                                                                                                    EMBL; M64276; AAA49228.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 19.5
Les 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vitellogenin 4 precursor.
VIT-4 OR F59D8.2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 TTGKLPVPWPTLVTALSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 TGEEIPV-WAANFVLMEYGTGAVMAVPGH-DQRD-YEFASKYGLTIKPVILAADGSEPDL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 RAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
                                                                                                                                                                 Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Hodden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAMAP; MF 00049; -; 1.

InterPro; IPR002302; Leu-tRNAsyntla.

InterPro; IPR001302; Leu-tRNA-synt_la.

InterPro; IPR001412; TRNA-synt_la.

InterPro; IPR001408; ValRS_IIERS_edit.

Pfam; PF00133; TRNA-synt_lī_1.

PRINTS; PR00185; TRNA-SYNTHEBU.

TIGRPAMS; TIGR00396; leuS_bact; 1.

PROSITE; PS001778; AA_TRNA_LIGASE_I; 1.

Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      371 SEQALTEKGVLFNSGEFDGLAFEAAFNALADKL------AEKGVGERKVNYRLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Bacteriol. 185:2330-2337(2003).
-!- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP +
diphosphate + L-leucyl-tRNA(Leu).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.9%; Score 87.5; DB 1; Length 860; 23.3%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "KMSKS" REGION.
ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21; Mismatches
                                                                                                                      STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
                            Enterobacteriaceae; Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AE016841; AA069822.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL627267; CAD05125.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 23.3%
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 413:848~852(2001).
                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BINDING
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 LAVNGQEVVKSETRAKVTFVEESKINR-EIK-----KVSGPKEEIVYSMENEKLIEQ 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 TAYGLRFGSEC------KECEKEGQFVQPQTVYTYTFKNEKLQESEVNSIYT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----NYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMAD 156
               Spieth J., Denison K., Kirtland S., Cane J., Blumenthal T.;
"The C. elegans vitellogenin genes: short sequence repeats in the
promoter regions and homology to the vertebrate genes.";
Nucleic Acids Res. 13:528-5295(1985).
-!- FUNCTION: Precursor of the egg-yolk proteins that are sources of
nutrients during embryonic development (Potential).
-!- SUBCELLULAR LOCATION: Spreted in Caenorhabditis only by 32 cells
building the intestine of adult hermaphroditic individuals; they
are cotranslationally secreted into the body cavity and
subsequently taken up by the gonad.
-!- SIMILARITY: Contains 1 VWFD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 MESDKDSLFFNVHEKTMEGDCEV---AYTIVQEG-GKTIYTKSVNFDKCITR-----PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LVTALSYGVQCFSRYPDHMKQHDFFKSAMPEG-YVQERTIF---FKDDG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last senotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS).
Salmonella typhi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.0%; Score 88.5; DB 1; Length 1603; 23.4%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VWFD.

Y -> V (IN REF. 3).

L -> V (IN REF. 2).

EVAYT -> RSRLH (IN REF. 2).

T -> S (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186307 MW; E303170325BC99BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 KQKNG-----IKVNFKIRHNIEDGSVQLADHYQQNTP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VITELLOGENIN 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                860 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Storage protein; Multigene family, Signal.
SIGNAL 1 15 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A43084; A43084.
Wormbep; F5908-2; CE26817.
InterPro; IPR001147; Libid transprt_N.
InterPro; IPR001846; VWF_D.
Pfam; PF01347; Vitellogenin_N; 1.
SMART; SM00638; LPD N; 1.
SMART; SM00216; VWD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AC024137; AAK09074.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M11498; AAA28163.1; -. EMBL; X02754; CAA26531.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1603
1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1603 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30
169
183
275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYL_SALTI
Q8ZBH5;
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CONFLICT CONFLICT

DOMAIN CHAIN

Query Match SEQUENCE

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25 GHKFSVS---GEGEGDATYGKLTLKFICTTGKLPVPWPTLVTALSYGVQCFSRYPDH--M 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 21.84
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           Rossier M.;
                           CANGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
CONFLICT
SEQUENCE
RESULT 8
CP51 CANGA
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                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 TIGKLPVPWPTLVTALSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 TGEEIPV-WAANFVLMEYGTGAVMAVPGH-DQRD-YEFASKYGLTIKPVILAADGSEPDL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 RAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 SEQALTEKGVLFNSGEFDGLAFEAAFNAIADKL------AEKGVGERKVNYRLR 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 H------NIEDGSVQLADHYQQNTPIGDGPVLLPDNHYL-STQSALSKDP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                419 DWGVSRQRYWGAPIPMVTLEDGTV-----LPTPEDQLPVILPEDVWMDGITSPIKADP 471
                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=LIZ / GSSCI412 / ATCC 700720;
MEDLINE=LIZ / GSSCI412 / LATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., "Aterston R., Wilson R.K."
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGRFAMS; TIGR00396; leus_bact; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
Aminoacyl-tRNA synthetase; Proteïn biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                               diphosphate + L-leucyl-tRNA(Leu).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS).
LEUS OR STWO648.
                                                                                                                           Salmonellą typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78; Indels
                                                                                                                                                                                                                                                                                                                                        Nature 413:852-856(2001).
-!- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "KMSKS" REGION.
ATP (BY SIMILARITY).
D5003584DFBCCAB6 CRC64;
                             860 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "HIGH" REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 6.9%; Score 87.5; I
Best Local Similarity 23.3%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP; MF 00049; -; 1.
InterPro; IPR002300; Leu-tRNAsyntla.
InterPro; IPR001300; TRNA-synt_la.
InterPro; IPR001412; TRNA-synt_l.
InterPro; IPR001408; ValRS_IleRS_edit.
                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 52 "H
619 623 "K
622 622 AT
860 AA; 96985 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE008725; AAL19599.1; -. StyGene; SG?????; leus.
                                                                                                                                                        Enterobacteriaceae; Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00133; tRNA-synt 1; 1
PRINTS; PR00985; TRNASYNTHLEU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
                                                                                                                                                                  NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42;
                           SYL SALTY
Q8ZQZ6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Geber A., Hitchcock C.A., Swartz J.E., Pullen F.S., Marsden K.E., Kwon-Chung K.J., Bennett J.E.; Fuller B. S., Bennett J.E.; Follerion of the Candida glabrata ERG3 and ERG11 genes: effect on cell viability, cell growth, sterol composition, and antifungal gusceptibility.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAINE-ATCC 2001;
MEDLINE-95081364; PubMed=7989540;
Burgener-Kairuz P., Zuber J.P., Jaunin P., Buchman T.G., Bille J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Rapid detection and identification of Candida albicans and Torulopsis (Candida) glabrata in clinical specimens by specific nested PCR amplification of a cytochrome P-450 lanosterol-alpha-demethylase (11A1) gene fragment.", J. Clin. Microbiol. 32:1902-1907(1994).

-!- FUNCTION: Catalyzes C14-demethylation of lanosterol which is critical for ergosterol biosynthesis. It transforms lanosterol into 4.4'-dimethyl cholesta-8,14,24-triene-3-beta-ol (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00086; CYTOCHROME P450; 1.
Electron transport; Oxidoreductase; Monooxygenase; Membrane; Heme;
Sterol biosynthesis; NADP.
                      P50859; 00312;
01-0CT-1996 (Rel. 34, Created)
01-0CT-2096 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Cytochrome P450 51 (EC 1.14.13.70) (CYPLI) (P450-LIA1) (Sterol 14-alpha-demethylase) (P450-14DM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC_ACTIVITY: Obtusifoliol + 3 O(2) + 3 NADPH = 4-alpha-
methyl-5-alpha-ergosta-8,14,24(28)-trien-3-beta-ol + formate +
                                                                                                                                                                                                                                                                         Candida glabrata (Yeast) (Torulopsis glabrata).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.8%; Score 86.5; DB 1; Length 533; 21.8%; Pred. No. 9.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      472 IRON (HEME AXIAL LIGAND)
64 I -> M (IN REF 2).
473 I -> T (IN REF 2).
61305 MW; A0506C17507E6EF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antimicrob. Agents Chemother. 39:2708-2717(1995).
533 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NADP(+) + 3 H(2)0.
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Pfam; PF00067; p450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: Obtusifoliol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96161286; PubMed=8593007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L40389; AAB02329.1; -. EMBL; S75389; AAB32679.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 60-473 FROM N.A.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            533 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=5478;
                                                                                                                                                                                                                                                      ERG11 OR CYP51
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6

Indels

80;

32; Mismatches

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                   ----KLEYNYNS
                                                            487 FFENYDNSKSDTSSNYKRTTYGSNVTL-GFPVNENNSYYVGLGHTYNKISNFALEYN---
                                                                                                            149 HNVYIMADKQK-NGIKVNFKIRHNIEDGSVQLADHYQQ------NTPIGDGPVLL
                                                                                                                                                        543 RNLYIQSMKFKGNGIKTN-----DFDFSFGWNYNSLNRGYFPTKGVKASLG-GRVTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Outer membrane protein D15 is conserved among Haemophilus influenzae species and may represent a universal protective antigen against invasive disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=Serotype B;
MEDLINE=95525676; PubMed=7737523;
Flack F.S., Loosmore S., Chong P., Thomas W.R.;
"The sequencing of the 80-kDa D15 protective surface antigen of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protective surface antigen D15 precursor (80 kDa D15 antigen)
Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   797 PROTECTIVE SURPACE ANTIGEN DIS. 87675 MW; 2F93DE538696AF1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - FKSAMPEGYVQE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Infect. Immun. 65:3701-3707(1997).
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SIMILARITY: Belongs to the surface antigen D15 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                     FFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNI---LGH---
                                                                                                                                                                                                                                      594 PGSDNKYYKLSADVQGFYPLDRDHLWVVSAKASAGYANG 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Minna / Serotype B, and Eagan / Serotype B; MEDLINE=97427952; PubMed=9284140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78;
                                                                                                                                                                                                      197 P--DNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.8%; Score 86.5; D
21.9%; Pred. No. 15;
ative 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, U60833; AAB61976.1; -.
PIR, JC4078, JC4078.
InterPro, IPR000184; Bac_surfAg_D15.
Pfam; PF01103; Bac_surface_Ag; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 LSYGVQCFSRYPDHMKQHDF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antigen; Outer membrane; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U13961; AAA85645.1; -. EMBL; U60832; AAB61974.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemophilus influenzae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48; Conservative
                                                                                                                                                                                                                                                                                                                                                                        STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 156:97-99(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                797 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klein M.H.;
                                                                                                                                                                                                                                                                                                                                                                        HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                     100
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Best Local S
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  : | | | | | | | -- FGKGVIYDCPNHRLM 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KQHDFFKSAM-PEGYV-----QERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDF 131
                                                                                                                                                             132 KEDGNILCHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 LSYGVQCFSRYPDHMKQHDF------RTSAMPEGYVQE-----RTI
                                                                                                               150 EÓKKFVKGÁLTKÉAFVRYVPLIAEÉLYKYFRNSKNFKINENNSGIVDVMVSQPÉM--TIF
                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAINSEA ( WAZO / ATCC 51907;
STRAINSEA ( WAZO / ATCC 51907;
BLEISCHMANN R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             P.1907-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Protective surface antigen D15 precursor (80 kDa D15 antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTECTIVE SURFACE ANTIGEN D15.
B85691FC22E6ED44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SIMILARITY: Belongs to the surface antigen D15 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01103; Bac_surface_Ag; T.
Antigen; Outer membrane; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                           795 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.8%; Score 86.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                           192 GPVLLPDNHYLSTQSALSKDPNEKRD 217
                                                                                                                                                                                                                                                                                      -----GTYMSLIKERREKND 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (D-15-Ag) (Outer membrane protein D15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000184; Bac_surfAg_D15.
109 GHEFIFNAKLADVSAEAAYSHLT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87478 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U32773; AAC22575.1; -. TIGR; H10917; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemophilus influenzae.
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20
795 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48;
                                                                                                                                                                                                                                                                                                                                                                                                                           D152 HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                     FFKDDGNYKTRAEVKFEGDTLVNRIBLKGIDFKEDGNI---LGH------KLEYNYNS 148
                                                                                                          542
                                                                                                                                                            HNVYIMADKQK-NGIKVNFKIRHNIEDGSVQLADHYQQ-----NTPIGDGPVLL 196
127 IGYGTESGISYQASVKQDNFLGTGAAVSIAGTKNDYGTSVNLGYTEPYFTKDGVSLGGNV 486
                                                                                                                                                                                                                    543 RNLYIQSMKFKGNGIKTN-----DFDFSFGWNYNSLNRGYFPTKGVKASLG-GRVTI 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=2242131; PubMed=12533478;

MEDLINE=2242131; PubMed=12533478;

Na Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,

Na Myaki C.Y., Furlan L.R., Camargo L.B.A., da Silva A.C.R., Moon D.H.,

Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,

Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M.,

A Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M.,

A Coutinio L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E.,

Marino C.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,

Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,

A Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.P., Kishi L.T.,

Leoni S.G., Oliveira A.R., Rosa V.E. Ur., Sassaki F.T., Sena J.A.D.,

de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G.,

Civerolo E.L., Simpson A.J.G., Almeida N.F. Ur., Setubal J.C.,
                                                                                                    437 FFENYDNSKSDTSSNYKRTTYGSNVTL-GFPVNENNSYYVGLGHTYNKISNFALEYN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGRFAMS; TIGR00396; leuS bact; 1.
PROSITIS; PS00178; AA TRNA_LIGASE I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS).
LEUS OR PD1230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Comparative analyses of the complete genome sequences of Pierce's disease and citrus variegated chlorosis strains of Xylella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEUS OR PD1230.
Xylella fastidiosa (strain Temeculal / ATCC 700964).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Bacteriol. 185:1018-1026(2003).
-!- CATALYTIC ACTIVITY: AFP + L-Leucine + tRNA(Leu) = AMP diphosphate + L-Leucyl-tRNA(Leu).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                       594 PGSDNKYYKLSADVQGFYPLDRDHLWVVSAKASAGYANG 632
                                                                                                                                                                                                                                                                         P--DNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              879 AA.
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INTERFN:0, IPR002302; Leu-tRNAByntla.
INTERFN:0; IPR001412; TRNA-SYNT_Ia.
INTERFN:0; IPR001412; TRNA-SYNT_I.
INTERFN:0; IPR009008; ValRS_ILERS_edit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kanthomonadaceae; Xylella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TAXID=183190;
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                                                                                                                                                                                                                                                                       107
                                                                                                                                                                                                                                                                                                             422 ---ROGRGORRVNYRLR----DWGVSRQRYWGCPIPVIYCPTCGAVPVPENQLPVILPEN 474
                                                                                                                                                                                                                                                                    50 TIGKLPVPWPTLVTALSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNY--
                                                                                                                                                                                                                                                                                                                                                                                             108 ------KTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYI
                                                                                                                                                                                                                                                                                                                                                                                                                         378 STWEPDVWRDWYADKTR---EFE---LINSAEFDGLDYQGAFEVLAERFE-----
                                                                                                                                                                                                            57; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-91037937; PubMed=2230718; Ozaki K.; Shikata S., Kawai S., Ito S., Okamoto K.; Ozaki K., Shikata S., Kawai S., Ito S., Okamoto K.; Molecular cloning and nucleotide sequence of a gene for alkaline cellulase from Bacillus Sp. KSM-635."; J. Gen. Microbiol. 136:137-1334 [1990].

-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic linkages in cellulose, lichenin and cereal beta-D-glucons.
-!- SIMILARITY: Belongs to cellulase family A (family 5 of glycosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF03424; CBM 17_28; 2.
Pfam; PF00150; cellulase; 1.
Pfam; PF00395; SiH; 3.
PROSITE; PS00659; GLYCOSYL_HYDROL_F5; 1.
PROSITE; PS01072; SLH DOMAIN; 2.
Cellulose degradation; Hydrolase; Glycosidase; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 16, Last sequence update)
10-OCT-2003 (Rel. 42, Last sannotation update)
Endoglucanase precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)
(Alkaline cellulase).
Bacillus sp. (strain KSM-63s).
Bacteria; Firmicutes; Bacillales; Bacillus.
                                                                                                                                                     DB 1; Length 879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hydrolases).
-!- SIMILARITY: Contains 3 S-layer homology (SLH) domains.
                                                                                                                                                                                                            Indels
                           "KMSKS" REGION.
ATP (BY SIMILARITY).
4C2EE01B8FDC497E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 MADKOKNG-IKVNFKIRHNIEDGSVQLADHYQQNTPI----
                                                                                                                                                                                                            69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                941 AA
                                                                                                                                                                             1 Similarity 22.2%; Pred. No. 17; 44; Conservative 28; Mismatches
                                                                                                                            6.8%; Score 86.5; I
   "HIGH" REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDB; 1G01; 31_DEC-02.
PDB; 1G02; 31_DEC-02.
InterPro; 1PR005086; CBM 17_28.
InterPro; 1PR008979; Gal_bind like.
InterPro; 1PR001547; Glyco_hydro_5.
InterPro; IPR00119; SLH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 -HYLSTQSALSKDPNEKR 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              475 VAFSGTGSPIKTDPEWRK 492
45 55 "H
637 641 "K
640 640 AT
879 AA; 99823 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M27420; AAA22304.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S29043; S29043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI TaxID=1415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GUN BACS6
P19424;
SITE
SITE
BINDING
SEQUENCE
                                                                                                                                                        Query Match
                                                                                                                                                                                Best Local
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
GUN BACS6
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174
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                                                                                                                                                                                                       75 YPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKED 134
                                                                                                                                                                                                                               319
                                                                                                                                                                                                                                                     135 GNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSV----QLADHYQQNTPIG 190
                                                                                                                                                                                                                                                                                                 191 DGPVLLPDNHYLSTQSALSKDPN-----EKRDHMVL 221
                                                                                                                                                                                                                                                                                                                        361 -----PKNHYIIWELANEPSPNNNGGPGLTNDEKGWEAVKEYAEPIVEMLREKGDNMIL 414
                                                                                                                                                                                 16 LVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTALS-YGVQCFSR 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Catalyzes the formation of 5-methyl-uridine at position 54 (M-5-U54) in all tRNA (By similarity) CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-homocysteine + tRNA containing thymine. SIMILARITY: Belongs to the RNA M5U methyltransferase family. TrmA
                                                                                                                                                                                                                             272 --EIVNENAFVALSNDWGSNMIRLAMYIGENGYATNPEVK---DLVYEGIELA----
                                                                                                                                                                                                                                                                           ----PEHDMYVIVDWH---VHAPGDPRADVYSGAYDFFEEIADHYKDH----
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20150912; PubMed=10688204; Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C., Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M., Whitehead S., Barrell B.G.; "The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
FINA (Uracil-5-)-methyltransferase (EC 2.1.1.35) (FRNA(M-5-U54)-TRMA OR CJ0831C.
                                                                                                                                     99;
                                                                                                                 Length 941;
                                 SLH 1.
SLH 2.
SLH 2.
SLH 2.
PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
8 MW, BEAZAC38169BFADA CRC64;
                                                                                                                                     61; Indels
                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                            357 AA
                                                                                                                         19.8%; Pred. No. 18;
tive 34; Mismatches
                       ENDOGLUCANASE
                                                                                                                Score 86.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reveals hypervariable sequences.";
Nature 403:665-668(2000).
                                                                                                                 6.8%;
                                                                                                                          1 Similarity 19.89
48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
           29
941
151
151
2225
485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Campylobacter jejuni.
                                                                                           941 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=NCTC 11168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     416
                                                                                                                                                                                                                                                                                                                                              223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subfamily.
3D-structure.
SIGNAL
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                                                                  ACT_SITE
ACT_SITE
SEQUENCE
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                                                                                                                 Query Match
                                                                                                                         Best Local
                      CHAIN
DOMAIN
DOMAIN
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                                                         DOMAIN
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 KOHDFFKSAMPEGYVOERTIFFKDDGNYKTRAEVKF--EGDTLV------NRIELKG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 LDFADEKICAFMPRLLEYLRQDNKLKEKL-----FGVEFLTTKQE--LSITLLYHKNIE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 IDFKED------GNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIE 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73
                                                                                           R PRIX; GB13-5.

R HAMAP; MP 01011; -1 1.

DR InterPro; IPR001056; SAM bind.

DR InterPro; IPR001566; TrmA.

DR PROSITE; PS01230; TRMA_1; 1.

DR PROSITE; PS01231; TRMA_2; FLSE_NEG.

KW Transferase; Methyltransferase; LENA processing; Complete proteome.

FT DOMAIN 207 213 SADENOSYLMETHIONINE BINDING (BY SIMILARITY).

SADENOSYLMETHIONINE BINDING (BY SIMILARITY).

ATE 315 BY SIMILARITY.

Transferase; Methyltransferase; LENA processing; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Virol. 62:3832-3839(1988).
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 EKHSFIKKYFKEFYTKDFKLFASKDKHYRTRAELSFYHENDTLFYAMFDPKSKKKYIIEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
P protein [Includes: DNA-directed DNA polymerase (EC 2.7.7.7); RNA-directed DNA polymerase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.4)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sprengel R., Kaleta B.F., Will H.; "Isolation and characterization of a hepatitis B virus endemic in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.8%; Score 86; DB 1; Length 357; Best Local Similarity 24.8%; Pred. No. 6.2; Matches 30; Conservative 18; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses, Retroid viruses, Hepadnaviridae, Avihepadnavirus VCBI_TaxID=28300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   788 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR, A30082; JDVLHH.
InterPro; IPR001462; DNApol_viral_C.
InterPro; IPR000201; DNApol_viral_N.
InterPro; IPR000477; VYTSe.
Pfam; PF00336; DNA_pol_viral_C; 1.
Pfam; PF00242; DNA_pol_viral_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M22056; AAA45738.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heron hepatitis b virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphomonoester.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ď 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D 174
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P13846;
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                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 TWEQKHLVPQQHGAYSSKINDRQESRRRRIITATSSRKNDSSRI-----FGAHN--- 245
                                                                                                                                                                                                                                                                                                                                                         58 WPTLVTALSYGVQCFSRYPDHMKQH-----DFFKSAMPEGYVQERT----IFFKDDGNYK 108
                                                                                                                                                                                                                                                                                                                                                                                                                        139 WPKSISYLPVHSGVKPKYPEFQONHESLVNDYLNKLFEAGILYKRVSKHLVTFK--GPYF 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 T-------RAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIM 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 ADKOKNGIKVNFKIRHNIEDGSVQLADHYQ------QNTPIGDGPVLL-PDNHYL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 ----NGRKISY---HSTRDGSHRLSGRTSDPTSRGALAGGDSTPIGPGSTAAHPSTHHV 297
                                 ProDom; PD000814; DNApol viral C; 1.
Transferase; RNA-directed DNA polymerase; PNA-directed DNA polymerase; Hydrolase; Nuclease; Endonuclease; DNA replication; DNA-binding.
SEQUENCE 788 AA; 90070 MW; FB44F38F75EADF44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Outer membrane protein D15 is conserved among Haemophilus influenzae species and may represent a universal protective antigen against
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
                                                                                                                                                                                                                                                                                       65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Protective surface antigen D15 precursor (80 kDa D15 antigen)
(D-15-Ng) (Outer membrane protein D15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 793;
                                                                                                                                                                                                                 DB 1; Length 788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTECTIVE SURFACE ANTIGEN D15.
51BFDB2036801A14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invasive disease.";
Infect. Immun. 6:3701-3707(1997).
-!- SUNGELLULAR LOCATION: Outer membrane.
-!- SIMILARITY: Belongs to the surface antigen D15 family.
                                                                                                                                                                                                                                                                                   66; Indels
                                                                                                                                                                                                          Query Match
6.7%; Score 85.5; Di
Best Loca: Similarity 19.7%; Pred. No. 18;
Matches 40; Conservative 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        793 AA
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6.7%; Score 85.5; D
Best Local Similarity 22.4%; Pred. No. 18;
Matches 49; Conservative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 STQ-----SALSKDPNEKR 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 DRRRROKGOGVLOAISREPSETR 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, U60834; AAB61977.1; -.
InterPro: IPR000184; Bac_surfag_D15.
Pfam; PF01103; Bac_surface_Ag; I.
Antigen; Outer membrane; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN:=PAK 12085;
MEDLINE=97427952; PubMed=9284140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87511 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
Pfam; PF00078; rvt; 1
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D153_HABIN
AC 032629;
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DT 16-OCT-2001
DE Protectity e species
CC NCBI_TAXID=7
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RC STRAINE-PAK 1
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                                                      100 FFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNI---LGH-----KLEYNYNS
 --FKSAMPEGYVQE---
                                                                                  149 HNVYIMADKOK-NGIKVNFKIRHNIEDGSVQLADHYQQ-----
                                                                                                                           197 P--DNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLG 233
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62 VTALSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
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Koranyi P., Berenyi M., Burg K.;

"Occurrence of green fluorescence protein in diazotrophic bacteria
Azomonas and Azotobacter.";

Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF324408; AAN86140.1; -..

GO; GO:000001; P:energy pathways; IEA.

InterPro; IPR000718 GFP like.

InterPro; IPR000786; Green_fl_protein.

Ffam; PF01229; GFLUORESCENT.

PRINTS; PR01229; GFLUORESCENT.

ProDom; PD013756; Green fl_protein; 1.

SEQUENCE 238 AA; 26914 MW; F84840FIF9064018 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azotobacter.
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2289GFP.
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NCBI_TaxID=354;
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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                  Azomonas agilis.
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11 VITFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTLV 120
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MEDLINE=96305137; PubMed=8707053;
Cornack B.P., Valdivia R.H., Falkow S.;
"FACS-optimized mutants of the green fluorescent protein (GFP).";
Gene 173:33-38(1996).
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A CORMACK B.P., Bertram G., Egerton M., Gow N.A.R., Falkow S.,
CORMACK B.P., Bertram G., Egerton M., Gow N.A.R., Falkow S.,
A Brown A.J.P.;
T "Yeast Enhanced Green Fluorescent Protein (yEGFP): a reporter of
T "Yeast Enhanced Green Fluorescent Protein (yEGFP): a reporter of
T "Y13901, AB18957.1; ".
Microbiology 0:0-0(1996).
R MSSP; P42212, 1BFP.
R HSSP; P42212, 1BFP.
R GO; GC:0006091; P:energy pathways; IEA.
R InterFro; IPR009017; GFP like.
R InterFro; IPR000786; Green_fl_protein.
                                                                                                                                                                                                                                                                                                                                                                                                                          Aequorea victoria (Jellyfish).
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
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PRINTS; PR01229; GFUGNESCEN:
ProDon; PD013756; Green [] protein; 1.
SRQUENCE 238 AA; 26840 WW; A28622809A9DEA60 CRC64;
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Pred. No. 2.2e-96;
2; Mismatches 5;
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01-MAR-2003 (TrEMBLrel. 23, Created)
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97.1%;
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01-FEB-1997 (TrEMBLrel. 02,
01-FEB-1997 (TrEMBLrel. 02,
01-OCT-2003 (TrEMBLrel. 25,
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Matches 231;
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Q8GHE4
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122 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
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"Occurrence of green fluorescence protein in diazotrophic bacteria
"Occurrence of green fluorescence protein in diazotrophic bacteria
Azonanas and Azotobacter.";

Bubmitted (NOV-2000) to LPBEL/GenBank/DDBJ databases.

EMBL, A7324405; AAN86137.1; ...

GO, GO,0006091; P:energy pathways; IEA.

InterPro; IPR009017; GFP_like.

InterPro; IPR009017; GFP_like.

Pram: PF01383; GFP; 1.

PRINTS; PR01229; GFLUORESCENT.

PRODOM; PD013756; Green_fl_protein; 1.

SEQUENCE 238 AA; 26902 MW; 15FE9B9C5B4F6B89 CRC64;
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Pseudomonadaceae; Azotobacter.
                                                                                                                         Bacteria; Froteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Azomonas.
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26887 MW; E0E1616BD2AF6188 CRC64;
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Last annotation update)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Green fluorescence protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 1233; DB 2; Local Similarity 97.1%; Pred. No. 3.3e-96; neg 231; Conservative 2; Mismatches 5;
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InterPro; IPR009017; GFP like.
InterPro; IPR0009086; Green_fl protein.
Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green_fl protein; 1.
SEQUENCE 238 AA; 26887 WW; EDE16, FRDDAR.
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121 NRIELKGIDFKEDGNILGHKMBYNYNSHNVYIMGDKPKNGIKVNFKIRHNIKDGSVQLAD 180
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                                                                                                                                               Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=6100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aeguorea macrodactyla.
Eukaryota; Metazoa; Chidaria; Hydrozoa; Hydroida; Leptomedusae;
Aeguoreidae; Aeguorea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 93.1%; Score 1185; DB 5; Length 238; Best Local Similarity 92.9%; Pred. No. 3.8e-92; Matches 221; Conservative 7; Mismatches 10; Indels
                                                                                                                                                                                                                                            Markins J.N., Campbell A.K.;

L Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.

R EMBL; X83960; CAA58790.1; -.

EMBL; SOS092; JO1514.

R HSSP; P42212; JBFP.

R GO; GO:0006091; P:energy pathways; JEA.

R InterPro; JFR0009017; GFP_like.

R InterPro; JFR0009076; Green_fl_protein.

R Pfam; PF01353; GFP; 1.

R PRINTS; PR01229; GFLUORESCENT.

R ProDom; PD013756; Green_fl_protein; 1.

R ProDom; PD013756; Green_fl_protein; 1.

R ProDom; PD013756; Green_fl_protein; 1.
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF435431; AAL33916.1; -
EG0; G0:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IPR000786; Green_fl_protein.
Pf01353; GFP; 1.
                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                      Green fluorescent protein (Fragment)
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                                                                                                                             Aequorea victoria (Jellyfish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25,
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                                                              2 VSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=6100;
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Watkins J.N., Campbell A.K.;

Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.

EMBL; X83959; CAAS8789.1; -.

PIR; JS0692; JG114.

HSSP; P42212; IGFL.

GO; GO:006091; P:energy pathways; IEA.

InterPro; IPR001796; Green_fl_protein.

Pfam; PF01353; GFP; 1.

PRINTS; PR01229; GFLUORESCENT.

ProDom; PD013756; Green_fl_protein; 1.

ProDom; PD013756; Green_fl_protein; 1.

NON TER 238 AA; 26950 MW; 26E2BE450E748E44 CRC64;
                       Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Green fluorescent protein (Fragment).
                     5,
  Pred. No. 4e-96;
2; Mismatches
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97.1%;
Best Local Similarity 97.1
Matches 231; Conservative
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RESULT 5
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                                                                                    PRELIMINARY;
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NCBI_TaxID=147615;
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                                                                                    Q8WTC4
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                                          RESULT 9
Q8WTC4
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STRAIN-GFPXm, and GFPdhaxm;

Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Qin Y.X., Pang S.Q.,

Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Qin Y.X., Pang S.Q.,

Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Qin Y.X., Pang S.Q.,

Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Qin Y.X., Pang S.Q.,

Submitted NOV-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AY013824; AAK02062.1; -.

EMBL, AY013824; AAK02065.1; -.

GO, GO.0006091; PAR02059.1; -.

InterPro; IPR009017; GFP_like.

InterPro; IPR009086; Green_fl_protein.
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Eukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Leptomedusae,
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                                                                                        Length 238;
                                                                                 Query Mat.th 84.8%; Score 1080; DB 5; Length 2 Best Local Similarity 81.9%; Pred. No. 2.8e-83; Matches 195; Conservative 20; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PR01229; GFLUORESCENT.
PD013756; Green fl protein; 1.
2 238 AA; 27015 MW; 6B8FD75E88926903 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aequoreidae, Aequorea.
NCBI_TaxID=147615;
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01-OCT-2003 (
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    PRINTS; 1
ProDom; 1
                                            SEQUENCE
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G08WP95
IO 08WP 98C
OO 01-M
DT 01-O
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61 VTTLGYGILCFARYPEHMKANDFFKSAMPEGYIQERTIFFQDDGKXKTRGEVKFEGDTLV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                           STRAIN=ShG24;
Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
Li S.J., Xia N.S.;
                                                                                                                                                                                                   Aequorea macrodactyla.
Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
YCBI_TaxID=147615;
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Eukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Leptomedusae,
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84.2%; Score 1072; DB 5; Length 238;
Best Local Similarity 82.4%; Pred. No. 1.3e-82;
Matches 196; Conservative 17; Mismatches 25; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       macrodactyla.";
Submitted (OCT-2011) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-2011) to the EMBL/GenBank/DDBJ databases.
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR00911; GFP_like.
InterPro; IPR00798; Green_fl_protein.
PRINTS; PR01259; GFL00RESCBNT.
Probom; P013756; Green fl_protein; 1.
SEQUENCE 238 AA; 26956 WW; 75521EAF0CEBA73A CRC64;
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238 AA
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121 NRIELKGMDFKEDGNILGHKLEYNFNSHNVYIMPDKANNGLKVNFKIRHNIEGGGVQLAD 180
122 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
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                                                                                                                              STRAIN=GFPxm162,
Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Aequorea macrodactyla.
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF415428; AAL33913.1; -.
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR00786; Green_fl_protein.
Pfam; PF01153; GFP; 1.
PRINTS; PR01229; GFU00RSCENT.
ProDom; PD013756; Green_fl_protein; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          013756; Green fl_protein; 1.
238 AA; 27031 MW; 5F80A19C19DC584D CRC64;
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Last annotation update)
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Last annotation update)
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81.1%; Pred. No. 2.4e-82;
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                                                                                                                                                                                                                                                                                                                        Created)
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08WTC7
10 Q8WTC7
AC Q8WTC
DT 01-MA
DT 01-MA
DT 01-OC
DB Green
GN GFP.
OS Aequo
OC Bukar
OC Bukar
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                                                                                                                                                                                                                                                                                                                                                                                                                                     62 VTALSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 VTALSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
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                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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                                                                                                                                                                                                                                         84.1%; Score 1070; DB 5; Length 238; 81.1%; Pred. No. 2e-82; ive 20; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 238;
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84.0%; Score 1069; DB 5; Length 2
Best Local Similarity 81.1%; Pred. No. 2.4e-82;
Matches 193; Conservative 20; Mismatches 25; Indels
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF435427, AAL33912.1; -. GO; 0006691, P:energy pathways; IEA. InterPro; IPR009017; GFP_like. InterPro; IRR000786; Green_fl_protein. PF01353; GFP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        macrodactyla.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF435429; AAL33914.1;
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP_1ike.
InterPro; IPR0090786; Green_fl_protein.
PF01353; GFP; 1.
                                                                                                                                        PRINTS; PR01229; GFUORESCENT.
ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 26997 MW; 5F80A192173CB84D CRC64;
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ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 27047 MW; 5F80A18FA1E7C84D CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                 Best_Local Similarity 81.1%
Matches 193; Conservative
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Gaps

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Length 238; Indels 61

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121 NRIELKGMDFKEDGNILGHKLEYNFNSHNVYIMPDKANNGLKVNFKIRHNIEGGGVQLAD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVQLAD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
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                                                                                     Chen M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aequorea macrodactyla.
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
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81.9%; Pred. No. 5.2e-82;
ive 17; Mismatches 26; Indels
                                                                                     S.W., Guan B.Q.,
                                                                                  Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Li S.J., Xia N.S.; "Color;ul mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 238;
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF415432; AAL33917.1; -.
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IPR0000786; Green_fl_protein.
                                                                                                                                                                                  macrodactyla.",
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, 187454330; 78AL33915.1; -.
GO, GO:0006091; P:energy pathways; IEA.
InterPro: JPR009017; GFP_11ke.
InterPro: JPR009086; Green_fl_protein.
Pfam; JP01153; GFP; 1.
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ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 27002 MW; BD5BA2982264C018 CRC64;
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E 238 AA; 27018 MW; 75521EA5534E573A CRC64;
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Last annotation update)
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81.1%; Pred. No. 3.5e-82;
ive 20; Mismatches 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Orange fluorescent protein.
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Best Local Similarity 81.1?
Matches 193; Conservative
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NCBI TaxID=147615;
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Q8WTC5
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71 CFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGID 130
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                                                                                                VTALSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
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                                      9
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                                                                                                                                                                                                                                                                                                                                                                                  17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cyan fluorescent protein (Fragment).
Montastrase cavernosa (great star coral).
Edwaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia; Favilna; Favilda; Montastraea.
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Falkowski P.G., Sun Y.;

Falkowski P.G., Sun Y.;

Falkowski P.G., Sun Y.;

Falkowski P.G., Sun Y.;

Submitted Cavernosa fluorescent protein.";

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

GO; GO:0006091; P:energy pathways; IEA.

InterPro; IPR000917; GFP_like.

InterPro; IPR000986; GFen_fluorenterpro; IPR000786; GFen_fluorenterpro; IPR00786; GFen_fluorenterpro; I
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ProDom; PD013756; Green_fl_protein; 1.
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SEQUENCE
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## ALIGNMENTS

Novel fluorescent protein in in vitro assay for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution, has a green fluorescent protein with F64L and E222G /note= "Wild type Glu substituted with Gly; This corresponds to position 222 in the wild type protein" /note= "Wild type Phe substituted with Leu; This corresponds to position 64 in the wild type protein" Jellyfish; green fluorescent protein, GFP; protein redistribution, cellular function; genetic reporter; mutant; Stoke's shift; mutein. Enhanced F64L-E222G jellyfish green fluorescent protein mutant Location/Qualifiers Thastrup 0; Ā 19-JUN-2000; 2000DK-0000953. 20-JUN-2000; 2000US-02126BIP. 10-MAY-2001; 2001DK-00000739. 10-MAY-2001; 2001US-0290170P. 18-JUN-2001; 2001WO-EP006848 (first entry)

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The invention relates to a fluorescent protein derived from green fluorescent protein (GFP) or its analogue. The GFP containing mutations at F64% and B226 has a bigger compared to other GFP's making it very cuitable for high throughput screening due to better resolution. The fluorescent protein is useful in invitro assays for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution. The fluorescent protein tags in transgenic animals, living and fixed cells; organelle tags, secretion marker and genetic reporter. The fluorescent protein is also useful as a cell or organelle integrity marker, a marker for changes in cell morphology, as transfection marker, and as a marker to be used in combination with fluorescence activated cand as a marker to be used in combination with fluorescence activated consitor is also useful as markers in transcriptional and translational protein is also useful as markers in transcriptional and translational contein is also useful. Transposon vector mutagenesis and as a reporter for batterial detection. Transposons encoding the fluorescent protein are useful for screening promoters and for tagging plasmids and chromosomes. The fluorescent protein are useful for designing diagnostic tool. The present sequence is a DNA encoding enhanced F64L-E222G jellyfish green fluorescent protein (GFP) mutant
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99.6%; Pred. No. 1.3e-122;
iive 0; Mismatches 1;
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The invention relates to a novel cell, comprising three heterologous conjugates (HC), a first HC (HC1) comprising an anchor protein that specifically binds to an internal structure within the cell conjugated to an interactor protein (IP) of type A, a second HC (HC2) comprising IP of type B conjugated to a first protein of interest, and a third HC (HC3) comprising a second protein of interest conjugated to detectable group. The cell is useful for detecting if a compound disrupts or induces the interaction between two intracellular proteins. The cell is also useful intracellular proteins. The present sequence is used in the exemplification of the invention
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                                                                                                                                    Disclosure; Page 112-113; 118pp; English
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29-MAY-2000; 2000DK-00000849.
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                                N-PSDB; ACC72604
                                                                                                                                                                                                                                                                                                                                                                                Sequence 363 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JAN-2002
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25-OCT-2001

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The invention relates to determining, if a compound, is a dislocator of PDB4. The method comprises testing if the compound removes PDB4 spots, which may optionally be induced by a Rolipram-like reference compound, and testing if it inhibits the catalytic activity of the PDB4, where the compound is a dislocator of PDB4, if it removes PDB spots and if it does not inhibit the catalytic activity of PDB4. The method is useful for identifying compounds useful for the treatment of diseases of the central continhibit as depression and for the treatment of inflammatory disease. The method is useful for identifying compounds useful for the treatment of inflammatory disease. CC disease, respiratory diseases, or normic obstructive pulmonary disease. CC disease, respiratory diseases, chronic obstructive pulmonary disease. CC disease, bone resorption diseases, repetitusion injury, cancer and HIV inflammatoric programment of a reagent that can mimic or reverse the effect of the compound with affinity for the catalytic site on intracallular distribution of the PDB for the preparation of a medicament. The present services are all and a sequence of a HSPDE4Al-E222G fusion
                                                                                                              Determining if a compound is a dislocator of PDE4 for identifying compounds for treating CNS and inflammatory disease comprises identifying compounds which remove PDE4 spots.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        715 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      775 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKOKTKVNFKIRHNIEDGSVOLA 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDE4; central nervous system; antiinflammatory; cytostatic; nootropic; autoimmune; ischemic; osteopathic; GFP; green fluorescent protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLIKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVTGLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL
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Thastrup O, Almholt DC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of HSPDE4A4-E222G fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1267; DB 4;
Pred. No. 9.1e-122;
0; Mismatches 1;
                                                                                                                                                                                             Example 1; Page 156-160; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG65782 standard; protein; 1132 AA
  Bjorn SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 99.4%;
Best Local Similarity 99.6%;
Matches 238; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
Scudder KM,
                                                      WPI: 2001-611727/70
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                                                                              N-PSDB; AAI66852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 893 AA;
                  Praestegaard M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fusion protein.
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The invention relates to determining, if a compound, is a dislocator of PDB4. The method comprises testing if the compound removes PDE4 spots, which may optionally be induced by a Roliptram-like reference compound, and testing if it inhibite the catalytic activity of the PDB4, where the compound is a dislocator of PDB4, if it removes PDE spots and if it does not inhibit the catalytic activity of PDB4. The method is useful for identifying compounds useful for the treatment of diseases of the central nervous system such as identifying compounds useful for the treatment of inflammatory diseases such as joint inflammation, Crohn's disease, inflammatory bowel disease, respiratory diseases, chronic obstructive pulmonary disease (ODPD), including asthma, chronic bronchtis, pulmonary emphysema, endotoxis shock toxic shock syndrome, systemic lugue srthematosis, bone resorption diseases, reperfusion injury, cancer and HIV infection. The use of a reagent that can mimic or reverse the effect of the compound with affinity for the catalytic site on intracellular distribution of the PDE for the preparation of a medicament. The present sequence represents the amino acid sequence of a HSPDB4A4-E222G fusion
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                                                                                                                                                                                                                                                                                                                                   Determining if a compound is a dislocator of PDE4 for identifying compounds for treating CNS and inflammatory disease comprises identifying compounds which remove PDE4 spots.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         894 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPMPT 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVOLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1074 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LVTGLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MVSKGBELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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0
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                                                                                                                                                                                                    Bjorn SP, Thastrup O, Almholt DC;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 162-167; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE17517 standard; protein; 239 AA
                                          11-APR-2001; 2001WO-DK000264.
                                                                                      17-APR-2000; 2000DK-0000651.
29-MAY-2000; 2000DK-00000849.
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                                                                                                                                                                                                    Scudder KM,
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                                                                                                                                                     (BIOI-) BIOIMAGE AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 1132 AA;
                                                                                                                                                                                                                                                                                           N-PSDB; AAI66853
                                                                                                                                                                                                                         Praestegaard M;
                                                                                                                                                                                                    BR,
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AAE17517
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181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239 

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Novel fluorescent protein in in vitro assay for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution, has a green fluorescent protein with F64L and E222G
                                                                            /note= "Wild type Phe substituted with Leu, This corresponds to position 64 in the wild type protein"
Jellyfish; green fluorescent protein; GFP; protein redistribution; cellular function; genetic reporter; mutant; Stoke's shift; mutein.
                                                         Location/Qualifiers
                                                                                                                                                                                                                                       Thastrup 0;
                                                                                                                                                                                                                                                                                                                                      Example 1; Page 35; 41pp; English.
                                                                                                                                                                           20-JUN-2000; 2000US-021268IP.
10-MAY-2001; 2001DK-00000739.
10-MAY-2001; 2001US-0290170P.
                                                                                                                                               18-JUN-2001; 2001WO-EP006848
                                                                                                                                                                    19-JUN-2000; 2000DK-00000953
                                                                                                                                                                                                                                      Bjorn SP, Pagliaro L,
                                                                                                                                                                                                                                                         WPI; 2002-098224/13.
                                                                                                                                                                                                                    (BIOI-) BIOIMAGE AS
                              Aequoraa victoria.
                                                                                                                                                                                                                                                                    N-PSDB; AAD28162
                                                                    Misc-difference
                                                                                                           WO200198338-A2
                                                                                                                              27-DEC-2001
                                         Synthetic.
                                                                                                                                                                                                                                                                                                                    mutation.
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The invention relates to a fluorescent protein derived from green fluorescent protein (GFP) or its analogue. The GFP containing mutations at F64L and E222G has a bigger compared to other GFP's making it very suitable for high throughput screening due to better resolution. The fluorescent protein is useful in invitro assays for measuring protein redistribution. The fluorescent protein is useful in studying cellular functions in living cells; as protein tags in transganic animals, living and fixed cells; organelle tags, secretion marker and genetic reporter. The fluorescent protein is also useful as a cell or organelle integrity marker, a marker to be used in combination with fluorescence activated cell sating (FACS). The novel proteins can also be used as resporters to monitor live or dead biomass of organisms, such as fungi. The fluorescent protein is also useful as markers in transcriptional and translational contents of the protein is also useful as markers in transcriptional and as a reporter content or an experient content or and as a marker of the protein is also as a reporter or and as a reporter or and as a marker or and as a marker or or content or or organisms, such as fungi. The fluorescent fusions for performing transposon vector mutagenesis and as a reporter or an experient or and as a reporter. for bacterial detection. Transposons encoding the fluorescent protein are 61 LVTGLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120 9 9 useful for screening promoters and for tagging plasmids and chromosomes. The fluorescent protein engineered into the genome of a phage is useful 1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPMPT 1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT Gaps The fluorescent protein engineered into the genome of a phage is usef for designing diagnostic tool. The present sequence is enhanced F64L jellyfish green fluorescent protein (GFP) mutant ö Length 239; 2; Indels Score 1259; DB 5; Pred. No. 8.7e-122; 0; Mismatches 98.7%; 237; Conservative Query Match Best Local Similarity Sequence 239 AA; Matches d 원 ò

121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180

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The invention relates to systems, methods and reagents for cell-based screening or detection of compounds which affect particular biological functions. The methods of the invention utilise fluorescent biodetector molecules which, when acted on by a compound of interest, cause an allocate actions. The methods of the biosensors comprise hear shock proteins alteration in the cellular distribution of at least the fluorescent conject. In one embodiment, the biosensors comprise hear shock proteins (HSPB) fused to a fluorescent protein (e.g., jellyfish green fluorescent protein (e.g., jellyfish green fluorescent protein so a stress activation translocate to the nucleus. In the cytoplasm, but on stress activation translocate to the nucleus. In another embodiment biodetector proteins can be used to detect protease activity. Such protease biodetector fusion proteins comprise one or more fluorescent proteins a recognition signal which is cleaved by the protease, and at least one cellular logalisation signal which is acted upon by the protease, or may be from heferologous sources. Due to the components of a single protein which is acted upon by the protease of interest, the region of the cell. Once acted on by the protease of interest, the fluorescent protein is cleaved from the localisation signal attached to the fluorescent protein signal attached to the fluorescent protein signal attached to the fluorescent protein of the protease recognition sequence. The compartment after cleavage of the protease recognition sequence change in distribution of the fluorescent protein of the fluorescent protein of the methods and imaging methods with a high degree of spatial resolution. The methods and imaging methods with a high degree of spatial resolution.
                                                                                                                                                                                                          Biodetector protein; fusion protein; recognition site; cellular targetting sequence; cellular localisation; fluorescent protein; protease activity detection; toxin detection; cellular stress detection; drug discovery; cell based screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Automated cell-based characterization of toxin by contacting cells containing luminescent reporter molecules with test substance and analyzing optically.
                                                                                                                                                                        Enhanced green fluorescent protein (EGFP), SEQ ID NO:46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 11; Fig 29A; 336pp; English.
                                           Ā
                                           AAB22882 standard; protein; 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0122152P.
99US-0123399P.
99US-00352171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-2000; 2000WO-US004794.
                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-594086/56.
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                                                                                                                                                                                                                                                                                                                                  Aequorea victoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAA93373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-JUL-1999;
                                                                                                                                 10-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                            31-AUG-2000
                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                       AAB22882;
RESULT 6
                       AAB22882
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cellular activities and to screen compounds which modulate these example, may be used for the screening of compounds which modulate apoptosis, while biosensors containing a recognition site for caspase, for apoptosis, while biosensors containing other protease recognition sites may be used for the detection of proteolytic toxins (such as anthrax lethal factor). The method provides improved target validation and candidate compound optimisation by combining many cell screening formats with fluorescence-based molecular reagents and computer-based feature and speed of data analysis and automation, resulting in increased quantity and speed of data collection and faster evaluation of drug candidates. Sequences AAB22881-B22885 represent fluorescent proteins which may used as components of biosensor fusion proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LVTGLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFFGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                  VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                                                                                                                                                                                     DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
 biosensors of the invention can be used to investigate a wide range of
                                                                                                                                                                                                                                                                                                                    1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pluorescent protein; green fluorescent protein, emission intensity; fluorescence, pH detection; pH sensor; EGFP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of the mutant green fluorescent protein EGFP.
                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                     Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "wild type Phe substituted with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "wild type Ser substituted with Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "wild type His substituted with Leu"
                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                    Score 1256; DB 3;
Pred. No. 1.8e-121;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY54349 standard; protein; 239 AA
                                                                                                                                                                                                                                                     98.5%;
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98US-00172063
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(UYOR-) UNIV OREGON STATE.
                                                                                                                                                                                                                                                                        Best Local Similarity 98.7
Matches 236; Conservative
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Misc-difference 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aequorea victoria.
                                                                                                                                                                                                                        Sequence 239 AA;
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                                                                                                                                                        protein based on the Aguarea green fluorescent protein (GFP). The emission intensity changes as pH varies between 5 and 10 of the present protein are novel. The functional engineered fluorescent proteins show reversable changes in fluorescence over physiological pH ranges. They can be used for determining the pH of samples and cells. The polynucleotides can also be used to praduce transgent enimals. The fluorescent protein pH sensors can be delivered to cells in the form of polynucleotides encoding the protein sensor fused to a targeting signal. The targeting signal directs the expression of the protein sensors to restricted cell locations. This makes it possible to measure the pH of a precisely defined cellular region or organelle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWVLGFVTAAGITLGMDELYK 239
                                                                     New functional engineered green fluorescent proteins, used for measuring the pH in biological samples and cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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                                                                                                                                             sequence represents a functional engineered fluorescent
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                                                                                                                                                                                                                                                                                                                                                                         Length 239;
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                                                                                                                                                                                                                                                                                                                                                                       98.5%; Score 1256; DB 3;
98.7%; Pred. No. 1.8e-121;
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                                                                                                                  Disclosure; Page 9; 89pp; English
Wachter RM;
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Llopis J,
                          WPI; 2000-116540/10.
N-PSDB; AAZ45642.
                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                           Sequence 239 AA;
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26-MAY-1999;
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Tsien RY,
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The present sequence is that of the EGFP signal domain, which can be included in novel recombinant protease biosensors (PBS) of the invention. The PBS (see AAY79638-54) comprise: a first domain (see AAY79679-87) comprising at least 1 detectable polypepticd signal such as the present sequence; a second domain (see AAY79688-622) comprising at least 1. See AAY79688-622 comprising at least 1. Comprising at least 1 reactant target sequence. A recombinant nucleic comprising at least 1 reactant target sequence. A recombinant nucleic acid (see AAA27627-43) encoding the PB, an expression vector, and a computing the reactant target sequence. A recombinant nucleic acid sentifying compounds that modify protease activity in a cell involves contacting a host cell that possesses the recombinant PB with a test compound, and determining the PB distribution in the host cell, where contacts in the distribution of the PB are correlated with modification of protease activity by the test compound. Claimed kits for identifying compounds that modify protease activity in a host cell include the protease activity by the test compound. Claimed kits for identifying compounds that modify protease activity in a host cell include the crecombinant nucleic acid, or the recombinant screens to detect in vivo activation of enzymatic activity, and to identify specific activity based on cleavage of a known recognition motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LVTGLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant nucleic acid encoding a protease biosensor useful for fluorescence based cell and molecular biochemical assays for drug discovery comprising three operably linked nucleic acid sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.5%; Score 1256; DB 3; Length 239; 98.7%; Pred. No. 1.8e-121; ive 1; Mismatches 2; Indels (
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                                                                                                                                                                        Claim 14; Fig 29A; 218pp; English
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                                        N-PSDB; AAA27573
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The present sequence is a fluorescnet protein used in the construction of a fluorescent protein indicator. The indicator comprises a sensor polypeptide that is responsive to a chemical, biological, electrical or physiological parameter, and a fluorescence protein functional group. The sensor polypeptide is operatively inserted into the fluorescent moiety. The fluorescent indicator is useful for detecting the presence of a response inducing member in a sample. The method involves contacting the sample with the indicator and detecting a change in fluorescence, in which a change is indicative of the effect of the parameter on the sensor polypeptide. The novel fluorescent proteins are advantageous due to their reduced size as compared to the FRET (fluorescence resonance energy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LVTGLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                                                  Novel fluorescent proteins comprising a sensor protein inserted into them, useful for measuring the response of a sensor biological, chemical, electrical or physiological parameter in vivo or in vitro.
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Pred. No. 1.8e-121;
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17-MAY-2000; 2000WO-US013684
                               99US-00316919
99US-00316920
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Best Local Similarity 98.7%;
Matches 236; Conservative
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                                                                                 (REGC ) UNIV CALIFORNIA
                                                                                                                    Tsien RY, Baird GA;
                                                                                                                                                    2001-032017/04
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                                                                                                                                                                     N-PSDB; AAC90488.
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                                 21-MAY-1999;
21-MAY-1999;
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                                                                                                                                                                                                         The invention provides melanin concentrating hormone (MCH) receptor (MCHR) chimeric and fusion proteins. The MCHR chimeric proteins comprise MCHR polypeptide regions from different species. The MCHR fusion protein comprise MCHR polypeptide region and a fluorescent polypeptide region and protein goined directly, or via a linker, to the carboxy side of the MCHR polypeptide region. The MCHR fusion proteins can be expressed by standard recombinant methodology. MCH action promotes feeding (orexigenic) and up regulation of MCH activity stimulates food intake. The present sequence represents a A. victoria green fluorescent protein (GFP) and a linker
                                                                                                                                                                                                                                                                                                                                                                                                                                              LVTGLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                           Fusion proteins comprising melanin concentrating hormone receptor peptides and fluorescent proteins, useful for identifying appetite
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1; Mismatches 2;
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                                                                                                                                                                                      Claim 2; Page 14; 71pp; English.
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                    14-MAR-2001; 2001WO-US008071.
                                          15-MAR-2000; 2000US-0189698P.
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                                                               (MERI ) MERCK & CO INC
                                                                                                          WPI; 2001-565791/63
                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aequorea victoria.
                                                                                                                       N-PSDB; AAH47304
                                                                                                                                                                                                                                                                                                                                  Sequence 239 AA;
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20-SEP-2001
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                                                                                                                                                               stimulants.
                                                                                      Marsh DJ;
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The specification describes a method for assessing the growth rate and death rate of a micro-organism within a predetermined time period in a desired environment. The method comprises introducing at least two reporter genes encoding luminescent and/or fluorescent products into the micro-organisms, incubating the micro-organism within the desired environment, and detecting luminescence and/or fluorescence after a predetermined time period. Use of two different markers within a micro-organism enables the differentiation between growth and death rates. The method is used to assess the growth rate and death rate of a micro-organism within a predetermined time period in a desired environment. The present sequence represents a green fluorescent protein (GFP), and is encoded by a plasmid which encodes luminescent and fluorescent proteins, and is used in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.5%; Score 1256; DB 4; Length 239; 98.7%; Pred. No. 1.8e-121; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A. victoria green fluorescent protein (EGFP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 27; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ā
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99FI-00001296
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Matches 236; Conservative
                                                                                                                                                                                                                             WPI; 2001-061737/07
                                                                                                                                                            Lilius E, Virta M;
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                                                                (LILI/) LILIUS E.
                                                                                               VIRTA M.
                                                                                                                                                                                                                                                               N-PSDB; AAC86954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 239 AA;
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07-JUN-1999;
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99US-00398965.
                                                                Kapur R;
                                                                                  2002-634730/68.
                                    GIULIANO K.
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                                                                                                                                                                                                                                                                                                                         screening system
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                                                                                            N-PSDB; ABS71491
       29-OCT-1999;
01-DEC-1999;
17-SEP-1999;
                                                                Giuliano K,
                                                                                                                                          identifiers
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                                              KAPU/)
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                                                                                                                                                                                                                                                                                                       LVTGLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                  The invention relates to a gene encoding proteins having cyan-green fluorescence characteristic and having a function of showing stable fluorescence characteristic in acid region. A method for the preparation of a cyan-green fluorescent protein is provided which involves a transformant transformed by a recombinant vector comprising the gene, where the transformant is cultured and the protein is collected from the culture. The present sequence represents the A. victoria green fluorescent protein (BGFP)
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                                                                                                                                                                                                                                                                                                                                                                                           Detection, classification, identification, toxin detection, protease, ADP-ribosylating toxin, cytotoxic phospholipase, exfoliative toxin, toxic threat agent.
                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                             Length 239;
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                                                                                                                                                                                                                             Score 1256; DB 5;
Pred. No. 1.8e-121;
1; Mismatches 2;
                                                                                   gene encoding cyan-green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protease biosensor signal sequence #6
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                                                                                                         Example; Page 14; 20pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-00810983.
98US-00031271.
99US-0123152P.
99US-0133399P.
99US-00352171.
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 04-AUG-2000; 2000JP-00237165
                    04-AUG-2000; 2000JP-00237165
                                      (RIKA ) RIKAGAKU KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                      Best Local Similarity 98. Matches 236; Conservative
                                                          WPI; 2002-299190/34
                                                                    N-PSDB; ABL40628
                                                                                                                                                                                                              Sequence 239 AA;
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12-JUL-1999;
31-AUG-1999;
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The invention describes methods of automated detection, classification and identification comprising treating cells containing luminescent reporter molecules (I) in array of locations with a test substance, where (C) are detectors, classifiers or identifiers, imaging cells in each clocation to obtain luminescent signals and converting optical information control digital data to interpret presence of toxins in the test substance. The method are useful for detection of toxins chosen from proteases, ADP-cribosylating toxins, cytocoxic phospholipases, and exfoliative toxins. Three classes of cell-based luminescent reporter molecules such as detectors, classifiers and identifiers are described and serve as creporters of toxic threat agents. The first two levels of characterisation ensure a rapid readout of toxin class without sacrificing the ability to detect many new mutant toxins or dissect several complex mixtures of known toxins. This is the amino acid sequence of a protease biosensor related signal sequence used in the cell-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
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                                                                                                                                                                                                                                                                                                                                                                                Automated cell-based toxin detection, classification, and/or identification by treating cells involves use of three classes of luminescent reporter molecules such as detectors, classifiers or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 10; Fig 29A; 214pp; English
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99US-00430656.
99US-0168408P.
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Matches 236; Conservative
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method for mutagenesis that comprises synthesising a mutated strand and a complementary strand by use of synthesising a mutated strand and a complementary strand by use of megaprimers. The method basically comprises a DNA synthesis in which one or more primers that have a nucleotide sequence containing at least one and then subjected to an elongation reaction using a thermostable bush. It idelity DNA polymerase, after which the phosphorylated 5'-terminus and the elongated terminus are ligated by means of a thermostable DNA ligase the step of DNA synthesis is repeated several times to amplify the DNA containing the primers; a digestion in which the step of DNA synthesis is repeated several fragments of amplify the DNA containing the primers and then, at least DNAs other than the amplified circular DNA are digested into several fragments obtained in the step of digestion as megaprimers, the megaprimers are annealed to the circular DNA synthesised above, followed by an elongation reaction performed using the thermostable high-fidelity DNA polymerase. The method is useful for mutagenesis, particularly for introducing certain mutations at certain sites of the nucleotide sequence. The present method is simple, speedy, economical and widely applicable. The present method is simple, a pepedy, economical and widely applicable. The present sequence is Aequorea victoria enhanced green fluorescent protein (GFP) sequence of Aequorea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Method for mutagenesis, e.g. for introducing certain or random mutations at certain sites of the nucleotide sequence, comprises synthesizing a mutated strand and a complementary strand by use of megaprimers.
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'note= "Wild-type GFP Met-Ser are replaced with Met-Val-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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                                                                                  'note= "GFP Phe64 is replaced by Leu"
                                                                                                              by Thr"
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ilarity 98.7%; Pred. No. 1.8e-121;
Conservative 1; Mismatches 2;
                                                                                                              /note= "GFP Ser65 is replaced
                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 13-14; 31pp; English.
              Location/Qualifiers
                                                                                                                                                                                                                           04-AUG-2000; 2000JP-00237166.
                                                                                                                                                                                               03-AUG-2001; 2001EP-00306650.
                                                                                                                                                                                                                                                                                  Miyawaki A, Sawano A;
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                                                                                              Misc-difference 66
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comprising a phosphorylation bolypeptide and a fluorescent protein or in operative linkage, a donor molecule, a phosphorylatable domain, a phosphorylation binding domain (PAABD) and an acceptor molecule. The phosphorylation indicators of the invention are useful for detecting kinases or phosphatases in a biological sample. They are also useful in high throughput analysis e.g. for detecting a kinase inhibitor or phosphatase inhibitor. The present sequence is Aequorea victoria enhanced green fluorescent protein (EGFP) used in the invention
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                                                                                                                                                                                                                                                                                                                                                                                                              Aequorea victoria enhanced green fluorescent protein (EGFP).
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131 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 239

Search completed: June 21, 2004, 15:54:08 Job time : 50.1111 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.
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61 LVTGLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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APPLICANT Myawaki, Ateushi
APPLICANT Lidpis, Juan
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APPLICANT Lidpis, Juan
APPLICANT Remington, S. James
TITLE OF INVENTION FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION MASSURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/071001
CURRENT APPLICATION NUMBER: US/09/172,063
CURRENT FILING DATE: 1998-10-13
EARLIER APPLICATION NUMBER: 09/094,359
EARLIER FILING DATE: 1998-06-09
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Pred. No. 1.1e-127;
1; Mismatches 2;
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US-09-417-197-71
US-09-417-197-119
US-09-513-783A-176
US-09-513-783A-176
US-09-417-197-141
US-09-417-197-179
US-09-513-783A-178
US-09-513-783A-178
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US-09-417-197-119
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US-09-417-197-43
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
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Best Local Similarity 98.7%;
Matches 236; Conservative
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ORGANISM: Aequorea victoria
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OTHER INFORMATION: EGFP
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US-09-513-783A-46
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Pred. No. 1.1e-127;
1; Mismatches 2; Indels
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                                                  | Patent No. 6416959 |
| Patent No. 6416959 |
| GENERAL INFORMATION: |
| APPLICANT: Giuliano, Kenneth A. |
| APPLICANT: Giuliano, Kenneth A. |
| TILLE OF INVENTION: A System for Cell Based Screening |
| TILLE REFERENCE: 97-022-L1 |
| CURRENT APPLICATION NUMBER: US/09/513,783A |
| CURRENT APPLICATION NUMBER: US/09/513,783A |
| CURRENT APPLICATION OF SEQ ID NOS: 180 |
| SOFTWARE: Patentin Ver. 2.0 |
| SEQ ID NO 46 |
| LENGTH: 239
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; Sequence 4. Application US/09316919
; Patent No. 6469154
; GENERAL INFORMITION:
; APPLICANT: Taien, Roger Y.
; APPLICANT: Baird, Geoffrey
; TITLE OF INVENTION: FULORESCENT PROTEIN INDICATORS
; FILE REFERENCE: 07257/073001
; CURRENT APPLICATION NUMBER: US/09/316,919
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FASTSEQ for Windows Version 4.0
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98.7%; Pred. No. 1.1e-127;
iive 1; Mismatches 2;
RESULT 2
US-09-513-783A-46
; Sequence 46, Application US/09513783A
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Best Local Similarity 98.7%;
Matches 236; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity 98.7
Matches 236; Conservative
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VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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APPLICANT: Miyawaki, Atsushi
APPLICANT: Miyawaki, Atsushi
APPLICANT: Miyawaki, Atsushi
APPLICANT: Lippis, Juan
APPLICANT: Remington, S. James
TITLE OF INVENTION: FLUCRESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: FLUCRESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/071001
CURRENT APPLICATION NUMBER: US/09/602,641
CURRENT APPLICATION NUMBER: 09/172,063
PRIOR PILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FASSESQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 239
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Pred. No. 1.1e-127;
1; Mismatches 2;
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                                                                                                                                                                                                                                                     Sequence 3, Application US/09602641
Patent No. 6608189
GENERAL INFORMATION:
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Best Local Similarity 98.73
Matches 236; Conservative
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GENERAL INFORMATION:
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Patent No. 6130313

GENERAL INFORMATION:

APPLICANT: Kain, Steve

APPLICANT: Li, Xiangiang

TITLE OF INVENTION: Rapidly Degrading GFP-Fusion Proteins and Methods

TITLE OF INVENTION: of Use

FILE REFERENCE: D6100

CURRENT APPLICATION NUMBER: US/09/062,102

CURRENT FILING DATE: 1999-04-17

EARLIER FILING DATE: 1997-10-02
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                                                                                                                                            Query Match
98.5%; Score 1256; DB 4; Length 239;
Best Local Similarity 98.7%; Pred. No. 1.1e-127;
Matches 236; Conservative 1; Mismatches 2; Indels
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98.7%; Pred. No. 1.4e-127;
live 1; Mismatches 2;
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2 LENGTH: 239
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                                                                                  ORGANISM: Aequorea victoria
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Best Local Similarity
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US-09-062-102-1
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                                                             TYPE: PRT
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APPLICANT: Li, Xianqiang
TITLE OF INVENTION: Rapidly Degrading GFP-Fusion Proteins and Methods
TITLE OF INVENTION: 6f use
File Reference: D6100C1P/D2
CURRENT APPLICATION NUMBER: US/09/364,946
CURRENT FILING DATE: 1999-07-30
EARLIER RFLING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Sequence of the EGFP-MODC422-461 fusion protein.; Patent No. 6306600
US-09-364-946-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1256; DB 4;
Pred. No. 1.4e-127;
1; Mismatches 2;
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Patent No. 6416959
GENERAL INFORMATION:
APPLICANT: Giuliano, Kenneth A.
APPLICANT: Kapur, Ravi
TITLE OF INVENTION: A System for Cell Based Scri
FILE REFERENCE: 97-022-L1
CURRENT APPLICATION NUMBER: US/09/513,783A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 180
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 294
Sequence 1, Application US/09364946
Patent No. 6306600
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ORGANISM: Artificial Sequence
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Best Local Similarity 98.7°
Matches 236; Conservative
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                                                   51 LVTGLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL
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| APPLICANT: INCOMENTATION:
| APPLICANT: INCOMENTATION:
| APPLICANT: Incomentation: Juan
| APPLICANT: Machter, Rebeeka M.
| APPLICANT: Wachter, Rebeeka M.
| APPLICANT: Remington, S. James
| TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
| TITLE OF INVENTION: MESSIGNING THE PH OF A BIOLOGICAL SAMPLE
| TITLE OF INVENTION: MESSIGNING THE PH OF A BIOLOGICAL SAMPLE
| FILE REFERENCE: 07257/071001
| CURRENT FILING DATE: 1998-10-13
| EARLIER FILING DATE: 1998-10-13
| EARLIER FILING DATE: 1998-06-09
| NUMBER OF SEQ ID NOS: 38
| SOFTWARE: PASSIGN FOR WINDOWS VERSION 4.0
| SEQ ID NO: 21
| LENGTH: 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.5%; Score 1256; DB 3; Length 323; 98.7%; Pred. No. 1.7e-127;
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ORGANISM: Aeguorea victoria
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; OTHER INFORMATION: GT-EGFP
US-09-172-063-21
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Best Local Similarity 98.7
Matches 236; Conservative
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Sequence 21, Application US/09602641; Patent No. 6608189; GENERAL INFORMATION:

US-09-602-641-21

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APPLICANT: Tsien, Roger Y. APPLICANT: Miyawaki, Atsushi APPLICANT: Llopis, Juan

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us-09-085-305-6
; Sequence 6, Application US/09085305
; Sequence 6, Application US/09085305
; Patent No. 6191269
; GENERAL INFORMATION:
    APPLICANT: Lovett, David H.
    APPLICANT: Lovett, David H.
    APPLICANT: Turck, Johanna
    TITLE OF INVENTION: Selective Induction of Apoptosis in
    TITLE OF INVENTION: Malignant Cancer Cells by Delivery of N-Terminal
    TITLE OF INVENTION: Malignant Cancer Cells by Delivery of N-Terminal
    TITLE OF INVENTION: Malignant Cancer Cells by Delivery of N-Terminal
    TITLE OF INVENTION: Malignant Cancer Cells by Delivery of N-Terminal
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    TITLE OF INVENTION: Malignant Cancer Cells by Delivery of N-Terminal
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APPLICANT: Wachter, Rebekka M.
APPLICANT: Remington, S. James
TITLE OF INVENTION: FLUCRESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/071001
CURRENT APPLICATION NUMBER: US/09/602,641
CURRENT FILING DATE: 2000-06-22
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 98.5%; Score 1256; DB 4; Length 323; Best Local Similarity 98.7%; Pred. No. 1.7e-127; Matches 236; Conservative 1; Mismatches 2; Indels
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ZIF: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: SYSTEM: DOS
CONFURER: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATE: US/09/085,305
APPLICATION NUMBER: US/09/085,305
"TING DATE: 29-MAY-1998
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ORGANISM: Aequorea victoria
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: VARIANT
; LOCATION: (0) ...(0)
OTHER INFORMATION: GT-EGFP
US-09-602-641-21
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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Sequence 127, Application US/09417197

Retent No. 6518021

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF THASTRUP, et al.
TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An Intile OF INVENTION: On A Cellular Response
TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An Intile OF INVENTION: On A Cellular Response
CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patentin version 3.0
SEQ ID NO 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           316 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 375
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                                                         181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
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                        181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
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                                                                                                                                                                                      Sequence 48, Application US/09800170; Sequence 48, Application US/09800170; Patent No. 6481667; GENERAL INFORMATION:
APPLICANIT KINSELLA, Todd
TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES; FILE REFERENCE: A-68614-1/DJB/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/800,170; CURRENT FILING DATE: 2001-08-28; PRIOR APPLICATION NUMBER: US 60/187,130; PRIOR FILING DATE: 2000-03-06; NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin version 3.1
SEQ ID NO 48
LENTH: 434
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98.7%; Pred. No. 2.8e-127;
tive 1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Synechocystis PCC6803
US-09-800-170-48
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ORGANISM: Artificial Sequence
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Best Local Similarity 98.74
Matches 236; Conservative
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                                                                                                                                                     RESULT 13
US-09-800-170-48
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APPLICANT: O1e THASTRUP, et al.
TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An TITLE OF INVENTION: On A Cellular Response
FILE REFERENCE: 3759-0110P
CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 305
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                                                                                                                                                                                                                                                                                                                                                                                                                     Length 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
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Pred. No. 2.1e-127;
1; Mismatches 2;
                                                                         6510/102US1
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Patent No. 6518021
                     NAME: Francis, Carol L
REGISTRATION NUMBER: 36,513
REFRENCE/DOCKET NUMBER: 6510
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
TELEFAX: 650-327-331
                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: amino acid
STRANDEDNESS: single
JOPOLOGY: linear
US-09-085-305-6
                                                                                                                                                                                                                                                                                                                                                                                                                     98.5%;
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ORGANISM: Artificial Sequence
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 98.7
Matches 236; Conservative
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US-09-417-197-129
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LENGTH: 379
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                                                              VNRIELKGIDPKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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Best Local Similarity 98.7%; Pred. No. 2.9e-127;
Matches 236; Conservative 1; Mismatches 2; Indels
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| Sequence 170, Application US/09513783A |
| Sequence 170, Application US/09513783A |
| Sequence 170, Application US/09513783A |
| GENERAL INFORMATION: |
| APPLICANT: Giuliano, Kenneth A. |
| TITLE OF INVENTION: Ravi Ravi TITLE OF INVENTION: |
| FILE REFREENCE: 97-022-11 |
| CURRENT FILING DATE: 2000-02-25 |
| NUMBER OF SEQ ID NOS: 180 |
| SEQ ID NO: 170 |
| SEQ ID NO: 170 |
| LENGTH: 459 |
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Sequence 4, Application US/09887784
Facent No. US20020177189A1
GENERAL INFORMATION:
APPLICANT: BJOORN, Sara et al
TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS
FILE REFERENCE: 3759-01159
CURRENT APPLICATION NUMBER: US/09/887,784
CURRENT FILING DATE: 2001-06-19
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
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ORGANISM: Aequoria Victoria
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1 MVSKGEELFTGVVPILVELD......VLLGFVTAAGITLGMDELYK
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Seguence 4. Appli	Sequence 4, Appli	Sequence 6, Appli	Sequence 30, Appl	Sequence 32, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 3, Appli	Sequence 13, Appl
SUMMARIES ID	US-09-887-784-4	US-10-296-953-4	4 US-10-270-223-6	US-10-257-909A-30	US-10-257-909A-32	US-09-887-784-2	US-10-296-953-2	US-09-920-922-2	US-09-999-745-4	US-09-866-538-4	US-09-797-496B-2	US-09-794-308-4	US-09-865-291-4	US-10-457-982-3	US-10-121-258-13
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* Query Match	99.4	99.4	99.4	99.4	99.4	98.7	98.7	98.5	98.5	98.5	98.5	98.5	98.5	98.5	98.5
Score	1267	1267	1267	1267	1267	1259	1259	1256	1256	1256	1256	1256	1256	1256	1256
Result No.	1	8	m	4	2	9	7	œ	6	10	11	12	13	14	15

Sequence 7, Appli Sequence 46, Appl Sequence 2, Appli Sequence 3, Appli Sequence 4, Appli	equence 1 equence 3 equence 3 equence 3 equence 3 equence 2 equence 2 equence 2 equence 3	28,000	equence 1 equence 1 equence 1 equence 1 equence 5 equence 5	equence 3, equence 9, equence 3, equence 33,
US-10-221-461-7 US-10-100-957A-46 US-10-177-390-2 US-10-338-411-3 US-10-370-570-4 US-10-389-640-3	10-314-861- 10-314-861- 10-314-861- 10-314-861- 10-100-9578- 10-314-861-	-10-314-861-3 -10-314-861-3 -10-033-717-3 -10-314-861-2 -10-314-861-2 -10-389-411-1	-10-338-411- -10-338-411- -10-389-640- -10-389-640- -10-314-861- -10-318-411-	0-388-611- 0-338-411- 0-389-640- 0-033-717-
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                                                                                          1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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                              Length 239;
                                                             Indels
                             Query Match 99.4%; Score 1267; DB 9;
Best Local Similarity 99.6%; Pred. No. 1.1e-123;
Matches 238; Conservative 0; Mismatches 1;
US-09-887-784-4
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Sequence 30, Application US/10257909A

Publication No. US20030187056A1

Publication No. US20030187056A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Live cell procedures to identify compounds modulating intracellularity of INVENTION: distribution of phosphodiesterase (PDE) enzymes
TITLE OF INVENTION: distribution of phosphodiesterase (PDE) enzymes
TITLE OF INVENTION: 20125P
CURRENT APPLICATION NUMBER: US/10/257,909A
CURRENT FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 30
LENGTH: 893
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                                                                              181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNBKRDHMVLLGFVTAAGITLGMDELYK 239
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                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 99.4%; Score 1267; DB 14; Best Local Similarity 99.6%; Pred. No. 7e-123; Matches 238; Conservative 0; Mismatches 1;
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US-10-257-909A-32
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99.4%; Score 1267; DB 14;
Best Local Similarity 99.6%; Pred. No. 1.9e-123;
Matches 238; Conservative 0; Mismatches 1;
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99.6%; Pred. No. 1.1e-123;
tive 0; Mismatches 1;
                                                                                   APPLICANT: BJORN, SARA P.
APPLICANT: BJORN, SARA P.
APPLICANT: BJORN, LEN
APPLICANT: BJORN, LEN
APPLICANT: PAGLIARO, LEN
APPLICANT: THASTRUP, OLE
TITLE GOT INVENTION: NOVEL FLUORESCENT PROTEINS
FILE REFRENCE: PL0095
CURRENT APPLICATION NUMBER: US/10/296,953
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: PA 2000 00953
PRIOR APPLICATION NUMBER: 60/212,681
PRIOR APPLICATION NUMBER: 60/290,170
PRIOR FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: 60/290,170
PRIOR APPLICATION NUMBER: 2001-05-10
PRIOR PILING DATE: 2001-05-10
NUMBER: CF SEQ ID NOS: 24
SOFTWARE: PATENTIN VOY: 2.1
                                          ; Sequence 4, Application US/10296953; Publication No. US20040072995A1; GENERAL INFORMATION:
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US-10-296-953-4
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Best Local Similarity
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APPLICANT: BJORN, SARA P.
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                                                                                             ; OTHER INFORMATION: Fusion between Aequorea victoria and human US-10-257-909A-32
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Pred. No. 7.2e-123;
0; Mismatches 2; Indels
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Pred. No. 9.8e-123;
0; Mismatches 1;
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Fatent No. US20020177189A1
GENERAL INFORMATION:
GENERAL INFORMATION:
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GENERAL INFORMATION:
FILE REFERENCE: 3759-0115P
CURRENT APPLICATION NUMBER: US/09/887,784
CURRENT FILING DATE: 2001-06-19
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 239
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Best Local Similarity 99.6%;
Matches 238; Conservative (
                                       TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 99.2%;
Matches 237; Conservative
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US-09-887-784-2
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US-09-887-784-2
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SEQ ID NO 32
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Pred. No. 7.2e-123;
0; Mismatches 2;
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Best Local Similarity 98.7%; Pred. No. 1.5e-122;
Matches 236; Conservative 1; Mismatches 2;
APPLICANT: BACLARO, LEN
APPLICANT: PAGLIRAC, LEN
APPLICANT: THASTRUD, OLE
ITTLE OF INVENTION: NOVEL FLUORESCENT PROTEINS
FILE REFERENCE: PLOO95
CURRENT APPLICATION NUMBER: US/10/296,953
CURRENT FILING DATE: 2002-11-26
CURRENT FILING DATE: 2000-06-19
PRIOR PELICATION NUMBER: 60/212,681
PRIOR APPLICATION NUMBER: 60/212,681
PRIOR APPLICATION NUMBER: 60/290,170
PRIOR PILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-10
PRIOR FILING DATE: 2001-05-10
PRIOR FILING DATE: 2001-05-10
PRIOR FILING DATE: 2001-05-10
NUMBER: PAPLICATION NUMBER: PA 2001 00739
PRIOR FILING DATE: 2001-05-10
NUMBER: PAPLICATION NUMBER: PA 2001 0739
PRIOR FILING DATE: 2001-05-10
NUMBER: PAPLICATION NUMBER: PA 2001 0739
PRIOR FILING DATE: 2001-05-10
NUMBER: PAPLICATION NUMBER: PA 2001 0739
PRIOR FILING DATE: 2001-05-10
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PRIOR FILING DATE: 2001-05-10
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PRIOR FILING DATE: 2001-05-10
NUMBER: PAPLICATION NUMBER: PA 2001 0739
PRIOR FILING DATE: 2001-05-10
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Patent No. US2002083488A1
GENERAL INFORMATION:
APPLICANT: Miyawaki, Atsushi
APPLICANT: Sawano, Asako
TITLE OF INVENTION: METHOD FOR MUTAGENESIS
FILE REFRENCE: 11283-012001
CURRENT APPLICATION NUMBER: US/09/920,922
CURRENT FILING DATE: 2001-08-02
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PRIOR APPLICATION NUMBER: JP 2000-237166
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 239
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Best Local Similarity 99.2%;
Matches 237; Conservative
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US-10-296-953-2
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US-09-920-922-2
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                                                                                                                                                                                                                     Sequence 4, Application US/0999745
; Sequence 4, Application US/0999745
; Patent Nc. US20020157120A1
; GENERAL INFORMATION:
    APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: Taien, Roger Y.
; APPLICANT: Baird, Geoffrey Y.
; APPLICANT: Baird, Geoffrey Y.
; TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
; FILE REFERENCE: REGENIA 70-1
; CURRENT APPLICATION NUMBER: US/09/999, 745
; FILE REPLICATION NUMBER: 09/316, 920
; PRIOR AFPLICATION NUMBER: 09/316, 920
; PRIOR FILING DATE: 1999-05-21
; NUMBER CF SEQ ID NOS: 67
; SOFTWARE: Patentin version 3.0
; SEQ ID NO, 4
LENGTH: 239
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                                                                              DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
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LVTGLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL
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Sequence 4, Application US/09866538

Publication No. US20030032088A1

GENERAL INFORMATION:
APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TELEN, ROSET

APPLICANT: Campbell, Robert

TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
FILE REFERENCE: REGENTS30-2

CURRENT APPLICATION NUMBER: US/09/866,538

CURRENT FILING DATE: 2001-05-24

NUMBER JF SEQ ID NOS: 29

SOGTWARE: PATEURIN VETSION 3.0
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Pred, No. 1.5e-122;
1; Mismatches 2;
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98.7%;
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ORGANISM: Aequorea victoria
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Best Local Similarity 98.7
Matches 236; Conservative
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LENGTH: 239
TYPE: PRT
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US-09-999-745-4
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US-09-999-745-4
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ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Aequorea victoria green fluorescent protein modified as described OTHER INFORMATION: in specification US-09-797-496B-2
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; Sequence 2, Application US/09797496B
; Publication No. US20030049597A1
; GENERAL INFORMATION:
; APPLICANT: Sinon, Sanford M.
; TITLE OF INVENTION: Chimeric Fluorescent Enzymes and Uses Thereof
; TITLE OF INVENTION: Chimeric Fluorescent Enzymes and Uses Thereof
; TILE REFERENCE: 600-1-267
; CURRENT FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 239
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; Sequence 10, US20030170911A1
; GENERAL INFORMATION:
; APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
98.5%; Score 1256; DB 10;
Best Local Similarity 98.7%; Pred. No. 1.5e-122;
Matches 236; Conservative 1; Mismatches 2;
                                                    Score 1256; DB 10;
Pred. No. 1.5e-122;
1; Mismatches 2;
                                                    98.5%;
Best Local Similarity 98.7%;
Matches 236; Conservative
, ORGANISM: Aequorea victoria
US-09-866-538-4
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US-09-797-496B-2
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US-09-794-308-4
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Publication No. US20030186229A1
CBUERAL INFORMATION:
APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TSIEN, ROGET
APPLICANT: TING, Alice
APPLICANT: TING, Alice
APPLICANT: TING, SICO
APPLICANTION: EMISSION RATIOMETRIC INDICATORS OF PHOSPHORYLATION
FILE REFERENCE: REGENISSO
CURRENT APPLICATION NUMBER: US/09/865,291
CURRENT APPLICATION NUMBER: 2001-05-24
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.0
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                APPLICANT: ZACHARIAS, David
APPLICANT: BAIRD, Geoffrey
TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
FILE REFERENCE: REGENIS30
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98.7%; Pred. No. 1.5e-122;
iive 1; Mismatches 2;
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Pred. No. 1.5e-122;
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                                                                                   CURRENT APPLICATION NUMBER: US/09/794,308
CURRENT FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 239
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98.7%;
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ORGANISM: Aequorea victoria
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US-09-794-308-4
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Best Local Similarity 98.7
Matches 236; Conservative
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TSIEN, Roger
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Best Local Similarity
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181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
                                    181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWVLLEFVTAAGITLGMDELXK 239
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FUBLICARIE US20030059835A1
GENERAL INFORMATION:
APPLICANT: Teien, Roger
APPLICANT: Campbell, Robert
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME
TITLE OF INVENTION: WONDER: US/10/121,258
CURRENT APPLICATION NUMBER: US/10/121,258
CURRENT FILING DATE: 2002-04-10
FRIOR APPLICATION NUMBER: 09/794,308
FRIOR APPLICATION NUMBER: 09/794,308
FRIOR APPLICATION NUMBER: 09/866,538
FRIOR PRING DATE: 2001-02-26
FRIOR PRING DATE: 2001-05-24
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APPLICANT: Myawaki, Asushi
APPLICANT: Miyawaki, Asushi
APPLICANT: Miyawaki, Juan
APPLICANT: Monter, Rebekka M.
APPLICANT: Remington, S. James
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MRASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 0725/7071001
CURRENT APPLICATION NUMBER: US/10/457,982
CURRENT FILING DATE: 2003-06-09
PRIOR PAPLICATION NUMBER: 09/172,063
PRIOR APPLICATION NUMBER: 09/172,063
PRIOR APPLICATION NUMBER: 09/172,063
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 38
SOFWWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 98.7%; Pred. No. 1.5e-122;
Matches 236; Conservative 1; Mismatches 2;
                                                                                                                                                                                                                 ; Sequence 3, Application US/10457982; Publication No. US20030212265A1; GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Aequorea victoria
                                                                                                                                                                                                                                                                                                                   APPLICANT: Tsien, Roger Y.
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OTHER INFORMATION: EGFP
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NAME/KEY: VARIANT
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US-10-457-982-3
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                                                                                                                               Query Match

98.5%; Score 1256; DB 14; Length 239;
Best Local Similarity 98.7%; Pred. No. 1.5e-122;
Matches 236; Conservative 1; Mismatches 2; Indels 0
, NUMBER OF SEQ ID NOS: 78

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13

LENGTH: 239

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Enhanced Green Fluorescent Protein (EGFP)
US-10-121-258-13
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Search completed: June 21, 2004, 16:09:25 Job time : 35.7778 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

June 21, 2004, 15:46:00; Search time 10.3333 Seconds (without alignments) 2224.817 Million cell updates/sec Run on:

US-09-887-784-64G

1275 1 MVSKGEBLFTGVVPILVELD......VLLGFVTAAGITLGMDELYK 239 BLOSUM62 Gapop 10.0 , Gapext 0.5 score: Scoring table: Sequence: Perfect

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	•
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
-	1234	96.8	238	-	JQ1514	green-fluorescent
7	106	8.3	785	0	H72228	hypothetical prote
m	92.5	7.3	797	N	JC4078	protective surface
4	92.5	7.3	808	~	F64102	protective surface
ß	92.5	7.3	941	~	S29043	cellulase (EC 3.2.
9	90.5	7.1	740	~	G95153	neuraminidase, pro
7	88.5	6.9	655	0	D83917	-ro
60	88.5	6.9	861	~	H64102	leucine-tRNA ligas
σ	87.5	6.9	370	~	E70390	iron-sulfur cofact
10	87.5	6.9	2518	7	AI2140	polyketide synthas
11	87.5	6.9	2573	~	D71614	hypothetical prote
12	87	6.8	752	Н	KXRTC1	proprotein convert
13	86.5	6.8	887	~	E82590	leucyl-tRNA synthe
14	86	6.7	357	N	G81355	tRNA (uracil-5-)-m
15	98	6.7	578	Н	140794	dihydrolipoamide d
16		6.7	217	~	S35324	expl protein - Brw
17	85.5	6.7	889	~	JC5576	inter-alpha-trypsi
18	82	6.7	281	~	AD2052	hypothetical prote
19	85	6.7	439	~	JH0414	synaptogamin 0-p65
20	84.5	9.9	613	~	A99552	oligoendopeptidase
21	84.5	9.9	788	Н	ЭДОЛГНН	DNA-directed DNA p
22	84.5	9.9	860	~	AC0582	leucyl-tRNA synthe
23	83.5	6.5	425	N	C97354	hypothetical prote
24	83.5		1134	~	A60234	IgA Fc receptor pr
25	83.5	6.5	1164	Н	FCSOAG	Fc receptor
56	83.5	6.5	1603	N	F89497	vit-5 [i
27		6.5	632	N	T06586	DNA-binding protei
28	83	6.5	782	7	S55094	probable membrane

coatomer complex a	imidazoleglycerol-	photosystem II chl	hypothetical prote	alpha-amylase homo	hypothetical prote	lipoxygenase (EC 1	water-stress-induc	synergohymenotropi	molybdenum formylm	vitellogenin vit-5	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	propionyl-CoA carb
ERHUAH	E84941	T06936	T27856	T39539	T42323	T11852	S53488	S68225	H69222	VJKWS	G86643	C64468	A75125	E75394	C72344
Т	7	7	7	7	7	7	7	7	7	7	~	N	~	~	7
1224	353	461	471	774	836	865	263	310	400	1603	1983	336	433	449	515
6.5	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4
82.5	82	82	82	82	82	82	81.5	81.5	81.5	81.5	81.5	81	81	81	81
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1	1514	

green-fluorescent protein [validated] - hydromedusa (Aequorea victoria) C;Species: Aequorea victoria

C;Species: Aequorea victoria C;Species: Aequorea victoria C;Date: 03-Dec-1999 #sequence revision 03-Dec-1999 #text_change 23-Mar-2001 C;Accession: 186692; JQ1514; PQ0335; S48693; S51330; S51331 R;Prasher, D.C.; Eckenrode, V.K.; Ward, W.W.; Prendergast, F.G.; Cormier, M.J. Gene 111, 229-233, 1992 A;Title: Primary structure of the Aequorea victoria green-fluorescent protein. A;Accession: JG0592 A;Molecule type: DNA A;Accession: JQ1514 A;Accession: PQ0335 A;Accession: PQ0335

A; Molecule type: protein
A; Residues: 46-64,74-122;132-151;154-183;185-200 <PRA3>
R; Inouve, S.; Tsuji, F.I.
FEBS Lett. 351, 211-214, 1994
A; Title: Evidence for redox forms of the Aequorea green fluorescent protein.
A; Reference number: 848693
A; Status: preliminary
A; Accession: 848693
A; Residues: 1-24,'Q',26-156,'P',158-171,'K',173-238 <INO>
A; Residues: 1-24,'Q',26-156,'P',158-171,'K',173-238 <INO>
A; Residues: 1-24,'Q',26-156,'P',158-171,'K',173-238 <INO>
A; Residues: 1-24,'Q',26-156,'P',158-171,'K',173-238 <INO>
A; Residues: 1-24,'Q',26-44,'N',46-153,'G',155-156,'P',158-171,'K',173-227,'R',;
A; Reference number: S51330
A; Reference number: S51330
A; Reference number: S51330
A; Residues: 1-13'',V',15-24,'Q',26-44,'N',46-153,'G',155-156,'P',158-171,'K',173-227,'R',;
A; Residues: 1-13'',V',15-24,'Q',26-44,'N',46-153,'G',155-156,'P',158-171,'K',173-227,'R',;
A; Residues: 1-13'',V',15-24,'Q',26-44,'N',A6-153,'G',155-156,'P',158-171,'K',173-227,'R',;
A; Residues: 1-13'',V',15-24,'Q',26-44,'N',A6-153,'G',155-156,'P',158-171,'K',173-227,'R',;
A; Residues: 1-13'',V',15-24,'Q',26-44,'N',A6-153,'G',155-156,'P',158-171,'K',173-227,'R',;
A; Residues: 1-13'',V',15-24,'Q',26-44,'N',A6-153,'G',155-156,'P',158-171,'K',173-227,'R',;
A; Residues: 1-13'',V',15-24,'Q',26-44,'N',A6-153,'G',155-156,'P',158-171,'K',173-227,'R',A6-153,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A6-155,'A

A,Accession: S51331 A,Molecule type: mRNA A,Residues: 1-24,'Q',26-29,'R',31-83,'L',85-153,'G',155-156,'P',158-171,'K',173-208,'Q','A A,Cross-references: EMBL:X83960; NID:9634010; PIDN:CAA58790.1; PID:9634011

A Experimental source: clone gfp2 R; Yang, F; Moss, LG., Phillips Jr., G.N. submitted to the Brookhaven Protein Data Bank, August 1996 A; Reference number: A65692; PDB:1GFL

A)Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 'A',2-79,'R',81-99. A,Note: engineered sequence based on JQ1514, cloned and expressed in Escherichia coli R;Yang, F.; Moss, L.G.; Phillips Jr., G.N.
Nat. Biotechnol. 14, 1246-1251, 1996
A;Title: The molecular structure of green fluorescent protein.
A;Ritle: The molecular structure of green fluorescent protein.

DNA-directed DNA p

1 JDVLD

836

6.5

82.5

59

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Matches
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A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A/Title: Evidence number: A72200; MUID:99287316; PMID:10360571

A/Accession: H7228

A/Accession: H7228

A/Accession: DNA

A/Accession: DNA

A/Accession: DNA

A/Accession: BNA

A/Accessi
A;Contents: annotation; X-ray crystallography, 1.9 angstroms
C;Comment: This protein is excited by the photoprotein aequorin (see PIR:AQJENV) emittin
C;Comment: The chromophore of this protein is formed by modification of Ser-dehydro-Tyr-G;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: green-fluorescent protein
C;Superfamily: green-fluorescent protein
C;Keywords: chromoprotein; luminescence
F;65-67/Cross-link: 5-imidazolinone (Ser-Gly) #status experimental
F;66/Modified site: dehydrotyrosine (Tyr) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D.H.; Hickey
hardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein TM1624 - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: In-un-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: H72228
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic.
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
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llarity 20.2%; Pred. No. 0.75;
Conservative 33; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                  Score 1234; DB 1;
Pred. No. 6.4e-96;
4; Mismatches 4;
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Best Local Similarity 96.6%;
Matches 230; Conservative
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Matches 47; Conserv
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A.Variety: type b
C.Date: 30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 29-Sep-1999
C.Date: 30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 29-Sep-1999
C.Daccession: JC407B b
C.Daccession: JC407B consorter, S.; Chong, P.; Thomas, W.R.
Gene 156, 97-99, 1995
A.Title: The sequencing of the 80-kDa D15 protective surface antigen of Haemophilus influAncession: JC407B MUD:95255676; PMID:7737523
A.Reference number: JC707 *FLAA
A.Residues: 1-797 *FLAA
A.Residues: 1-797 *FLAA
A.Residues: T-797 *FL
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Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
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F.1-19/Domain: signal sequence #status predicted <SIG>
F.20-797/Product: protective surface antigen D-15 #status predicted
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12.3%; Pred. No. 10;
ve 30; Mismatches
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22.3%; Pred. No. 10;
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C;Superfamily: protective surface antigen D-15
C;Keywords: surface antigen
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Best Local Similarity 22.3
Matches 49; Conservative
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C;Accession: G95153
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heide on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, I snson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Tile: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MuID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                A,Cross-references: GB:AE005672; PIDN:AAK75424.1; PID:g14972808; GSPDB:GN00164; TIGR:SP48
A,Experimental source: strain TIGR4
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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and careference number: A83650; MUID:20512582; PMID:11058132
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A;Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB05859.1; GSPDB:GN001
A;Experimental source: strain C-125
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C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
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Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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21.9%; Pred. No. 17;
tive 37; Mismatches
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Matches 53; Conserv
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A; Residues: 1-740 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: S29043; PC4404 — R;Oxaki, K.; Shikata, S.; Kawai, S.; Okamoto, K. J. Shikata, S.; Kawai, S.; Ito, S.; Okamoto, K. J. Microbiol. 136, 1327-1334, 1990 A;Title: Molecular cloning and nucleotide sequence of a gene for alkaline cellulase from A;Reference number: S29043; MUID:91037937; PMID:2230718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:M27420; NID:g142664; PIDN:AAA22304.1; PID:g142665
R;Shirai, T.; Yamane, T.; Hidaka, T.; Kuyama, K.; Suzuki, A.; Ashida, T.; Ozaki, K.; Itc
B;Shirai, T.; Kamane, T.; Hidaka, T.; Kuyama, K.; Suzuki, A.; Ashida, T.; Ozaki, K.; Itc
A;Title: Crystallization and preliminary X-ray analysis of a truncated family A alkaline
A;Reference number: PC4404; MUID:98060488; PMID:9399567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Pathway: celluiose degradation
C; Superfamily: Bacillus sp. KSM-635 alkaline cellulase; S-layer repeat homology; Thermot
C; Keywords: glycosidase, hydrolase; polysaccharide degradation
C; Keywords: glycosidase; hydrology (SELR)
F; 11-153/Domain: S-layer repeat homology (SELR)
F; 101-153/Domain: S-layer repeat homology (SERS)
F; 164-219/Domain: S-layer repeat homology (SERS)
F; 166-908/Domain: Thermotoga xylanase A amino-terminal repeat homology (TXA)
  148 SHNVYIMADKQK-NGIKVNFKIRHNIEDGSVQLADHYQQ-------NTPIGDGPVL 195
                                                                                                                                           556 -RNLYIQSMKFKGNGIKTN-----DFDFSFGWNYNSLNRGYFFTKGVKASLG-GRVT 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 YPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKED 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 GNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSV----QLADHYQQNTPIG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----PKNHYIIWELANEPSPNNNGGPGLINDEKGWEAVKEYAEPIVEMLREKGDNMIL 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 LVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTGLS-YGVQCFSR 74
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G95153
neuraminidase, probable [imported] - Streptococcus pneumoniae (strain TICR4)
                                                                                                                                                                                                                                                                                                                                                                                                cellulase (EC 3.2.1.4) - Bacillus sp.
N;Alternate names: endo-1,4-beta-glucanase
C;Species: Bacillus sp.
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 01-Dec-2000
C;Accession: S29043; PC4404
E;Ozaki, K.; Shikata, S.; Kawai, S.; Ito, S.; Okamoto, K.
J. Gen. Microbiol. 136, 1327-1334, 1990
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                                                                                                                                                                                                                                   196 LP--DNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLG 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Pred. No. 13; 34; Mismatches
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20.2%; Pred. No. 13
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Best Local Similarity 20.23
Matches 49; Conservative
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A; Molecule type: DNA
A; Residues: 1-941 <OZA>
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VG 416
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A/Status: preliminary; nucleic acid sequence not shown; translation not shown A/Status: preliminary; nucleic acid sequence not shown; translation not shown A/Molecule type: DNA A/Molecule type: DNA A/Molecule type: DNA A/Molecule type: DNA A/Residues: 1-370 <AQF>
A/Residues: 1-370 <AQF>
A/FORDERS: 1-370 <AQF>
A/FORDERS: GB.AB000720; NID:g2983529; PIDN:AAC07111.1; PID:g2983536; GB.AB000657. A/Gonetics: A/Gonetic
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polyketide synthase [imported] - Nostoc sp. (strain PCC 7120)

Cipportes: Nostoc sp. PCC 7120

Ciportes: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

Ciportes: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

Ciportes: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

Ciportes: Noston N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 ERSPSISSVIMPKFFGAEIVNKLSEKGIYCSTGSACLSGEYEPNKHMLKWGFSQEKALRM 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 TGKLP-----VPWPTLVTGLSYGVQCFSRYPDHMKQ-HDFFKSAMPEGYVQERTIFFKDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 NGKRSGTENVVGILSLAKALEIIVSNFSRYQEQLKKKLRDLFENLLLEA-LPDAQIVGKDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 KGVPLLTDAVQAIGKIPIELKNISYATFSGHKFHAIKGSGFLYISDEANYEPLIVGGGQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 370;
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llarity 24.5%; Pred. No. 1.2e+02;
Conservative 24; Mismatches 69;
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Best Local Similarity 25.4%; Pred. No. 9.9;
Matches 49; Conservative 30; Mismatches
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Matches 48; Conserv
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Accession: E70390
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Identrate names: leucyl-tRNA synthetase
C.Species: Haemophilus influenzae (strain Rd KW20)
N.Alternate names: leucyl-tRNA synthetase
C.Species: Haemophilus influenzae
C.Species: Haemophilus influenzae
C.Species: Haemophilus influenzae
C.Species: Haemophilus influenzae
C.Species: Haug-1995 #sequence_revision 18-Aug-1995 #text_change 03-Jun-2002
C.Accession: H64102
C.Accession: H64102
R.Fileischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, R.Fileischmann, R.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kchley, J.M.; Weidman, J. D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Puhrmann, J.L.; Geoghagen, N.S.M.; Science 265, 496-512, 1995
A.Authors: Ganehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Recession: H64102
A;Readues: 1061 - TIGR>
A;Residues: 1061 - TIGR>
A;Residues: 1-861 - TIGR>
A;Cross-references: GB:U32774; GB:L42023; NID:g1573942; PIDN:AAC22581.1; PID:g1573943; T
C;Genetics:
A;Genetics:
C;Superfam:ly: leucine-tRNA synthetase; ligase; protein biosynthesis
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;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
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                        SVUNALSEWLIVEIKRDGWVYEQRFENGGKPSTTLEKKGKTRQTGTTIHFKPDPTVFSTT 182
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                                                                                                                            --NYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADK----
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Matches 46; Conserv
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Length 2518;

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Cispecies: Xylella fastidiosa
Cibate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
Cibate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
Rianonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Title: The genome A82315, MUID:20365717, PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
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R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carraro, J.C.; Carraro, D.M.; Carraro, J.C.; Carraro, J.C.; Carraro, J.C.; Carraro, J.C.; Carraro, J.C.; Marcines, M.C.; Franco, M.C.; Frohme J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Marques, M.V.; Martins, E.A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracaca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.C.; Goliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak, A.; Suuhors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, P.A.; Reference number: AS9328
A; Gontents: annotation
                                           C; Keywords: glycoprotein; hydrolase; serine proteinase
1-24/Domain: signal sequence #status predicted <51G>
F;12-3.110/Domain: propeptide #status predicted <PRO>
F;111-752/Product: prohormone-processing proteinase PC1 #status predicted <MAT>
F;183-396/Domain: subtilitiain homology <58T>
F;167,208,382/Acrive site: Asp, His, Ser #status predicted
F;167,208,382/Acrive site: Carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   595 ----SSQPEHMKQ-----PRVYT-----SYNTVQNDRRGVEKMVNVVEEKP
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ilarity 22.2%; Pred. No. 38;
Conservative 29; Mismatches
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Best Local Similarity 25.69
Matches 53; Conservative
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-887 <SIM>
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                                                                                                                                                                                                                                  "Species: Plasmodium falciparum" (") Species: Plasmodium falciparum")
C; Bate: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C; Accession: D71614
S; Accession: D71614
S; Activates, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; F, Fardner, M.J.; Pattelin, H.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O. Science 282, 1126-1132, 1998
A; Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A; Reference number: A71600; MUID:99021743; PMID:9804551
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-2573 cGAR>
A; Cross-references: GB:AE001365; GB:AE001362; NID:G3845188; PIDN:AAC71881.1; PID:G384519
C; Genetics: Contraction of the Contraction of Contracti
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NiAlternate names: furin homolog PC1; kexin homolog PC1; prohormone cleavage enzyme; pro
C;Species Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text_change 19-May-2000
C;Accession: A41556; S27361; $36358
R;Bloomquist, Br.; Expept, B.A.; Mains, R.B.
Mol. Endocrinol. 5, 2014-2024, 1991
A;Title: Prohormone-converting enzymes: regulation and evaluation of function using anti
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A;Residues: 1-752 <BLO>
A;Cross-references: GB:N76705; NID:g203508; PIDN:AAA40945.1; PID:g203509
A;Cross-references: GB:N76705; NID:g203508; PIDN:AAA40945.1; PID:g203509
R;Hakes, D.U.; Birch, N.P.; Mezey, A.; Dixon, J.E.
Endocrinology 129, 3053-3063, 1991
A;Title: Isolation of two complementary decoxyribonucleic acid clones from a rat insulinc
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Best Local Similarity 26.2%; Pred. No. 1.2e+02;
Matches 34; Conservative 30: Mismatches 53.
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R;Hakes, D.J.; Birch, N.P.; Mezey, A.; Dixon, J.E.
submitted to the EMBL Data Library, February 1992
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A;Residues: 1-513,'A',515-752 <HAK>
---PINLWLVTQGAIS 1711
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A;Accession: S36358
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52;

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124 IELKGIDFKEDG---NILGHKLEYNYNSHNYYIMADKQKN--GIKVNFKIRHNIEDGSVQ 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;5-77/Domain: lipoyl/biotin-binding homology <LPB>F;177-145/Region: beta-alpha-beta FAD nucleotide-binding fold F;117-145/Region: beta-alpha-beta ephydrogenase homology <DLD>F;119-561/Domain: dibydrolipoamide dehydrogenase homology <DLD>F;287-315/Region: beta-alpha-beta NAD nucleotide-binding fold F;153-158/Disulfide bonds: redox-active #status predicted
                                                                                                                                                                                     ch 6.7%; Score 86; DB 1; Length 578; Smilarity 23.5%; Pred. No. 24; 54; Conservative 39; Mismatches 85; Indels
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Matches 54
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dihydrolippamide dehydrogenase (EC 1.8.1.4) [validated] - Clostridium magnum Ajlternate names: 2-oxoglutarate dehydrogenase complex chain E3; acetoin dehydrogenase hydrogenase complex chain E3; S-complex 50K chain C;Species: Clostridium magnum C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000 C;Accession: 140794
R;Kruger, N.; Oppermann, F.B.; Lorenzl, H.; Steinbuchel, A.
J. Bacteriol. 176, 3614-3630, 1994
R;Kruger, N.; Oppermann, F.B.; Discoular characterization of the Clostridium magnum acetoin de A;Title Biochemical and molecular characterization of the Clostridium magnum acetoin de A;Title Biochemical and molecular characterization of the Clostridium magnum acetoin de A;Reference number: 140789; MUID:94266715; PMID:8206840
A;Reference number: 140789; MUID:94266715; PMID:910840
A;Reference number: 140789; MUID:94266715; PMID:910840
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A;Reference number: 140789; MUID:9426715; PMID:9306840
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C;Punction:
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C;Punction:
A;Reference number: 140789; MUID:9472324; PIDN:AAA21748.1; PID:9472330
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A;Reference number: 140789; MUID:9472324; PIDN:AAA21748.1; PID:9472330
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Cibate: 31-Mar-2000 #text_change 03-Jun-2002
Cibate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
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Cibate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
Cibate: 31-Mar-2000
Ripatrili, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A; Reference number: A81250; MUID:20150912; PMID:10688204
A; Reference number: A81250; MUID:20150912; PMID:10688204
A; Residues: Traininary
A; Molecule type: DNA
A; Residues: 1-357 PPRN>
A; Cross-references: GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB73096.1; PID:g696827
A; Cross-references: GB:AL139076; GB:AL111168
C; Genetics:
C; Genetics:
A; Gene: trnuA; Cj0831c
C; Keywords: methyltransferase; S-adenosylmethionine
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                                                                                        429
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                             -----KTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYI
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                                                                     Length 357;
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6.7%; Score 86; DB 2; Length 357
Best Local Similarity 24.8%; Pred. No. 13;
Matches 30; Conservative 18; Mismatches 39; Indels
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OM protein - protein search, using sw model

June 21, 2004, 15:42:24 ; Search time 6.44444 Seconds (without alignments) 1931.085 Million cell updates/sec Run on:

US-09-887-784-64G 1275 1 WOSKGEELFTGVVPILVELD.......VLLGFVTAAGITLGMDELYK 239 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

141681

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	212	_	P44935 haemophilus		P19424 bacillus sp	_	~	7					P97280 mesocricetu	P24506 discopyge o				9		Q8zqz6 salmonella		Q87c65 xylella fas	P27951 streptococc			ношо	P53621 homo sapien	P57203 buchnera ap	4	O42918 schizosacch	-	4	Q7vnf0 haemophilus
SUMMARIES	ID	GFP AEQVI	VIT4 CAEEL	D152 HAEIN	D151 HAEIN	GUN BACS6	CP51 CANGA	D153 HAEIN	SYL HAEIN	NECI_RAT	SYL_XYLFA	TRMA CAMJE	EXPI_ERWCA	ITH3_MESAU	SY62 DISOM	GLNA_AZOCA	AMPA_WIGBR	PEPF_MYCPU	DPOL_HPBHE	SYL_SALTI	SYL_SALTY	YCO3 KLEPN	SYL_XYLFT	BAG_STRAG	YM62_YEAST	PORL_BUCAP	ADAS_HUMAN	COPA HUMAN	HIS7_BUCAI	PSBC_CYAPA	AMY2_SCHPO	FMDC_METTH		SYD_HAEDU
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Q8ehp4 shewanella P06125 caenorhabdi	Q58743 methanococc P23865 escherichia	P21662 mus musculu	025443 helicobacte	088900 rattus norv	P53917 saccharomyc	P21951 saccharomyc		P91679 drosophila	P49052 bacillus li
SYL_SHEON VITS_CAEEL	YD48 METJA PRC ECOLI	NECI MOUSE	TRMB HELPY	GRBE_RAT	YNM7 YEAST	DPOE YEAST	AC2L_HUMAN	OPT1 DROME	SLAP_BACLI
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859 1603	336 682	753	393	538	953	2222	689	737	874
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81.5	81 81	81	80.5	80.5	80.5	80.5	80	80	80
34 35	36 37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

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62 VTGLSYGVOCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VITFSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 NRIBLKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                             5-imidazolinone (Ser-Gly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26886 MW; EASAGF21FBFBGE05 CRC64;
                                                                                                                                                                                                                        Z, 3-IDEHYDROTYROSINE.

F -> Y.

I -> M.

L -> M.

S -> G (IN REF. 3).

S -> G (IN REF. 2).

O -> R (IN REF. 2).

O -> P (IN REF. 2).

E -> K (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR009017; GFP like.
InterPro; IPR000786; Green_fl_protein.
                                                                                                                                          Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
Probom; PD013756; Green_fl_protein; Luminescence; 3D-structure.
CROSSLNK 65
                                                                                                                                                                                                                                 66
100
100
108
141
219
22
22
22
22
119
1157
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10-APR-02.
28-OCT-98.
                                                                     PDB; 2EMN; 20-AUG-97.
PDB; 2EMO; 20-AUG-97.
                                                    20-AUG-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 233; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 AA;
                    1KYS;
1YFP;
                                                        2EMD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation use by mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                           1155UE SECLETIOIN: FINDUCTYCES.

1. PTM: Contains a covalently attached chromophore, which is composed of modified amino acid residues. The chromophore is formed upon cyclization of the residues. The chromophore is formed upon cyclization of the residues Ser-dehydrofyr-GP.

1. BIOTECHNOLOGY: Has become useful and ubiquitous tool for making chimmeric proteins of GFP linked to other proteins where it functions as a fluorescent protein tag. GFP tolerates N-and C-terminal fusion to a broad variety of proteins. It has been expressed in Dacteria, yeast, slime mold, plants, Drosophila, zebrafish, and in mammalian cells. As a noninvasive fluorescent marker in living cells, it allows for a wide range of applications where it may function as a cell lineage tracer, reporter of gene expression, or as a measure of protein-protein interactions.

NOTE: Issue il of June 2001;

WHW="http://www.expasy.org/spotlight/articles/sptlt011.html".
                                                                                                                                                                           Elsiger M.A., Wachter R.M., Hanson G.T., Kallio K., Remington S.J.;
Elsiger M.A., Wachter R.M., Hanson G.T., Kallio K., Remington S.J.;
Elsiger M.A., Wachter R.M., Hanson G.T., Kallio K., Remington S.J.;

Structural and spectral response of green fluorescent protein

T variants to changes in pH.";

Blochemistry 38:5296-530(1999).

- !- PUNCTION: Bnergy-transfer acceptor. Its role is to transduce the blue chemiluminescence of the protein aequorin into green fluorescent light by energy transfer. Fluoresces in vivo upon receiving energy from the Ca(2+)-activated photoprotein aequorin. Aksorbance peak at 470 nm. The fluorescence emission spectrum peaks at 590 nm with a shoulder at 540 nm.

- !- SUBUNIT: Monomer.

- I TISSUE SPBEIRICITY: Photocytes.
                  X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF MUTANT WITH YELLOW EMMISSION. MEDLINE=99455509; PubMed=9782051; Wachter R.M., Elslider M.A., Kallio K., Hanson G.T., Remington S.J.; "Structural basis of spectral shifts in the yellow-emission variants of green fluorescent protein."; Structure 6:1267-1277(1998).
                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=99238303; PubMed=10220315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M62654; AAA27722.1; --
EMBL; M62653; AAA27721.1; --
EMBL; L29345; AAA58246.1; --
EMBL; X96418; CAA65278.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR, (30662), JO1514.
PDB, 11B9C, JT.-NOV-00.
PDB, 11BFP, 07-71LL-97.
PDB, 11EMA, 98-NOV-96.
PDB, 11EMA, 98-NOV-96.
PDB, 11EMA, 16-JUN-97.
PDB, 11EMC, 20-AUG-97.
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0; Gaps

Length 238; Indels 61 9 HYQONTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239

182

· &

07-JAN-03. 28-AUG-02. 10-APR-02.

g

181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238

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                                                                                                                                                                                                                                                                                                                                                                                                                                                Spieth J., Denison K., Kirtrand S., Cane J., Blumenthal T.,
"The C. elegans vitellogenin genes: short sequence repeats in the
promoter regions and homology to the vertebrate genes.";

"The C. elegans vitellogenin genes: short sequence repeats in the
promoter regions and homology to the vertebrate genes.";

"In subclaic Acids Res. 13:5283-5295(1985).

"I- FUNCTION: Precursor of the egg-yolk proteins that are sources of
nutrients during embryonic development (Potential).

"SUBCELLULAR LOCATION: Secreted.

"I SSUB SPECIFICITY: Synthesized in Caenorhabditis only by 32 cells
building the intestine of adult hermaphroditic individuals; they
are cotranalationally secreted into the body cavity and
subsequently taken up by the goand.

"SIMILARITY: Contains 1 VWFD domain.
                                                                                                                                                           Caenorhabditis elegans.
Eukaryota: Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.4%; Score 94.5; DB 1; Length 1603; 23.9%; Pred. No. 7.8; ive 32; Mismatches 68; Indels 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VWFD.

Y -> V (IN REF. 3).

L -> V (IN REF. 2).

EVAYT -> RSRLH (IN REF. 2).

T -> S (IN REF. 2).

7 MW; E303170325BC99BB CRC64;
                                                                                                                                                                                                                                                                                        Waterston R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                            Blumenthal T., Spieth J., Zucker E.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
                                 VIT4_CAEEL STANDARD; PRT; 1603 AA. P18947; Q9BPP3; CORPED 1; Created) 10-OCT-2003 (Rel. 42, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) VIT-4 OR F5998.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VITELLOGENIN 4.
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SIGNAL 1 15 POTENTIAL.
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Wormbep; F59D8.2; CE26817.
InterPro; IPR001747; Lipid_transprt_N.
InterPro; IPR001846; VWF D.
Pfam; PF01347; Vitellogenin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-71 FROM N.A.
MEDLINE=85269643; PubMed=4022780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AC024137; AAK09074.1; -.
EMBL; M11498; AAA28163.1; -.
EMBL; X02754; CAA26531.1; -.
                                                                                                                                                                                                                                                                                                                                               FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00638; LPD N; 1.
SMART; SM00216; VWD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 23.9
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 16
183 18
275 27
1603 AA;
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-282
                                                                                                                                                                                                             NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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RESULT 2
VIT4_CAEEL
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12;

Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                 258 INVNGQEVVKSETRAKVTPVESKINR-EIK-----KVSGPKEEIVYSMENEKLIEQ 308
                                                                                                         106 -----NYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMAD 156
                                        162 MESDKDSLFFNVHEKTMEGDCEV---AYTIVQEG-GKTIYTKSVNFDKCITR-----PE 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86
1 MVSKGBELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                   61 LVTGLSYGVQCFSRYPDHMKQHDFFKSAMPEG-YVQERTIF---FKDDG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --FKSAMPEGYVQE-----RT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;

Pleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.E., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Witcherback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Protective surface antigen D15 precursor (80 kDa D15 antigen)
(D-15-Ag) (Outer membrane protein D15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.3%; Score 92.5; DB 1; Length 795; Best Local Similarity 22.3%; Pred. No. 4.9; Matches 49; Conservative 30; Mismatches 78; Indels 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN 20 795 PROTECTIVE SURFACE ANTIGEN D1S SEQUENCE 795 AA; 87478 MW; B85691FC22E6ED44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the surface antigen D15 family.
                                                                                                                                                                                                                                                         157 KOKNG-----IKVNFKIRHNIEDGSVQLADHYQQNTP 188
                                                                                                                                                                                                                                                                                    309 FYKQGDKAEVNPFKAIEIEQKV-EQLEEIFRQIQEH-EQNTP 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR000184; Bac surfAg D15.
Pfam; PF01103; Bac surface Ag; I.
Antigen; Outer membrane; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 GLSYGVQCFSRYPDHMKQHDF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U32773; AAC22575.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=727;
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D152 HAEIN
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STANDARD;
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373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1415;
                                                                                                                                                                                                                                                                              GUN_BACS6
P19424;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
126 GIGYGTESGISYQASVKQDNFLGTGAAVSIAGTKNDYGTSVNLGYTEPYFTKDGVSLGGN 485
                              ---KLEYNYN 147
                                                                                         148 SHNVYIMADKQK-NGIKVNFKIRHNIEDGSVQLADHYQQ------NTPIGDGPVL 195
                                                                                                                      543 -RNLÝLOSMKFKGNGÍKTŇ-----DFDFSFGWNÝNSLNRGYFPTKGVKASLG-GRVT 592
                                                            486 VFFENYDNSKSDTSSNYKRTTYGSNVTL-GPPVNENNSYYVGLGHTYNKISNFALEYN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Outer membrane protein D15 is conserved among Haemophilus influenzae species and may represent a universal protective antigen against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STEAIN=Minna / Serotype B, and Eagan / Serotype B;
MEDLINE=97427952; PubMed=9284140;
Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Flack F.S., Loosmore S., Chong P., Thomas W.R.; "The sequencing of the 80-kDa D15 protective surface antigen of Haemophilus influenzae."; Gene 156:97-99(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63;
                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protective surface antigen D15 precursor (80 kDa D15 antigen)
(D-15-Ag) (Outer membrane protein D15).
Haemophilus influencae.
Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
PROTECTIVE SURFACE ANTIGEN D15.
2F93DE538696AF1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Infect. Immun. 65:3701-3707(1997).
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SIMILARITY: Belongs to the surface antigen D15 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78; Indels
                              99 IFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNI---LGH-
                                                                                                                                                        LP--DNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLG 233
                                                                                                                                                                          7.3%; Score 92.5; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 4.9;
                                                                                                                                                                                                                                                                    797 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U60833; AAB61976.1; -.
PIR; JC4078; JC4078
InterPro; IPR000184; Bac_surfAg_D15.
Pfam; PF01103; Bac surface Ag; I.
Antigen; Outer membrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95255676; PubMed=7737523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20. 797 PJ
797 AA; 87675 MW;
                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U13961; AAA85645.1; -.
EMBL; U60832; AAB61974.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 22.39 Sonservative
                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              species and may re
invasive disease."
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Serotype B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=727;
                                                                                                                                                                                                                                                                    D151_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                          196
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Best Local 6
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64 GLSYGVQCFSRYPDHMKQHDF----

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99 IFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNI---LGH------KLEYNYN 147
                                                                                     542
                                                                                                                        148 SHNVYIMADKQK-NGIKVNFKIRHNIEDGSVQLADHYQQ------NTPIGDGPVL 195
                                                                                                                                                           592
                                                                            -----DFDFSFGWNYNSLNRGYFPTKGVKASLG-GRVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-91037937; PubMed=2230718;
Ozaki K., Shikata S., Kawai S., Ito S., Okamoto K.;
Ozaki K., Shikata S., Kawai S., Ito S., Okamoto K.;
"Molecular cloning and nucleotide sequence of a gene for alkaline cellulase from Bacillus Sp. KSM-635.";
J. Gen. Microbiol. 136:1327-1334 (1990).
-!- CAPMALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic linkages in cellulose, lichenin and cereal beta-D-glucons.
-!- SIMILARITY: Belongs to cellulase family A (family 5 of glycosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00659; GLYCOSYL HYDROL_F5; 1.
PROSITE; PS01072; SLH_DOMAÏN; 2.
Cellulose degradation; Hydrolase; Glycosidase; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                       01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Endoglucanase precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)
(Alkaline cellulase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hydrolases).
-!- SIMILARITY: Contains 3 S-layer homology (SLH) domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104628 MW; BEAZAC3B169BFADA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus sp. (strain KSM-615).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                                                                                                                                                                  196 LP--DNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLG
                                                                                                                                                                                                                                                                                                                        941 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENDOGLUCANASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDB; 1601; 31-DEC-02.
PDB; 1601; 31-DEC-02.
PDB; 1605; 31-DEC-02.
InterPro; IPR005086; CBM 17_28.
InterPro; IPR00199; Gal_bind like.
InterPro; IPR001919; SLH.
Pfam; PF0044; CBM 17_28; 2.
Pfam; PF00150; cellulase; 1.
Pfam; PF00150; cellulase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLH 1.
SLH 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLH 3.
                                                                                                                                                              543 -RNLYIQSMKFKGNGIKTN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M27420; AAA22304.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         485
941 AA;
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                                                                                                                                                                                                                                                                                                    75 YPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKED 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 GNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSV----QLADHYQQNTPIG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------PVQLRGMSTHGLQWFG- 271
                                                                                                                                                          74
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Kwon-Chung K.J., Bennett J.E.;
"Deletion of the Candida glabrata ERG3 and ERG11 genes: effect on cell
                                                                                                                                              LVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTGLS-YGVQCFSR
                                                                                                                                                                                                                                                                                                                                               ----EKRDHMVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | CPS1 CANGA |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Rapid detection and identification of Candida albicans and Torulopsis (Candida) glabrata in clinical specimens by Species-specific nested PCR amplification of a cytochrome P-450 lanosterol-alpha-demethylase (LiA1) gene fragment.";
J. Clin. Microbiol. 32:1902-1907(1994).
-! FUNCTION: Catalyzes C14-demethylation of lanosterol which is critical for ergosterol biosynthesis. It transforms lanosterol into 4.4' dimethyl cholesta-8,14,24-triene-3-beta-ol (By Similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: Obtusifoliol + 3 O(2) + 3 NADPH = 4-alpha-methyl-5-alpha-ergosta-8,14,24(28)-trien-3-beta-ol + formate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burgener-Kairuz P., Zuber J.P., Jaunin P., Buchman T.G., Bille J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Candida glabrata (Yeast) (Torulopsis glabrata).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                               . 66
7.3%; Score 92.5; DB 1; Length 941; 20.2%; Pred. No. 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               viability, cell growth, sterol composition, and antifungal susceptibility.";
                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antimicrob. Agents Chemother. 39:2708-2717(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 DGPVLLPDNHYLSTQSALSKDPN-------
                                                                       34; Mismatches
                                                                                                                                                                                                 240 LVELNG----QLTLAGE---DGT-----
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MEDLINE=95081364; Pubmed=7989540;
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                                                                       Conservative
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                                   Similarity
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   Query Match
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                       and for commercial
                       loved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                     10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 GHEFIFNAKLADVSAEAAYSHLTT-------PVFGKGVIY--DC----PNHRLM 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 KQHDFFKSAM-PEGYV-----QERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDF 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 TASRSLIGKEMRDKLDTDFAYLYSDLDKGFTPINF-VFPNLPLEHYRKRDHAQQAIS--- 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 GHKFSVS---GEGEGDATYGKLTLKFICTTGKLPVPWPTLVTGLSYGVQCFSRYPDH--M 79
    6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRON (HEME AXIAL LIGAND) (BY SIMILARITY)
I -> M (IN REF. 2).
I -> T (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Outer membrane protein D15 is conserved among Haemophilus influenzae species and may represent a universal protective antigen against invasive disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=PAK 12085;
MEDLINE=97427952; PubMed=9284140;
Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                   PROSITE; PS00086; CYTOCHROME P450; 1.
Electron transport; Oxidoreductase; Monooxygenase; Membrane; Heme;
Sterol biosynthesis; NADP.
  as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                     49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protective surface antigen D15 precursor (80 kDa D15 antigen)
(D-15-Ag) (Outer membrane protein D15).
                                                                                                                                                                                                                                                                                                                                                                                                  Match 7.2%; Score 91.5; DB 1; Length 533; Local Similarity 22.3%; Pred. No. 3.7; es 46; Conservative 32; Mismatches 79; Indels 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLUTAR LOCATION: Outer membrane.
                                                                                                                                                                                                                                                                                                                                                          533 AA; 61305 MW; A0506C17507E6EF7 CRC64;
                  modified and this statement is not removed.
entities requires a license agreement (See h
or send an email to license@isb-sib.ch).
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institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264 -----GTYMSLIKERREKND 278
                                                                                                                                                    InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Infect. Immun. 65:3701-3707(1997).
                                                                                                           EMBL; L40389; AAB02329.1; -. EMBL; S75389; AAB32679.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                64
473
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  non-profit
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                                                                                                                                                                                                                                                                                                                                     473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAEIN
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                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use ky non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce) or serd an email to license@isb-sib.ch).
                                                                                                                                  11;
                                                                                                                                                                                                                                148 SHNVYIMADKOK-NGIKVNFKIRHNIEDGSVQLADHYQQ------NTPIGDGPVL 195
                                                                                                                                                                            99 IFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNI---LGH-----KLEYNYN 147
                                                                                                                                                                                                                                                                                            543 -RNLYIQSMKFKGNGIKTN-----DFDFSFGWNYNSLNRGYFPTKGVKASLG-GRVT 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN=RG / KW20 / ATCC 51907;

MTDLINE=95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F.,

Kerlavage A.K., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.X., Hanna M.C., Nayven D.T., Saudek D.M., Brandon R.C.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP + diphosphate + L-leucyl-tRNA(Leu).

diphosphate + L-leucyl-tRNA(Leu).
SUBUNIT: Monomer. (By similarity).
SUBCELIULAR LOCATION: Cytoplasmic.
SUBCELIULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
18-FEB-2003 (Rel. 41, Last annotation update)
Leucyl-ERNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
LEUS OR HI0921.
                                                                                                                                  63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemophilus influenzae.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                        DB 1; Length 793;
                                                                 SURFACE ANTIGEN D15.
                                                                                                                                                            --FKSAMPEGYVOE
                                                                                                                               79; Indels
                                                                             51BFDB2036801A14 CRC64;
                                                                                                                                                                                                                                                                                                                        LP--DNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLG 233
                                                                                                                                                                                                                                                                                                                                                 593 IPGSDNKYYKLSADVQGFYPLDRDHRWVVSAKASAGYANG 632
                                                                                                                                                                                                                                                                                                                                                                                                                   861 AA
                                                                                                        Score 91.5; DI
Pred. No. 5.9;
                                                                                                                                  28; Mismatches
           InterPro; IPR000184; Bac_gurfAg_D15.
Pfam; Pf01103; Bac_surface Ag; 1.
Antigen; Outer membrane; Signal.
SIGNAL 1 19 POTENTIAL.
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                             793 AA; 87511 MW;
                                                                                                                                                            54 GLSYGVQCFSRYPDHMKQHDF
                                                                                                      7.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U32774; AAC22581.1; -.
 EMBL; 1J60834; AAB61977.1; -.
                                                                                                     Query Match
Best Local Similarity 22.78
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                SYL HAEIN
P43827;
                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                        196
                                                                   CHAIN
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SYL_HAEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 DGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADK-QKNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----IADKLEKLGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 ---KVNFKIRH-------NIEDGSVQLADHYQQNTPIGDGPVLLPDNHYL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=92168040; PubMed=1791845;
Bloomquist B.T., Eipper B.A., Mains R.E.;
"Prohormone-converting enzymes: regulation and evaluation of function
                                                                                                                                                                                                                                                                                                                                                                                                   50 TTGKLPVPWPTLVTGLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKD-----
HAMAP; MF 00049; -; 1.
InterPro; IRRO01302; Leu-tRNAsyntla.
InterPro; IRRO01302; LRNA-synt la.
InterPro; IRRO01412; tRNA-synt la.
InterPro; IRRO01402; tRNA-synt l.
InterPro; IRRO01808; ValRS_IRRS_edit.
PFO0133; tRNA-synt l. 1.
PRINTS; PR00985; TRNASYNTHLEU.
TIGREPAMs; TIGREPAMs; TIGRES_EDACE, 1.
PROSITE; PS00178; AA TRNA_ILGASE l; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Neuroendocrine convertase 1 precursor (EC 3.4.21.93) (NEC 1) (PC1)
PCSKI OR NEC1 OR NEC-1 OR BDP.
                                                                                                                                                                                                                                                                                                                                                              59;
                                                                                                                                                                                                                                                                                                                    6.9%; Score 88.5; DB 1; Length 861; 4.1%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                         122 ATP (BY SIMILARITY).
97750 MW; EB93304F6B4C8FB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        365 DEBIDLTKQAFVEHGKLVNSDEFDGKNF--DGAFNG-----
                                                                                                                                                                                                                                                                                                                                                                909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      752 AA
                                                                                                                                                                                                                                                                                                                          Guery Match
6.9%; Score 88.5; D'
Best Local Similarity 24.1%; Pred. No. 12;
Matches 46; Conservative 26; Mismatches
                                                                                                                                                                                                                      "HIGH" REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Endocrinol. 5:2014-2024(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 STOSALSKDPN 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :|::||
462 GVKSPINADPN 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat)
                                                                                                                                                                                                                          52
623
622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      using antisense RNA.
                                                                                                                                                                                                                                                                  622 6
861 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                          Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                             619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEC1 RAT P28840;
                                                                                                                                                                                                                                                 SITE
BINDING
                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 VQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 IDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 ELDGDVNGHK-----VPWPTLVTGKLTLKFICTTGKLP-----VPWPTLVTGLSYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     540 ERDTSPNGFKNWDFMSVHTWGENPV--GTWTLKVTDMSGRMONEGRIVNWKLILHGT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                             Microry; Sac. V.Z.;
InterPro; IPR002094; Peptidase S8.
InterPro; IPR002099; Peptidase S8.
InterPro; IPR002090; Protease inhib.
InterPro; IPR009020; Protease inhib.
Pfam; PF01483; P. proproten; I.
Pfam; PF00082; Peptidase S8; I.
PRONTS; PR00723; SUBTILIASI.
PROSITE; PS00136; SUBTILASE ASP; I.
PROSITE; PS00137; SUBTILASE HIS; I.
PROSITE; PS00138; SUBTILASE SER; I.
Hydrolase; Serine protease; Glycoprotein; Zymogen; Calcium; Signal.
SIGNAL
CATALYTIC ACTIVITY: Release of protein hormones, neuropeptides renin from their precursors, generally by cleavage of -Lys-Arg-
                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
                             COFACTOR: Calcium.
SUBCELLULAR LOCATION: Localized in the secretion granules.
SIMILARITY: Belongs to peptidase family S8. Furin subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
T - TT (IN REF 2)
E -> A (IN REF 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.8%; Score 87; DB 1; Length 752; Best Local Similarity 25.6%; Pred. No. 13; Matches 53; Conservative 20; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                             NEUROENDOCRINE CONVERTASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84120 MW; F630AD830A076DED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             (BY
(BY
                                                                                                                                                                                                                                                                                                                                                                                                                   (BY
                                                                                                                                                                                                                                                                                                                                                                                 AMPHIPATHIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                            CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 40, Created)
(Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 IGDGPVLLPDNHYLSTQSALSKDPNEK 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------SKQS--SKIPSAK 691
                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC
                                                                                                                                                            EMBL; M76705; AAA40945.1; -. EMBL; M83745; AAA41476.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 645
366
514
                                                                                                                                                                                                                                                                                                                                                  110
752
410
751
167
208
382
173
401
                                                                                                                                                                                 PIR; A41556; KXRTC1.
HSSP; Q45670; 1DBI.
MEROPS; S08.072; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                752 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYL XYLFA
Q9PBG8;
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
ACT_SITE
ACT_SITE
ACT_SITE
CAREOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
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                                                                                                                                                                                                                                                                                                                                                             CHAIN
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ID SYL X
AC Q9PEG
DT 16-OC
DT 16-OC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10,
                                                                                                                                                                                                      PRINTS; PR00995; TRNAŠYNTHÍEU.
TIGRPAMS; TIGR00396; leuS bact; 1.
PROSITE; PS00178; AA TRNA_SIRSI; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diphosphate + L-leucyl-tRNA(Leu).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
28-FEB-2003 (Rel. 41, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
LEUS OR XF2176.
                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.8%; Score 86.5; DB 1; Length 879; 22.2%; Pred. No. 17; ive 29; Mismatches 68; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "KMSKS" REGION.
ATP (BY SIMILARITY).
9FDCCB992092919E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "HIGH" REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAMAP; MF_00049; -; 1.
InterPro; IPR002302; Leu-tRNAsyntla.
InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR009008; ValRS_ILERS_edit.
Pfam; PF00133; tRNA-synt_l; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE004031; AAF84975.1; ALT_INIT.
                                                                                                                                                                                              MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99796 MW;
                                                                                                  Kanthomonadaceae; Xylella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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641
640
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879 AA;
                                                       fastidiosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 44; Conserv
                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
                                                                                                                    NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BINDING
SEQUENCE
                                                           Kylella
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Query Match
Best Local
                                                                                                                        174
                                                                                                                                               126
                                                                                                                                                                                                                                                                                                                                                                                                                                        Erwinia
                                                                                                                                                                                                                       P33882;
                                                                                                                                                                                    RESULT 12
EXPLERWCA
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Matches
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                                                                                               154 MADKQKNG-IKVNFKIRHNIEDGSVQLADHYQQNTPI------GDGPVLLPDN 199
                                                                                                                 TIGKL PVPWPTLVTGLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNY-- 107
                321 TNEQLPV-WVANFVLMAYGTGAVMAVPGHDQRDQFF--ANKYGLPIRQVIALKEPRNQDE 377
                                                 ---KIRAEVKFEGDILVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!-FUNCTION: Catalyzes the formation of 5-methyl-uridine at position 54 (M-5-U54) in all tRNA (By similarity).
-!-CATIALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-hcmocysteine + tRNA containing thymine.
-!-SIMILARITY: Belongs to the RNA M5U methyltransferase family. TrmA
                                                             378 STWEPDVWRDWYADKTR---BFE---LINSAEFDGLDYQDAFEVLAERFE-----
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20150912; PubMed=10688204; Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C., Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Dagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M., Whitehead S., Barrell B.G.; "The genome sequence of the food-borne pathogen Campylobacter jejuni Nature 403:665-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS01230; TRMA 1; 1.
PROSITE; PS01231; TRMA 2; FALSE NEG.
Transferase; Methyltransferase; TRNA processing; Complete proteome.
DOMAIN 207 213 S-ADENOSYLMETHIONINE BINDING (BY
                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter.
NCBI_TaxID=197;
                                                                                                                                                                                                                                                   zo-rkb-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
tRNA (Gracil-5-)-methyltransferase (EC 2.1.1.35) (tRNA(M-5-U54)-methyltransferase) (RUMT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
BY SIMILARITY.
CECS328347CEE497 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 86; DB :
Pred. No. 6.5;
                                                                                                                                                                                                                                       357 AA.
                                                                                                                                                                           475 VAFSGTGSPIKTDPEWRK 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; G81355, G81355.
HAMAP; MF 01011, -; I
InterPro; IPR000511, SAM bind.
InterPro; IPR001566; TrmA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL139076; CAB73096.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315 F
42276 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.78;
                                                                                                                                                   -HYLSTQSALSKDPNEKR
                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                          Campylobacter jejuni.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            315 3
357 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subfamily.
                                                                                                                                                                                                                                          TRMA CAMJE
09PP92;
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SEQUENCE
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24.8%;

Best Local Similarity

Query Match

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                80 KQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKF--EGDTLV-----NRIELKG 128
                                                                                                                                                            -----GNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIE 173
                                                                                                                                                                                              55
                                                                                                        73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heikinheimo R., Mae A., Flego D., Pirhonen M., Koiv V., Palva E.T.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: REQUIRED FOR THE SYNTHEGIS OF OHHL (N-(3-OXOHEXANOYL)-L-HOMOSERINE LACTONE), AN AUTOINDUCER MOLECULE WHICH BINDS TO EXPR AND THUS ACTS IN VIRULANCE (SOFT ROT DISEASE) THROUGH THE ACTIVATION OF GENES FOR PLANT TISSUE MACERATING ENZYMES.
-!- SIMILARITY: Belongs to the autoinducer synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 KGEELFTGVVPILVELDGD------VNGHKFSVSGEGEGDATYGKLTLKFICTTGKLP
                                                                                  14 EKHSPIKKYFKEFYTKDFKLFASKDKHYRTRABLSFYHENDTLFYAMFDPKSKKKYIIEY
  34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=SCC3193;
MEDLINE=92285117; PubMed=8508772;
Pirhonen M., Flego D., Heikinheimo R., Palva E.T.;
Pirhonen M., Flego D., Heikinheimo R., Palva E.T.;
a small diffusible signal molecule is responsible for the global control of virulence and exoenzyme production in the plant pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::
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Enterobacteriaceae, Pectobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57;
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  39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12F0979D20FDFE5D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27; Mismatches
     18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYNTH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement ( or send an email to license@isb-sib.ch)
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Pfam; PF00765; Autoind synth; 1.
PRINTS; PR01549; AUTOINDCRSYN.
ProDom; PD002752; Autoind synth; 1.
PROSITE; PS00949; AUTOINDUCERS SYNTH; Quorum sensing; Autoinducer synthesis.
SEQUENCE 217 AA; 25321 MW; 12F0979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X72891; CAA51409.1; -.
EMBL; X80475; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Autoinducer synthesis protein expl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBO J. 12:2467-2476(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
     30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                            129 IDFKED-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 28, (Rel. 28, 1) (Rel. 40, 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  carotovora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Erwinia carotovora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-SCC3193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=554;
                                                                                                                                                                                                                                                                             D 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001
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EMBL; D89287; BAA13940.1;

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117
                                    VPWPTLVTGLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKF 115
                                                                                                                  ----- EYNYNSH 149
                                                                                                                                                     118 PVSTMFFLATVNYSKSKGY----DGVYTIVSHPMLTILKRSGWKISIVEQGMSEKHERVY 173
16 KSEELFT----LRKETFKDRLNWAVKCINGMEFDQYDDDNATYLFGVEGDQVICSSRLIE 71
                                                                         72 TKYPNMITG-----TFFPY-----FEKIDIPEGKYIESSRFFVDKARSKTILGNSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heavy-chain
hamster:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             one or two heavy chains (Hi, H2 or H3) and one light chain, bikunin. Inter-alpha-inhibitor (I-alpha-I) is composed of H1, H2 and bikunin, inter-alpha-like inhibitor (I-alpha-L1) of H2 and bikunin, and pre-alpha-inhibitor (P-alpha-I) of H3 and bikunin. PTM: Heavy chains are interlinked with bikunin via a chondroitin 4-sulfate bridge to the their C-terminal aspartate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: I-alpha-I plasma protease inhibitors are assembled from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamamoto T., Yamamoto K., Sinohara H.;
"Inter-alpha-trypsin inhibitor and its related proteins in Syrian hamster urine and plasma.";
J. Biochem. 120:145-152(1996).
-!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;
"Molecular cloning and sequencing of cDNAs encoding three heavy-chai
precursors of the inter-alpha-trypsin inhibitor in Syrian hamster:
implications for the evolution of the inter-alpha-trypsin inhibitor
                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Inter-alpha-trypsin inhibitor heavy chain H3 precursor (III heavy chain H3) (Inter-alpha-inhibitor heavy chain 3) (HC3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 31-50; 446-472 AND 504-523, AND SUBUNITS
                                                                                                                116 EGDTL-----VNRIELKGIDFKEDG--NILGHKL-----
                                                                                                                                                                                                                                                                                                                                    886 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the ITIH family.
-!- SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                            150 NVYIMADKOKNGIKVNFKIRHNIE 173
                                                                                                                                                                                                                               174 LLFLPVDNESQDVLVR-RINHNQE 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97420688; PubMed=9276673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97018241; PubMed=8864857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. 122:71-82(1997).
                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10036;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mesocricetus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 YPDHMKQHDFFKSAMPEGYVQERT----IFFKDDGNYKTRAEVKFEGD----TLVNRIE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                  476 YPENAIL-DLTKNSYPHFYDGSETAVAGRLADSDMNNFK--ADVKGHGALNDLTFTEEVD 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 LKGID--FKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHY 183
                                                                                                                                       POTENTIAL.
BY SIMILARITY.
INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: Homodimer or homotrimer (possible).
-!- SUBCELLULAR LOCATION: Synaptic vesicles in neurons.
-!- TISSUE SPECIFICITY: Spinal cord, brainstem, midbrain and electric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: May have a regulatory role in the membrane interactions
                                                                                                                                                                                                                                                                                                                                                                     19; Gaps
                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. ..) (POTENTIAL).
CHONDROITIN 4-SULFATE, CROSS-LINK SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   during trafficking of synaptic vesicles at the active zone of the synapse. It binds acidic phospholipids with a specificity that requires the presence of both an acidic head group and a diacyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chondrichthyes;
                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichtl
Elasmobranchii, Squalea, Hypnosqualea, Pristiorajea, Batoidea,
Torpediniformes, Narcinoidei, Narcinidae, Discopyge.
                                                                                                                                                                                                                                                                                                                                     6.7%; Score 85.5; DB 1; Length 886;
                                                                                                          Repeat; Signal; Multigene family,
                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wendland B., Miller K.G., Schilling J., Scheller R.H., "Differential expression of the p65 gene family."; Neuron 6:993-1007(1991).
                                                                                                                                                                                                                                                                                                     AC0594C6852576B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Belongs to the synaptotagmin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synaptotagmin B (Synaptic vesicle protein O-p65-B).
                                                                                                                                                                                                                                                                                                                                                                   62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 QONTPIGDGPVLLPDNHYLSTQSALSKDPNE 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    590 HFVTPLTPMVVTKPEDN--EDQTSIADKPGE 618
                                                                                                                                                                                                                                                                                      (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                   34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               439 AA.
                                                                                                                                                                                                        SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=91273991; PubMed=2054189;
                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 2 C2 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Discopyge ommata (Electric ray)
                                                                                                                                                                                                                                                                                                     99018 MW;
                                                                                                                                                                                                                                                                                                                                                    23.8%;
             InterPro; IPR006587; VIT.
InterPro; IPR002035; VWF_A.
                                                          SMART; SM00609; VIT; 1.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
Serine protease inhibitor;
                                                                                                                                                                                                                                                                                                                                                                     36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                          18
30
646
                                                                                                                                                                                                        886
439
88
577
646
                                           Pfam; PF00092; vwa; 1.
                                                                                                                                                                                                                                                                                                     886 AA;
                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 36; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7785;
                                                                                                                                                                                                                                                                     646
                                                                                                                             Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISOM
                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                     BINDING
                                                                                                                                        SIGNAL
                                                                                                                                                                                                        PROPEP
                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                          CHAIN
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DISOM
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SY62_DI
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Interric, IPR00213-,
Pfam; PF00168; C2; 2.
SMART; SM00239, C2; 2.
SMART; SM00239, C2; 2.
SMART; SM00239, C2; 2.
FROSITE; PS00049; C2 DOMAIN 2; 2.
PROSITE; PS0004; C2 DOMAIN 2; 2.
Transmembrane; Repeat; Synapse; Multigene family; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHOLIPID BINDING (PROBABLE).
C2 DOWAIN 1.
C2 DOWAIN 2.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
2033F05FDBC69F39 CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
20-FBS-2003 (Rel. 41, Last annotation update)
61utamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GQVTVLMTKVDLGQQLEEWRDLESAEKEEPEKLGDICTSLRYVPTAG 305
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Hyphomicrobiaceae, Azorhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.7%; Score 85; DB 1; Length 439; 19.2%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46; Mismatches 94; Indels
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                                                                                                                                                                                                                                                       EMBL; M64276; AAA49228.1; -. PIR; JH0414, JH0414. HSSP, P21707; IBYN. InterPro; IPR000008; C2. InterPro; IPR008973; C2_Calb. InterPro; IPR008973; C2_Calb.
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55, Conserv
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P94125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 R----TIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNI-----LGHKLEYNY 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
       ENZYME REGULATION: The activity of this enzyme is controlled by adenylation. The fully adenylated enzyme complex is inactive. SUBUNIT: Oligomer of 12 subunits arranged in the form of two hexagons (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to the glutamine synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          397 AMP (UNDER CONDITIONS OF ABUNDANT GLUTAMINE) (BY SIMILARITY).
52359 MW, 36C759B9C95D5303 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 NSHNV-----YIMADKQKNGIKVNFKIRHNIEDGSVQ-
   L-glutamine.
ENZYME REGULATION: The activity of this enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.6%; Score 84.5; D
24.9%; Pred. No. 12;
Live 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam, PP00120; gln-synt; 1.

Pfam, PP03951; gln-synt, N; 1.

ProDom; PD010557; Gln synt_C; 1.

TIGRFAMs; TIGR00653; GlnA; 1.

PROSITE; PS00180; GLNA 1; 1.

PROSITE; PS00181; GLNA ATP; 1.

PROSITE; PS00181; GLNA AADP; 1.

PROSITE; PS00181; GLNA ADP; 1.

PROSITE; PS00181; GLNA ADP; 1.

PROSITE; PS00181; GLNA ADENYLATION; 1.

Nitrogen fixation; Ligase.

BINDING 397 397 AMP (UNDER C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR008147; Gln synt beta.
Interpro; IPR008146; Gln synt C.
Interpro; IPR004809; GlnA.
Interpro; IPR001637; GlnA adenyltn S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          June 21, 2004, 15:55:19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Y10213; CAA71265.1; -.
HSSP; P06201; 1LGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 24.9
Matches 45; Conservative
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June 21, 2004, 15:45:30 ; Search time 30.6667 Seconds (without alignments) 2458.984 Million cell updates/sec
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1 MVSKGEELFTGVVPILVELD......VLLGFVTAAGITLGMDELYK
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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	Description	O8qhe2 azotobacter	093125 aequorea vi	Q8ghe4 azomonas ag	Q8ghe3 azotobacter	Q17105 aequorea vi	Q17106 aequorea vi	Q8wtc6 aequorea ma	Q8wp95 aequorea ma	Q8wtc4 aequorea ma	Q8wtd0 aequorea ma	Q8wtc8 aequorea ma	Q8wtc9 aequorea ma	Q8wtc7 aequorea ma	Q8wtc5 aequorea ma	Q95ua7 montastraea	Q7z0w5 montastraea
SUMMARIES	QI	O8GHE2	093125	Q8GHE4	Q8GHE3	Q17105	017106	QBWTC6	Q8WP95	Q8WTC4	Q8WTD0	QBWTC8	Q8WTC9	Q8WTC7	Q8WTC5	Q95UA7	Q7Z0W5
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62 VTGLSYQVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121

Q963f5 montastraea Q8t6u0 dendronepht Q816j8 trachyphyll Q720w9 montastraea Q9u6y3 clavularia Q720w4 montastraea Q8t5f1 montastraea Q8t5f1 montastraea Q8t5f1 montastraea Q720w6 montastraea Q720w7 montastraea Q9t5f2 montastraea Q9u6y6 anemonia su Q9bly9 renilla mue Q9bly9 renilla mue Q9bly9 renilla su Q9bly9 cenilla su Q9bly9 discosoma su Q9ct0 montastraea Q720w8 montastraea Q720w8 montastraea Q720w8 montastraea Q9ct0 montastraea Q8ct0 montastraea Q8ct0 montastraea Q8ct0 meandrina m Q8ct0 meandrina m Q9u6y7 discosoma s	A.  update) n update) n update) in diazotrophic bacteria DBJ databases. 64018 CRC64; DBS_2; Length 238;	e-96; 4; Indels 0; Gaps 0;
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01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25, Green fluorescence protein.
01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25, Green fluorescence protein.
                                                                                                                                         Bacteria; Proteobacteria; G
Pseudomonadaceae; Azomonas.
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                                                                                            VTTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVQLAD 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96305137; PubMed=8707053; Cormack B.P., Valdivia R.H., Falkow S.; "FACS-optimized mutants of the green fluorescent protein (GFP)."; Gene 173:33-38(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Cormack B.P., Bertram G., Egerton M., Gow N.A.R., Falkow S.,
Brown A.J.P.;

Brown A.J.P.;

"Yeast Enhanced Green Fluorescent Protein (YEGFP): a reporter of expression in Candida albicans.";

Microficlogy 0:0-0(1996).

EMBL; 073901; AAB18957.1; -.

HSSP; P42212; 1BFP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aequorea victoria (Jellyfish).
Bukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Leptomedusae,
Aequoreidae, Aequorea.
NCBI_TaxID=6100,
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PRINTE; PR01229; GFLUORESCENT.
PRODEX: PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 26840 WW; A28622809A9DEA60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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Pred. No. 8.7e-96;
2; Mismatches 5;
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InterFro; IPR009017; GFP_like.
InterFro; IPR000786; Green_fl_protein.
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01-FEB-1997 (TrEMBLrel. 02,
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Matches 231; Conservative
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62 VTGLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
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Azomonas and Azotobacter.";

Bubmitted (NOV-2000) to HEBL/GenBank/DDBJ databases.

EMBL; AF324406; AAN86138.1; -..

GO; GO:0006091; P:energy pathways; IEA.

InterPro; IPR009017; GFP like.

InterPro; IPR009017; GFP like.

Pfam; PF01333; GFP; 1.

PRINTS; PR01229; GFLUORESCENT.

PRINTS; PR01229; GFLUORESCENT.

SEQUENCE 238 AA; 26887 MW; E0E1616BD2AF6188 CRC64;
                                                                                                                                                                                                                                                                              Sociation F. Merchyi M., Burg K.;
"Occurrence of green fluorescence protein in diazotrophic bacteria Azomans and Azotobacter.";
Azomans and Azotobacter.";
Submitted (NOV-2000) to HEBEL/GenBank/DDBJ databases.
EMBL; AF324405; AAN86137.1; -.
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP-like.
PRAM: PF01153; GFP: 1.
PRINTS; PR01229; GFPUORESCENT.
BRINTS; PR01229; GFUORESCENT.
SEQUENCE 238 AA; 26902 MW; 15FE9B9C5B4F6B89 CRC64;
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Pseudomonadaceae, Azotobacter.
                                                                                                                                        Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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96.5%; Score 1231; DB 2; Length 238;
Best Local Similarity 97.1%; Pred. No. 1.3e-95;
Matches 231; Conservative 2; Mismatches 5; Indels
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Last annotation update)
Last sequence update)
Last annotation update)
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Aeguorea victoria (Jellyfish)
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                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                                                                                                                        61 VITESYGVQCFSRXPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFRGDTLV 120
                                                                                                                                                                                                                                                                                              NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
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Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=6100;
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Pred, No. 1.6e-95;
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1 Similarity 93.7%; Score 1198; DB 5; Length 2

223; Conservative 6; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Watkins J.N., Campbell A.K.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, X83959; CAA58789.1; -.
PIR; JS0692; JQ1514.
HSSP; P42212; 1GFL.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Green fluorescent protein (Fragment).
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                                              2; Mismatches
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InterPro; IPR009017; GFP like.
InterPro; IPR000786; Green fl protein.
PERN; PF01153; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
Prodom; PD013756; Green fl protein; 1.
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                    97.1%;
                       Best Local Similarity 97.1
Matches 231; Conservative
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Q17105;
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PRELIMINARY;

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61 VITFSYGVQCFSRYPDHMKQHDFLKSAMPEGYVQERIFYKDDGNYKTRAEVKFEGDTLV 120
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                                                                                                                                                                                                                                           Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aeguoreidae; Aeguorea.
NCBI_TaxID=6100;
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q.,
Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 92.8*; Score 1183; DB 5; Length 238; Best Local Similarity 92.9*; Pred. No. 1.4e-91; Matches 221; Conservative 7; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; X83960; CAA58790.1; -.
PIR; JG0692; JG1514.
HSSP; P42212; JBFP.
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009786; Green_fl_protein.
Pfam; PF0153; GFP, 1.
PRINTS; PR01229; GFLUORESCENT.
ProDom; P013756; Green_fl_protein; 1.
PRODOM; P013756; Green_fl_protein; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   macrodactyla.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF495431; AAL33916.1; -.
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR000786; Green_fl_protein.
Ffam; PF0153; GFP; II.
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1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Green fluorescent protein (Fragment).
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                      NCBI_TaxID=147615;
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                                                                                                                                                                                                                                                                                                                                                         STRAIN=ShG24;
                                                                                                                     01-MAR-2002
                                                                                                                                                               01-OCT-2003
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                                   RESULT 9
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STRAIN-GFPAM, and GFPdnaxm;

Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Qin Y.X., Pang S.Q.,

Li S.J., Xia N.S.;

Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

ENBL, AY013824; AAK02062.1;

ENBL, AY013824; AAK02059.1;

GO, GC:0006091; P:energy pathways; IEA.

InterFro; IPR009017; GFP_like.

InterFro; IPR00786; Green_fl_protein.
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Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aeguoreidae; Aeguorea.
NCBI_TaxID=147615;
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                                                                           Query Match

84.5%; Score 1078; DB 5; Length 238;
Best Local Similarity 81.9%; Pred. No. 9.6e-83;
Matches 195; Conservative 20; Mismatches 23; Indels
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PRODOW; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 27049 MW; 8185D0E55529012B CRC64;
PR01229; GFLUORESCENT.
PD013756; Green fl protein; 1.
3 238 AA; 27015 MW; 6B8FD75E88926903 CRC64;
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Last annotation update)
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Matches 194; Conservative
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  PRINTS; PR
ProDom; PC
SEQUENCE
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AC CQBWP
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Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                            Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
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Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
                                                                                                                                             Aequorea macrodactyla.
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 238;
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                                                                                                                                                                                                                                                                                                                                                                                  macrodactyla.;
Submitted (OCT-2011) to the EMBL/GenBank/DDBJ databases.
EMBL; AF435433; AAL33918.1;
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IPR00786; Green_fl_protein.
Pfan; PF01239; GFP, I.
PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green_fl_protein; 1.
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82.4%; Pred. No. 4.5e-82;
Live 17; Mismatches 25;
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238 AA
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Matches 196; Conservative
                                                                                                              Green fluorescent protein.
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122 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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PRODOM; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 27031 MW; 5F80A19C19DC584D CRC64;
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Last annotation update)
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InterPro; IPR009017; GFP_like.
InterPro; IPR000786; Green_fl_protein.
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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81.1%; Pred. No. 8.1e-82;
ive 20; Mismatches 25; Indels
                                                                                                                                                                                                                                                                         Length 238;
                                                                                                                                                                                                                                                                                                                               25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         macrodactyla.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF435429; AAL33914.1;
GO; 60:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IPR000786; Green_fl_protein.
(OCT-2001) to the EMBL/GenBank/DDBJ databases.
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PRINTS; PR01229; GFLVORESCENT.
ProDom; P0013756; Green fl protein; 1.
SEQUENCE 238 AA; 26997 WW; 5F80A192173CB84D CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                         83.8%; Score 1068; DB 5;
81.1%; Pred. No. 6.7e-82;
                                                                                                                                                                                                                                                                                             81.1%; Pred. ...
rive 20; Mismatches
                   EMBL, AF435427, AAL33912.1; -. GO: GO:0006091; P:energy pathways; IEA.
ThrerPro: IPR009017; GFP_like.
                                                                         InterPro, IPR009017; GFP like.
InterPro, IPR000786; Green fl protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Green fluorescent protein.
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Matches 193; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTGLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                    Chen M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Eukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Leptomedusae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                             Duo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.4%; Score 1063; DB 5; Length 238; 81.9%; Pred. No. 1.8e-81; ive 17; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is.J., Xia N.S.; "Colorful mutants of green fluorescent protein from Aeguorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25; Indels
                                                                                                                                                                     macrodactyla.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF435430; AAL33915.1;
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IPR0090786; Green_fl_protein.
PF01353; GFP; 1.
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PRODOM; PD013756; Green_fl_protein; 1.
SEQUENCE 238 AA; 27018 MW; 75521EA5534E573A CRC64;
                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01229; GFLUORESCENT.
Prodom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 27002 MW; BD5BA2982264C018 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.5%; Score 1065; DB 5;
81.1%; Pred. No. 1.2e-81;
iive 20; Mismatches 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Orange fluorescent protein.
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Matches 195; Conservative
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Best Local Similarity 81.19
Matches 193, Conservative
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NCBI_TaxID=147615;
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                                                        STRAIN=GFPxm191uv;
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                                                                                       Luo W.X.,
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99
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                                                                                                                                                                                                                                                                                                                                                                                                                                               62 VIGLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Montastraea cavernosa (great star coral).
Bukaryota, Metazoa, Cnidaria, Anthozoa, Zoantharia, Scleractinia,
Favina, Favinae, Montastraea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 225;
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"Montastraea cavernosa fluorescent protein.";
"Montastraea cavernosa fluorescent protein.";
submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AYO56460; AAL17905.1;
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR000786; Green_fl_protein.
Pfan; PP01353; GFP; I.
PRINTS; PR01229; GFLUORESCENT.
PRODE, PR01375; Green_fl_protein; I.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cyan fluorescent protein (Fragment).
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June 21, 2004, 15:41:49; Search time 47.1111 Seconds (without alignments) 1433.395 Million cell updates/sec
GenCore version 5.1.6
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                    Copyright
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US-09-887-784-64L 1273 1 WVSKGEELFTGVVPILVELD......VLLGFVTAAGITLGMDELYK 239 Title: Perfect score: Sequence:

1586107 seqs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

1586107 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

A\_Geneseq\_29Jan04:\*
1: geneseqp1980s:\*
2: geneseqp1990s:\*
4: geneseqp2000s:\*
5: geneseqp2001s:\*
6: geneseqp2003as:\*
7: geneseqp2003bs:\*
8: geneseqp2003bs:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|   | Description    | Aae17    | 52 Abr40352 Human ami |         |          |          | 82 Aab22882 Enhanced | 49 Aay54349 Amino aci | Aay79584 |          | 00 Aab85900 A. victor | 71 Aab31171 Amino aci | 98 Aag66198 A. victor |          | Aae14599 | Aae34958 | Aag79829 | Abr83616 | Ada38074 | Abu63204 | 58 Adc18358 EGFP (enh | 14 Abw00914 Aequorea | Ade28570 | 11 Abm79011 Enhanced | 19 Aaq68319 Jellyfish |   |
|---|----------------|----------|-----------------------|---------|----------|----------|----------------------|-----------------------|----------|----------|-----------------------|-----------------------|-----------------------|----------|----------|----------|----------|----------|----------|----------|-----------------------|----------------------|----------|----------------------|-----------------------|---|
|   | Ω              | AAE17518 | ABR40352              | AAG6578 | AAG65782 | AAE17517 | AAB22882             | AAY54349              | AAY79584 | AAB50804 | AAB85900              | AAB31171              | AAG66198              | ABG94444 | AAE14599 | AAE34958 | AAG79829 | ABR83616 | ADA38074 | ABU63204 | ADC18358              | ABW00914             | ADE28570 | ABM7901              | AAG68319              |   |
|   | DB             | i ru     | φ                     | 4       | 4        | ß        | m                    | ٣                     | m        | 4        | 4                     | 4                     | ß                     | Ŋ        | S        | 9        |          | 9        | 9        | 7        | 7                     | 7                    | 7        | 7                    | 'n                    | • |
|   | Length         | 239      | 363                   | 893     | 1132     | 239      | 239                  | 239                   | 239      | 239      | 239                   | 239                   | 239                   | 239      | 239      | 239      | 239      | 239      | 239      | 239      | 239                   | 239                  | 239      | 246                  | 248                   |   |
| æ | Ouery<br>Match | 9.66     | 99.6                  | 99.66   | 9.66     | 0.66     | 98.7                 | 98.7                  | 98.7     | 98.7     | 98.7                  | 98.7                  | 98.7                  | 98.7     | 98.7     | 98.7     | 98.7     | 98.7     | 98.7     | 98.7     | 98.7                  | 98.7                 | 98.7     | 98.7                 | 98.7                  | ( |
|   | Score          | 1268     | 1268                  | 1268    | 1268     | 1260     | 1257                 | 1257                  | 1257     | 1257     | 1257                  | 1257                  | 1257                  | 1257     | 1257     | 1257     | 1257     | 1257     | 1257     | 1257     | 1257                  | 1257                 | 1257     | 1257                 | 1257                  |   |
|   |                | 1        | 7                     | e       | 4        | ហ        | 9                    | 7                     | 80       | 0        | 10                    | 11                    | 12                    | 13       | 14       | 15       | 16       | 17       | 18       | 19       | 20                    | 21                   | 22       | 23                   | 24                    |   |

Novel fluorescent protein in in vitro assay for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution, has a green fluorescent protein with F64L and E222G

Claim 9; Page 37; 41pp; English.

mutation.

| Wild-type<br>Biomembra<br>Biomembra<br>Biomembra<br>Biomembra<br>Biomembra<br>Biomembra<br>Green five<br>EGFP-MODC<br>EGFP-MODC<br>EGFP-MODC<br>EGFP/ hum<br>EGFP/ | _        |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------|
| Aaw97451 Aau99803 Aau99800 Aau99800 Aau99800 Aay42181 Abay42181 Abay42181 Abay42181                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Abr83621 |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |          |
| AAW97451 AAU99800 AAU99800 AAU99800 AAU99800 AAU99801 AAU59801 AAU5080 AAU5080 AAU5080 AAU5080 AAY2181 AAY43181                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ABR83621 |
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| 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 323      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 98.7     |
| 1257<br>1257<br>1257<br>1257<br>1257<br>1257<br>1257<br>1257                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 1257     |
| 00000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 45       |

## ALIGNMENTS

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/note= "Wild type Glu substituted with Gly; This corresponds to position 222 in the wild type protein"
                                                                                                                                                                                   /note= "Wild type Phe substituted with Leu; This
corresponds to position 64 in the wild type protein"
Misc-difference 223
                                                                                                          Jellyfish; green fluorescent protein; GFP; protein redistribution; cellular function; genetic reporter; mutant; Stoke's shift; mutein.
                                                                                     Enhanced F64L-E222G jellyfish green fluorescent protein mutant
                                                                                                                                                                         Key Location/Qualifiers
Misc-difference 65
                                                                                                                                                                                                                                                                                                                                                                                                        Thastrup 0;
                    AAE17518 standard; protein; 239 AA.
                                                                                                                                                                                                                                                                                                                             19-JUN-2000; 2000DK-00000953.
20-JUN-2000; 2000US-0212681P.
10-MAY-2001; 2001DK-00000739.
10-MAY-2001; 2001US-0290170P.
                                                                                                                                                                                                                                                                                                          18-JUN-2001; 2001WO-EP006848
                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                          Bjorn SP, Pagliaro L,
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-098224/13.
N-PSDB; AAD28163.
                                                                                                                                                                                                                                                                                                                                                                                   (BIOI -) BIOIMAGE AS.
                                                                                                                                       Aequorea victoria.
Synthetic.
                                                                                                                                                                                                                                                               WO200198338-A2
                                                                22-APR-2002
                                                                                                                                                                                                                                                                                    27-DEC-2001.
                                          AAE17518;
RESULT 1
AAE17518
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The invention relates to a fluorescent protein derived from green fluorescent protein (GFP) or its analogue. The GFP containing mutations at Felf. and E2266 has a bigger compared to other GFP's making it very suitable for high throughput screening due to better resolution. The fluorescent protein is useful in invitro assays for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution. The fluorescent protein tags in transgenic animals, living and fixed cells; organelle tags, secretion marker and genetic reporter. The fluorescent protein is also useful as a cell or organelle integrity marker, a marker for changes in cell morphology, as transfection marker. The fluorescent protein is also useful as a cell or organelle integrity marker, a marker to be used in combination with fluorescence activated cell sorting (FACS). The novel proteins can also be used as reporter to monitor live or dead biomass of organisms, such as fungi. The fluorescent protein is also useful as markers in transcriptional and translational protein for bacterial detection. Transposons encoding the fluorescent protein are useful for screening promoters and for tagging plasmids and as a reporter for bacterial detection. Transposons encoding the fluorescent protein are useful for designing diagnostic tool. The present sequence is a DNA encoding conhanced F64L-E222G jellyfish green fluorescent protein (GFP) mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1268; DB 5; Length 239;
Pred. No. 2e-122;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; heterologous conjugate; intracellular protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human amino acid sequence SEQ ID NO: 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR40352 standard; protein; 363 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.6%;
al Similarity 99.6%;
238; Conservative (
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11-OCT-2001; 2001US-0328896P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002; 2002WO-DK000651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BIOL-) BIOLMAGE AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aequoria victoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 239 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-JUL-2003
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Best Local S
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The invention relates to a novel cell, comprising three heterologous conjugates (HC), a first HC (HC1) comprising an anchor protein that specifically binds to an internal structure within the cell conjugated to an interactor protein (IP) of type A, a second HC (HC2) comprising IP of type B conjugated to a first protein of interest, and a third HC (HC3) comprising a second protein of interest conjugated to detectable group. The cell is useful for detecting if a compound disrupts or induces the interaction between two intracellular proteins. The cell is also useful for screening compounds that modulate the interaction between two intracellular proteins. The present sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                            Novel cell for identifying modulators of protein interaction, contains a first conjugate comprising anchor protein, second conjugate having type B interactor protein and third conjugate with detectable group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 VARIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDE4; central nervous system; antiinflammatory; cytostatic; nootropic; autoimmune; ischemic; osteopathic; GPP; green fluorescent protein; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPMPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MVSKGBELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPMPT
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0
                                                                                                                                                                                                                                                                                                                                                                                                              Length 363;
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                                                                                                                                                                                                                                                                                                                                                                                                            Score 1268; DB 6;
Pred. No. 3.7e-122;
                                                                                                                                                                                                                                                                                                                                                                                                99.6%; Scor.
99.6%; Pred. No. 3...
0; Mismatches
                                                                                                                                 Disclosure; Page 112-113; 118pp; English
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29-MAY-2000; 2000DK-00000849.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 238; Conservative
                2003-430211/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BIOI - ) BIOIMAGE AS
                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                WPI; 2003-430211/
N-PSDB; ACC72604.
                                                                                                                                                                                                                                                                                                                                                                            Sequence 363 AA;
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Best Local 8
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셤
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25-OCT-2001.

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The invention relates to determining, if a compound, is a dislocator of PDB4. The method comprises testing if the compound removes PDB4 spots, which may optionally be induced by a Roliprami-like reference compound, and testing if it inhibits the catalytic activity of the PDB4, where the compound is a dislocator of PDB4, if it removes PDB spots and if it does not inhibit the catalytic activity of PDB4. The method is useful for the treatment of diseases of the central dentifying compounds useful for the treatment of diseases of the central nervous system such as joint inflammation, Crohn's diseases of inflammatory bowel disease, respiratory diseases, cronn's disease, inflammatory bowel compound as than, chronic bronchitis, pulmonary disease (CODD), including asthma, chronic bronchitis, pulmonary disease condotoxic shock, toxic shock syndrome, systemic lupus erthematosis, postiaeis, bone resorption diseases, repetitusion injury, cancer and HIV infection. The use of a reagent that can mimic or reverse the effect of the compound with affinity for the catalytic site on intracellular distribution of the PDB for the preparation of a medicament. The present serion can distribution of the PDB for the preparation of a HSPDB4A1-E222G fusion
                                                                                                                              Determining if a compound is a dislocator of PDE4 for identifying compounds for treating CNS and inflammatory disease comprises identifying compounds which remove PDE4 spots.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLDVPWPT 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVTLLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        715 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               775 VNRIELKGIDPKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNPKIRHNIEDGSVQLA 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DHYQONTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    835 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWVLLGFVTAAGITLGMDELYK 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDE4; central nervous system; antiinflammatory; cytostatic; nootropic; autoimmune; ischemic; osteopathic; GFP; green fluorescent protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 99.6%; Score 1268; DB 4; Length 893; Best Local Similarity 99.6%; Pred. No. 1.4e-121; Matches 238; Conservative 0; Mismatches 1; Indels C
Bjorn SP, Thastrup O, Almholt DC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of HSPDE4A4-E222G fusion protein.
                                                                                                                                                                                                                     Example 1; Page 156-160; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG65782 standard; protein; 1132 AA
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  Scudder KM,
                                                                WPI; 2001-611727/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aequorea victoria.
                                                                                       N-PSDB; AAI66852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 893 AA;
                    Praestegaard M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fusion protein.
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The invention relates to determining, if a compound, is a dislocator of PDB4. The method comprises testing if the compound removes PDB4 spots, which may optionally be induced by a Rollpram-like reference compound, and testing if it inhibite the catalytic activity of the PDB4, where the compound is a dislocator of PDB4, if it removes PDE spots and if it does not inhibit the catalytic activity of PDB4. The method is useful for identifying compounds useful for the treatment of diseases such as joint inflammation, cron's disease such as joint inflammation, cron's disease, inflammatory bowel disease, respiratory diseases, chronic obstructive pulmonary disease (ODPD), including asthma, chronic bronchitis, pulmonary emphysema, endotoxic shock toxic shock syndrome, systemic lupus erthematosis, bone resorption diseases, reperfusion injury, cancer and HIV psection. The use of a reagent that can mimic or reverse the effect of the compound with affinity for the catalytic site on intracellular distribution of the PDE for the preparation of a medicament. The present sequence represents the amino acid sequence of a HSPDB4A4-E222G fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .014 VNRIELKGIDFKEDGNILGHKLEYNYNSHNYYIMADKQKNGIKVNFKIRHNIEDGSVQLA 1073
                                                                                                                                                                                                                                                                                     Determining if a compound is a dislocator of PDE4 for identifying compounds for treating CNS and inflammatory disease comprises identifying compounds which remove PDE4 spots.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LVTLLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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                                                                                                                                                                       Thastrup O, Almholt DC;
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0; Mismatches 1
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                                                                                                                                                                         Bjorn SP,
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                                    11-APR-2001; 2001WO-DK000264.
                                                                          17-APR-2000; 2000DK-0000651.
29-MAY-2000; 2000DK-00000849.
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Matches 238; Conservative
                                                                                                                                                                         Scudder KM,
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N-PSDB; AA166853.
                                                                                                                                   (BIOI-) BIOIMAGE AS
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                                                                                                                                                                                        Praestegaard M;
                                                                                                                                                                         Terry BR,
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The invention relates to a fluorescent protein derived from green fluorescent protein (GFP) or its analogue. The GFP containing mutations at F641 and E322G has a bigger compared to other GFP's making it very suitable for high throughput screening due to better resolution. The fluorescent protein is useful in invitro assays for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution. The fluorescent protein is useful in studying cellular functions in living cells, as protein tags in transgenic animals, living and fixed cells; organelle tags, secretion marker and genetic reporter. The fluorescent protein is also useful as a cell or organelle integrity marker, a marker for changes in cell morphology, as transfection marker, and as a marker to be used in combination with fluorescence activated cell systing (FACS). The novel proteins an also be used as reporters to monitor live or dead biomass of organisms, such as fungi. The fluorescent protein as markers in transcriptional and translational fusions for performing transposons encoding the fluorescent protein are useful for screening promoters and for tagging plasmids and chromosomes. The fluorescent protein engineered into the genome of a phage is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel Eluorescent protein in in vitro assay for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution, has a green fluorescent protein with F64L and E222G
                                                                                                                                                               /note= "Wild type Phe substituted with Leu; This corresponds to position 64 in the wild type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for designing diagnostic tool. The present sequence is enhanced F64L
Jellyfish; green fluorescent protein; GFP; protein redistribution; cellular function; genetic reporter; mutant; Stoke's shift; mutein.
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                                                                                                                        Location/Qualifiers
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20-JUN-2000; 2000US-0212681P.
10-MAX-2001; 2001DK-00000739.
10-MAY-2001; 2001US-0290170P.
                                                                                                                                                                                                                                                                                                           18-JUN-2001; 2001WO-EP006848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2302-098224/13.
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                                                              Aequorea victoria.
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                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mutation.
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61 LVTLLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120 1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGGEGDATYGKLTLKFICTTGKLPVPWPT MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT Gaps . 0 99.0%; Score 1260; DB 5; Length 239; 99.2%; Pred. No. 1.3e-121; 2; Mismatches 2; Indels 237; Conservative Local Similarity Query Match Best Local Matches g à 음

Sequence 239 AA;

9 9 121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180

Biodetector protein; fusion protein; recognition site; cellular targetting sequence; cellular localisation; fluorescent protein; protease activity detection; toxin detection; cellular stress detection; 181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239 Automated cell-based characterization of toxin by contacting cells containing luminescent reporter molecules with test substance and analyzing optically. Enhanced green fluorescent protein (EGFP), SEQ ID NO:46. drug discovery; cell based screening. Example 11; Fig 29A; 336pp; English. AAB22882 standard; protein; 239 AA 99US-0122152P. 99US-0123399P. 99US-00352171. 25-FEB-2000; 2000WO-US004794. (first entry) Giuliano KA, Kapur R; (CELL-) CELLOMICS INC WPI; 2000-594086/56. Aeguorea victoria. N-PSDB; AAA93373. WO200050872-A2. 26-FEB-1999; 08-MAR-1999; 10-JAN-2001 12-JUL-1999; 31-AUG-2000 Synthetic. AAB22882; AAB22882 RESULT ò 셤 

The invention relates to systems, methods and reagents for cell-based screening or detection of compounds which affect particular biological tunctions. The methods of the invention utilise fluorescent biodetector molecules which, when acted on by a compound of interest, cause an afteration in the cellular distribution of at least the fluorescent context. In one embodiament, the biosensors comprise hear shock proteins a least to a fluorescent protein (e.g., jellyfish green fluorescent protein (e.g., jellyfish green fluorescent protein (e.g., jellyfish green fluorescent proteins can be used to detect protesse activity such protease biodetector proteins can be used to detect protesse activity. Such protease biodetector fusion proteins comprise one or more fluorescent proteins, a recognition signal which is cleaved by the protease; and at least one cellular localisation signal the latter two components may be from heterologous sources. Due to the protease, or may be from heterologous sources. Due to the components of a single protein which is acted upon by the protease of interest, the region of the cell. Once acted on by the protease of interest, the coalisation signal attached from the localisation sequence, and is free to migrate to other locations within the cell. The presence of a second localisation signal attached to a different cellular compartment after cleavage of the protease recognition sequence. The change in distribution of the fluorescent protein of the fluorescent protein of the fluorescent protein compartment after cleavage of the protease recognition sequence in magning methods with a high degree of spatial resolution. The methods and imaging methods with a high degree of spatial resolution. The methods and

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cellular activities and to screen compounds which modulate these example, may be used for the screening of compounds which modulate these apoptosis, while biosensors containing a recognition site for caspase, for appoptosis, while biosensors containing other protease recognition sites may be used for the detection of proteolytic toxins (such as anthrax candidate compound optimisation by combining many cell screening formats with fluorescence-based molecular reagents and computer-based feature and speed of data analysis and automation, resulting in increased quantity and speed of data collection and faster evaluation of drug candidates. Sequences AAB22881-B22885 represent fluorescent proteins which may used as components of biosensor fusion proteins of the invention
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biosensors of the invention can be used to investigate a wide range of
                                                                                                                                                                                                                                                                                                                           MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                          Length 239;
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                                                                                                                                                                                                                                                          Score 1257; DB 3;
Pred. No. 2.7e-121;
1; Mismatches 2;
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                                                                                                                                                                                                                                                                                          Matches 236; Conservative
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                                                                                                                                                                                                                             Sequence 239 AA;
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                                                                                                                                                                protein based on the Advance green fluorescent protein (GFP). The emission intensity changes as pH varies between 5 and 10 of the present protein are novel. The functional engineered fluorescent proteins show reversible changes in fluorescence over physiological pH ranges. They can be used for determining the pH of samples and cells. The polymucleotides can also be used to produce transgenic animals. The fluorescent protein pH sensors can be delivered to cells in the form of polymucleotides encoding the protein sensor fused to a targeting signal. The targeting signal directs the expression of the protein sensors to restricted cell locations. This makes it possible to measure the pH of a precisely defined cellular region or organelle
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                                                                           fluorescent proteins, used for measuring
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                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                      sequence represents a functional engineered fluorescent
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                                                                                                                                                                                                                                                                                                                                                                                      Length 239;
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                                                                                                                                                                                                                                                                                                                                                                                   Score 1257; DB 3;
Pred. No. 2.7e-121;
1; Mismatches 2;
                                                                           New functional engineered green fluores
the pH in biological samples and cells.
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                                                                                                                        Disclosure; Page 9; 89pp; English
 Wachter RM;
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                                                                                                                                                                                                                                                                                                                                                                                      98.78;
98.78;
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nes 236; Conservative
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 Llopis J,
                              WPI; 2000-116540/10.
N-PSDB; AAZ45642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGFP signal domain.
                                                                                                                                                                                                                                                                                                                                                         Sequence 239 AA;
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26-MAY-1999;
                                                                                                                                                        present
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Tsien RY,
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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AABS0804 standard; protein; 239 AA
                                Claim 14; Fig 29A; 218pp; English.
                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                         Jellyfish GFP mutant EGFP
                                                                                                                                      Best Local Similarity 98.7
Matches 236; Conservative
                                                                                                                                                                                                                                                                                 Aequorea victoria
   WPI; 2000-365644,
N-PSDB: AAA27573
                                                                                                                          Sequence 239 AA;
                                                                                                                                                                                                                                                                                          WO200071565-A2.
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                                                                                                                                  Query Match
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The present sequence is a fluorescnet protein used in the construction of a fluorescent protein indicator. The indicator comprises a sensor polypeptide that is responsive to a chemical, biological, electrical or physiological parameter, and a fluorescence protein functional group. The sensor polypeptide is operatively inserted into the fluorescent moiety. The fluorescent indicator is useful for detecting the presence of a response inducing member in a sample. The method involves contacting the sample with the indicator and detecting a change in fluorescence, in which a change is indicative of the effect of the parameter on the sensor polypeptide. The novel fluorescent proteins are advantageous due to their reduced size as compared to the FRET (fluorescence resonance energy transfer)-based sensors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                                                                                                                                                                                                                            Novel fluorescent proteins comprising a sensor protein inserted into them, useful for measuring the response of a sensor biological, chemical, electrical or physiological parameter in vivo or in vitro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGGGATYGKLTKFICTTGKLPVPWPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fluorescent polypeptide; orexigenic; anabolic; food intake; GFP; green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A. victoria green fluorescent protein (GFP) and linker sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

98.7%; Score 1257; DB 4; Length 239;
Best Local Similarity 98.7%; Pred. No. 2.7e-121;
Matches 236; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 24; 94pp; English.
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17-MAY-2000; 2000WO-US013684.
                                                      99US-00316919.
99US-00316920.
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                                                                                                                                       (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                Baird GA;
                                                                                                                                                                                                                                                    WPI; 2001-032017/04.
                                                                                                                                                                                                                                                                                 N-PSDB; AAC90488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 239 AA;
                                                      21-MAY-1999;
21-MAY-1999;
                                                                                                                                                                                                Tsien RY,
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                                                                                                                                                                                                                                                                   The present sequence is that of the BGFP signal domain, which can be included in novel recombinant protease biosensors (PBS) of the invention. The PBIS (see AAY79638-54) comprise: a first domain (see AAY79579-87) comprising at least 1 detectable polypeptide signal such as the present sequence; a second domain (see AAY79588-622) comprising at least 1 least the present comprising at least 1 reactant target sequence. A recombinant nucleic comprising at least 1 seactant target sequence. A recombinant nucleic acid (see AAA27627-43) encoding the PB, an expression vector, and a CG acid (see AAA27627-43) encoding the PB, an expression vector, and a cG dentifying engound that modify protease activity in cell involves contacting a host cell that possesses the recombinant PB with a test compound, and determining the PB distribution in the host cell, where CG changes in the distribution of the PB are correlated with modification of protease activity in a host cell include the compounds that modify protease activity in a host cell include the compounds that modify protease activity in a host cell include the crocmbinant nucleic acid, or the recombinant PB, or the vector, or the host cell. The PB is useful in high content screens to detect in vivo activation of enzymatic activity, and to identify specific activity based con cleavage of a known recognition motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 LVTLLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LVITLIYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDIL 120
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                                                                                                                Recombinant nucleic acid encoding a protease biosensor useful for fluorescence based cell and molecular biochemical assays for drug discovery comprising three operably linked nucleic acid sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.7%; Score 1257; DB 3; 98.7%; Pred. No. 2.7e-121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
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fusion;

Aequorea victoria.

Synthetic.

WO200168706-A1

9

0; Gaps

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The specification describes a method for assessing the growth rate and death rate of a micro-organism within a predetermined time period in a desired environment. The method comprises introducing at least two reporter genes encoding luminescent and/or fluorescent products into the micro-organisms, incubating the micro-organism within the desired environment, and detecting luminescence and/or fluorescence after a predetermined time period. Use of two different markers within a micro-organism enables the differentiation between growth and death rates. The method is used to assess the growth rate and death rate of a micro-organism within a predetermined time period in a desired environment. The present sequence represents a green fluorescent protein (GFP), and is encoded by a plasmid which encodes luminescent and fluorescent proteins, and is used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LVITLIYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LVTLLSYGVOCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                                                                                                                           Assessing growth and death rates of a micro-organism in a desired environment, by introducing 2 reporter genes encoding luminescent and fluorescent products and detecting luminescent fluorescence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.7%; Score 1257; DB 4; Length 239; 98.7%; Pred. No. 2.7e-121; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A. victoria green fluorescent protein (EGFP).
                                                                                                                                                                                                                                                                                                               Disclosure; Page 27; 32pp; English.
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                     99FI-00001296
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Matches 236; Conservative
                                                                                                                                                                 WPI; 2001-061737/07
                                                                                                                        Lilius E, Virta M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aequorea victoria
                                                            (LILI/) LILIUS E. (VIRT/) VIRTA M.
                                                                                                                                                                                         N-PSDB; AAC86954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 239 AA;
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                     07-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                      The invention provides melanin concentrating hormone (MCH) receptor (MCHR) chimeric and fusion proteins. The MCHR chimeric proteins comprise MCHR polypeptide regions from different species. The MCHR fusion protein comprise MCHR polypeptide region and a fluorescent polypeptide region of polypeptide region protein solypeptide region. The MCHR fusion proteins can be expressed by standard recombinant methodology. MCH action promotes feeding (orexigenic) and up regulation of MCH activity stimulates food intake. The present sequence represents a A. victoria green fluorescent protein (GFP) and a linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LVTLLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                  Fusion proteins comprising melanin concentrating hormone receptor peptides and fluorescent proteins, useful for identifying appetite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Growth rate, death rate, reporter gene, luminescent protein, fluorescent product, luciferase, green fluorescent protein, GFP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1257; DB 4; Length 239;
Pred. No. 2.7e-121;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of a green fluorescent protein (GFP).
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                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 14; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.7%;
98.7%;
                                      14-MAR-2001; 2001WO-US008071.
                                                                             15-MAR-2000; 2000US-0189698P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 236; Conservative
                                                                                                                    (MERI ) MERCK & CO INC
                                                                                                                                                                                                      WPI; 2001-565791/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                                             N-PSDB; AAH47304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 239 AA;
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20-SEP-2001
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                                                                                                                                                                                                                                                                                                           stimulants.
                                                                                                                                                               Marsh DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB31171;
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Gaps ; 0

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99US-00398965.
                                                                     Kapur R;
                                                                                         2002-634730/68.
                                        (GIUL/) GIULIANO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aequorea victoria.
                                                                                                                                                                                                                                                                                                                                                screening system
                                                                                                                                                                                                                                                                                                                                                                   Sequence 239 AA;
                                                                                                   N-PSDB; ABS71491
         29-OCT-1999;
01-DEC-1999;
 17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAY-2002
                                                                     Giuliano K,
                                                                                                                                                     identifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19
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                                                  KAPU/)
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                                                                                                                                                                                                                                                                                                                                                51 LVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                    VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                              The invention relates to a gene encoding proteins having cyan-green fluorescence characteristic and having a function of showing stable fluorescence characteristic in acid region. A method for the preparation of a cyan-green fluorescent protein is provided which involves a transformant transformed by a recombinant vector comprising the gene, where the transformant is cultured and the protein is collected from the culture. The present sequence represents the A. victoria green fluorescent protein (BGFP)
                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                           DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                     1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                       1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detection, classification, identification, toxin detection, protease, ADP-ribosylating toxin, cytotoxic phospholipase, exfoliative toxin,
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                               Length 239;
                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                              Score 1257; DB 5;
Pred. No. 2.7e-121;
                                                                                                                                                                                                                                                                   5
                                                                                          encoding cyan-green fluorescent protein.
                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protease biosensor signal sequence #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG94444 standard; protein; 239 AA
                                                                                                                Example; Page 14; 20pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-00810983.
98US-00031271.
99US-0123152P.
99US-013399P.
99US-00352171.
                                                                                                                                                                                                                                               98.7%;
98.7%;
   04-AUG-2000; 2000JP-00237165
                       04-AUG-2000; 2000JP-00237165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-00513783
                                           (RIKA ) RIKAGAKU KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                        Best Local Similarity 98.7
Matches 236; Conservative
                                                              WPI; 2002-299190/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    toxic threat agent
                                                                          N-PSDB; ABL40628.
                                                                                                                                                                                                                            Sequence 239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6416959-B1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAR-1999;
12-JUL-1999;
31-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-NOV-2002
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26-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                               51
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                                                                                                                                                                                                                                                 Query Match
                                                                                             gene
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The invention describes methods of automated detection, classification and identification comprising treating cells containing luminescent containing luminescent reporter molecules (I) in array of locations with a test substance, where (I) are detectors, classifiers or identifiers, imaging cells in each location to obtain luminescent signals and converting optical information into digital data to interpret presence of toxins in the test substance. The method are useful for detection of toxins chosen from proteases, ADP-ribosylating toxins, cytotoxic phospholipases, and exfoliative toxins. Three classes of cell-based luminescent reporter molecules such as detectors, classifiers and identifiers are described and serve as reporters of toxic threat agents. The first two levels of characterisation ensure a rapid readout of toxin class without several complex mixtures of known toxins. This is the amino acid sequence of a protease biosensor related signal sequence used in the cell-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWYLGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutagenesis; enhanced green fluorescent protein; EGFP; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGBGEGDATYGKLTLKFICTTGKLPVPWPT
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                                                                                                                                                                                                                                                                                                                                                                                                Automated cell-based toxin detection, classification, and/or identification by treating cells involves use of three classes luminescent reporter molecules such as detectors, classifiers o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1257; DB 5; Length 239; Pred. No. 2.7e-121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 10; Fig 29A; 214pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ą.
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99US-00430656.
99US-0168408P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 98.7
Matches 236; Conservative
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120

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181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
               DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Col 56-57; 38pp; English
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                                                                                                                 AAE34958 standard; protein; 239
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98.7%;
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                                                                                                                                                                                                                                                                                                                                                                                            24-MAY-2001; 2001US-00865291
                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 98.77
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2003-148474/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ting AY,
                                                                                                                                                                                                                                                                            Aequorea victoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     operative linkage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-148474/
N-PSDB; AAD53428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 239 AA;
                                                                                                                                                                                                                                                                                                        WO200295058-A2
                                                                                                                                                                         28-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tsien RY,
               181
                                                                                                                                            AAE34958;
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                                                                                      RESULT 15
                                                                                                  AAE34958
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                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method for mutagenesis that comprises synthesising a mutated strand and a complementary strand by use of synthesising a mutated basically comprises a DNA synthesis in which one cor more primers that have a nucleotide sequence containing at least one or more primers that have a nucleotide sequence containing at least one mutation and a phosphorylated 5-terminus are annealed to a template DNA and then subjected to an elongation reaction using a thermostable high-containing then subjected terminus are ligated by means of a thermostable high-containing the primers; a digestion in which the stop of DNA synthesis is repeated several lines to amplify the DNA containing the primers and then, at least DNAs other than the amplified circular DNA are digested into several fragments obtained in the step of DNA synthesis in which, with the several fragments obtained in the step of digestion as megaprimers the megaprimers are annealed to the circular DNA synthesised above, followed by an elongation reaction performed using the thermostable high-fidality DNA polymerase. The method is useful for mutagenesis, particularly for introducing centain mutations at certain sites of the nucleotide sequence. The present method is simple, speedy, economical and widely applicable. The present sequence is certain sites of the nucleotide sequence. The present sequence is mutagenesis in an exemplification of the invention. The EGPP used for mutagenesis in an exemplification of the invention. The EGPP is derived intering the green fluorescent protein (GFP) sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVTLLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNRIBLKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNYYIMADKOKNGIKVNFKIRHNIEDGSVOLA 180
                                                                                                                                                                                                                                                                                                                                                               Method for mutagenesis, e.g. for introducing certain or random mutations at certain sites of the nucleotide sequence, comprises synthesizing a mutated strand and a complementary strand by use of megaprimers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                              . .3
note= "Wild-type GFP Met-Ser are replaced with Met-Val-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 239;
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                                                                                   Phe64 is replaced by Leu"
                                                                                                               "GFP Ser65 is replaced by Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1257; DB 5;
Pred. No. 2.7e-121;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 13-14; 31pp; English.
               Location/Qualifiers
                                                                                                                                                                                                    03-AUG-2001; 2001EP-00306650.
                                                                                   "GFP
                                                                                                                                                                                                                               04-AUG-2000; 2000JP-00237166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.7%;
ilarity 98.7%;
Conservative
                                                                                    /note=
                                                                                                                 /note=
                                                                                                                                                                                                                                                                                        Miyawaki A, Sawano A;
                                                                                                                                                                                                                                                                                                                     WPI; 2002-208112/27.
                                                                                                Misc-difference 66
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                                                                                                                                                                                                                                                          (RIKE ) RIKEN KK.
                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAD27910.
                           Misc-difference
                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 239 AA;
                                                                                                                                            EP1178109-A1
                                                                                                                                                                       06-FEB-2002
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comprising a phosphorylation polypeptide and a fluorescent protein or in operative linkage, a donor molecule, a phosphorylatable domain, a phosphorylation indicators of the invention an acceptor molecule. The phosphorylation indicators of the invention are useful for detecting kinases or phosphatases in a biological sample. They are also useful in this throughput analysis e.g. for detecting a kinase inhibitor or phosphatase inhibitor. The present sequence is Aequorea victoria enhanced green fluorescent protein (EGFP) used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphorylation indicator, fluorescent protein; detection; phosphatase; kinase; enhanced green fluorescent protein; EGFP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel chimeric phosphorylation indicators, useful for detecting
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Pred. No. 2.7e-121;
1; Mismatches 2;
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131 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 239

Search completed: June 21, 2004, 15:54:10 Job time: 48.1111 secs us-09-887-784-641.rai

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Sequence 46, Appl
Sequence 4, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 6, Appli
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Sequence 129, Appli
Sequence 127, Appli
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Sequence 2, App
Sequence 6, App
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                                                                June 21, 2004, 15:46:55 ; Search time 12.7778 Seconds
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/RecoMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-513-783A-46

US-09-503-783A-46

US-09-602-641-3

US-09-602-102-1

US-09-513-783A-2

US-09-513-783A-2

US-09-513-783A-2

US-09-602-641-21

US-09-602-641-21

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Maximum Match 100%
Listing first 45 summaries
                                           protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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| Sequence 3, Application US/09172063
| Patent No. 6150176
| GENERAL INPORMATION:
| APPLICANT: INPORMATION:
| APPLICANT: Injois, Juan
| APPLICANT: Injois, Juan
| APPLICANT: Remington, S. James
| TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
| TITLE OF INVENTION: PLOYERSCENT PROTEIN SENSORS FOR
| TITLE OF INVENTION: WORDSER: US/09/172,063
| TITLE OF INVENTION: WORDSER: US/09/172,063
| CURRENT FILING DATE: 1998-10-13
| EARLIER PILICATION NUMBER: US/09/172,063
| SERVILER PILICATION NUMBER: US/09/172,063
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Pred. No. 9.3e-127;
1; Mismatches 2;
                                                                                                  US-09-417-197-75
US-09-417-197-75
US-09-417-197-139
US-09-417-197-139
US-09-417-197-141
US-09-417-197-143
US-09-417-197-197-197-197
US-09-417-197-197-197
US-09-417-197-61
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98.7%;
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ORGANISM: Aequorea victoria
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Best Local Similarity 98.7
Matches 236; Conservative
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RESULT 1
US-09-172-063-3
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181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239

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RESULT 5
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                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: EGFP
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                      Sequence 46, Application US/09513783A

Patent No. 641659
GENERAL INFORMATION:
APPLICANT: Giulano, Kenneth A.
TITLE OF INVENTION: A System for Cell Based Screening
TITLE OF INVENTION: A System for Cell Based Screening
TITLE OF INVENTION: A System for Cell Based Screening
CURRENT APPLICANION NUMBER: US/09/513,783A
CURRENT FILING DATE: 2000-02-25
NUMBER CF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SEQ ID NC 46
LENGTH: 239
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; GENERAL INFORMATION:
APPLICANT: Taien, Roger Y.
; APPLICANT: Baird, Geoffrey.
; TITLE OF INVENTION: FIUORESCENT PROTEIN INDICATORS
; TITLE OF INVENTION: FIUORESCENT
; CURRENT APPLICATION UNMER: US/09/316,919
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 63
; SOFFTARR: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4
; SEQ ID NO 4
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Patent No. 6469154
                                                                                                                                                                                                                                                                   TYPE: FRT
ORGANISM: Artificial Sequence
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US-09-316-919-4
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RESULT 2
US-09-513-783A-46
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US-09-316-919-4
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APPLICANT: Taion, Roger Y.
APPLICANT: Miyawaki, Arsushi
APPLICANT: Llopis, Juan
APPLICANT: William Miyawaki, Arsushi
APPLICANT: Wachter, Rebekka M.
APPLICANT: Wemington, S. James
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MESSURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07227/071001
CURRENT APPLICATION NUMBER: US/09/602,641
CURRENT FILING DATE: 1998-10-13
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 239
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98.7%; Pred. No. 9.3e-127;
tive 1; Mismatches 2;
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; Sequence 2, Application US/09920922
; Patent No. 6673610
; GREERAL INFORMATION:
    APPLICANT: Miyawaki, Atsushi
    APPLICANT: Miyawaki, Atsushi
    APPLICANT: Sawano, Abako
    TITLE OF INVENTION: METHOD FOR MUTAGENESIS
    TILE REFERENCE: 11203-01201
; CURRENT APPLICATION NUMBER: US/09/920,922
CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: JP 2000-237166
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                  Sequence 3, Application US/09602641
Patent No. 6608189
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FEATURE:
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Best Local Similarity 98.79
Matches 236; Conservative
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OTHER INFORMATION: EGFP
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ORGANISM: Artificial Sequence FEATURE:
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APPLICANT: Li, Xianqiang
TITLE OF INVENTION: Rapidly Degrading GFP-Fusion Proteins and Methods
TITLE OF INVENTION: of Use
TITLE OF INVENTION: of Use
TITLE PEPERENCE: D6100
CURRENT APPLICATION NUMBER: US/09/062,102
CURRENT APPLICATION NUMBER: US 60/060,855
EARLIER APPLICATION NUMBER: US 60/060,855
EARLIER PILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Sequence of the EGFP-MODC422-461 fusion protein. Patent No. 6130313
US-062-102-1
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                                                                                                                                                                     Query Match

98.7%; Score 1257; DB 4; Length 239;
Best Local Similarity 98.7%; Pred. No. 9.3e-127;
Matches 236; Conservative 1; Mismatches 2; Indels
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Pred. No. 1.2e-126;
1; Mismatches 2;
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2 LENGTH: 239
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Patent No. 6130313
GENERAL INFORMATION:
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                                                                                                ; ORGANISM: Aequorea victoria
US-09-920-922-2
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Best Local Similarity 98.7
Matches 236; Conservative
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                                                                         TYPE: PRT
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Sequence 1, Application US/09364946

Sequence 1, Application US/09364946

Sequence 1, Application US/09364946

GENERAL INFORMATION:

APPLICANT: Kain, Steve

APPLICANT: Kain, Steve

TITLE OF INVENTION: Rapidly Degrading GFP-Fusion Proteins and Methods

TITLE OF INVENTION: of Use

TITLE OF INVENTION: of Use

CURRENT APPLICATION NUMBER: US/09/364,946

CURRENT PILING DATE: 1999-07-30

CURRENT PILING DATE: 1999-07-30

SARLIER PLICATION NUMBER: US 09/191,233

EARLIER FILING DATE: 1998-11-13

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 1

LENGTH: 281
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| Sequence 2. Application US/09513783A |
| Patent NO. 6416959 |
| GENERAL INFORMATION: |
| APPLICANT: Giuliano, Kenneth A. |
| APPLICANT: Kapur, Ravi |
| TITLE OF INVENTION: A System for Cell Based Screening |
| FILE REFERENCE: 97-022-11 |
| CURRENT FILING DATE: 2000-02-25 |
| NUMBER OF SEQ ID NOS: 180 |
| SOFTWARE: PatentIn Ver. 2.0 |
| SEQ ID NO 2 |
| LENGTH: 294 |
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                                         51 LVTLLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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Sequence 21, Application US/09172063
Sequence 21, Application US/09172063
Sequence 21, Application US/09172063
Sequence 21, Application US/09172063
Sequence 21, Application Sequence 21, Applicant Mayawaki, Atsushi
APPLICANT: Machier, Rebecka M. APPLICANT: Remington, S. James
STITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR TITLE OF INVENTION: MASASURING THE PH OF A BIOLOGICAL SAMPLE FILE REPERENCE: 07257/071001
CURRENT APPLICATION NUMBER: 09/094,359
SEALLER APPLICATION NUMBER: 09/094,359
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: GT-EGFP US-09-172-053-21
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Matches 236; Conservative
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                                                                                                                                                                                                                                                                                                                   RESULT 9
US-09-172-053-21
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US-09-602-641-21
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APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
APPLICANT: Llopis, Juan

GENERAL INFORMATION:

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85 MYSKGEBLFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKPICTTGKLPVPWPT 144
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Patent No. 6191269
Patent No. 6191
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APPLICANT: Wachter, Rebekka M.
APPLICANT: Wachter, S. James
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/071001
CURRENT FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/172,063
PRIOR PILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 323
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Pred. No. 1.5e-126;
1; Mismatches 2;
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast5EQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,305
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STREET: 285 Hamilton Ave, Suite 200
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 98.7%;
Matches 236; Conservative
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FEATURE:
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OTHER INFORMATION: GT-EGFP
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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US-09-085-305-6
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                                                321 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 379
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                       181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
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                                                                                                                                                                   Sequence 48, Application US/09800170

Batent No. 6481667

GENERAL INFORMATION:

APPLICANT: Kinsella, Todd

TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES

FILE REPRENEUR: A-68614-1/DJB/RMS/RMK

CURRENT APPLICATION NUMBER: US/09/800,170

CURRENT FILING DATE: 2001-08-28

PRIOR PILIONG DATE: 2000-03-06

NUMBER OF SEQ ID NOS: 90

SOFTWARE: PatentIn version 3.1

SEQ ID NO 48

LENGTH: 434
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Pred. No. 2.3e-126;
1; Mismatches 2;
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98.7%; Pred. No. 2.3e-126;
tive 1; Mismatches 2;
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US-09-800-170-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 98.7%;
Matches 236; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity
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US-09-417-197-127
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                                                                                                                                  RESULT 13
US-09-800-170-48
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Patent No. 6518021
GENERAL INFORMATION:
APPLICANT: OLE THASTRUP, et al.
TITLE OF INVENTION: On A Cellular Response
FILE OF INVENTION: On A Cellular Response
FILE REPERENCE: 3759-0110P
CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LVTLLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                                                                                                                                                                                                                                                             Length 364;
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                                                                                                                                                                                                                                                                                                                                                        Score 1257; DB 3;
Pred. No. 1.8e-126;
1; Mismatches 2;
                    NAME: Francis, Carol L
REGISTRATION NUMBER: 36,513
REPERENCE/DOCKET NUMBER: 6510/102US1
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
TELEFAX: 650-327-3231
                                                                                                                                                                                                                                                                                                                                                           98.7%;
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ORGANISM: Artificial Sequence
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 98.7
Matches 236; Conservative
                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
US-09-085-305-6
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US-09-417-197-129
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LENGTH: 379
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61 LVTLLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                     61 LVTLLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                         1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT 60
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US-09-513-783A-170
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98.7%; Score 1257; DB 4; Length 459;
Best Local Similarity 98.7%; Pred. No. 2.5e-126;
Matches 236; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                            ; Sequence 170, Application US/09513783A; Sequence 170, Application US/09513783A; Patent NO. 6416959; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.; APPLICANT: Kapur, Ravi; TITLE OF INVENTION: A System for Cell Based Screening; FILE REFERENCE: 97-022-L1; CURRENT APPLICATION NUMBER: US/09/513,783A; CURRENT FILING DATE: 2000-02-25; NUMBER CF SEQ ID NOS: 180; SOFTWARE: PatentIn Ver. 2.0; SEQ ID NC: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: FRT ORGANISM: Artificial Sequence
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US-09-513-783A-170
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Search completed: June 21, 2004, 16:04:02 Job time: 13.7778 secs

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61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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Pred. No. 4e-124;
US-10-221-461-7
US-10-100-957A-46
US-10-110-957A-46
US-10-318-411-3
US-10-318-640-3
US-10-314-861-35
US-10-314-861-35
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US-10-314-861-35
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US-10-318-411-11
US-10-318-411-13
US-10-318-411-13
US-10-318-411-13
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US-10-318-411-13
US-10-318-411-13
US-10-318-411-13
US-10-318-411-5
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09887784
Patent No. US20020177189A1
GENERAL INFORMATION:
APPLICANT: BJORN, Sara et al
TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS
FILE REFERENCE: 3759-0115P
CURRENT FILING DATE: 2001-06-19
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.0
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    ORGANISM: Aequoria Victoria
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Best Local Similarity 99.6
Matches 238; Conservative
  SEQ ID NO 4
LENGTH: 239
TYPE: PRT
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Sequence 30, Appl
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Sequence 2, Appli
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1940.117 Million cell updates/sec
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Sequence 4, Al
Sequence 3, Al
Sequence 13,
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                                                                                 June 21, 2004, 15:54:20 ; Search time 34.7778 Seconds
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1 MVSKGEELFTGVVPILVELD......VLLGFVTAAGITLGMDELYK
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/ Cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.ppp:*
/ Cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.ppp:*
/ Cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.ppp:*
/ Cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.ppp:*
/ Cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.ppp:*
/ Cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.ppp:*
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/ Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
/ Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
/ Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
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             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-270-223-6

US-10-257-909A-32

US-10-257-909A-32

US-10-257-909A-32

US-10-297-784-2

US-10-296-953-2

US-10-296-953-2

US-09-999-745-4
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US-09-797-496B-2
US-09-794-308-4
US-09-865-291-4
US-10-121-258-13
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                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                            protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Length 239; 1; Indels 9 9

Result

Sequence 29, Appl Sequence 11, Appl Sequence 21, Appl Sequence 7, Appl Sequence 13, Appl Sequence 13, Appl Sequence 16, Appl Sequence 16, Appl Sequence 5, Appli Sequence 5, Appli Sequence 9, Appli Sequence 9, Appli

Sequence Sequence

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US-10-257-909A-30
US-10-257-909A-30
Sequence 30, Application US/10257909A
Sequence 30, Application No. US20030187056A1
Sequence 30, Decedures to identify compounds modulating intracellulication No. US2003018708E
FERRAL INFORMATION: Live cell procedures to identify compounds modulating intracellulication of INVENTION: distribution of phosphodiesterase (PDE) enzymes
FILE REPREBRICE: 3759-0125P
CURRENT APPLICATION NUMBER: US/10/257,909A
CURRENT FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 30
LENGTH 893
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| Sequence 32, Application US/10257909A
| Sequence 32, Application US/10257909A
| Sequence 32, Application O. US20030187056A1
| Sequence 32, Application No. US20030187056A1
| GENERAL INFORMATION:
| APPLICANT: Bernard R. TERRY et al. |
| TITLE OF INVENTION: distribution of phosphodiesterase (PDE) enzymes
| FILE REPERENCE: 3759-0125P |
| CURRENT APPLICATION NUMBER: US/10/257,909A |
| CURRENT PILING DATE: 2002-10-17 |
| NUMBER OF SEQ ID NOS: 36 |
| SOFTWARE: FastSEQ for Windows Version 3.0
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                                   1 MVSKGBELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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| Sequence Application US/1027023
| Publication No. US20030143634A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| TITLE OF INVENTION: INTRACT LIVING CELLS, AND TO EXTRACT QUANTITATIVE INFORMATION:
| TITLE OF INVENTION: INTRACTIONS BY FLUCRESCENCE REDISTRIBUTION.
| TITLE OF INVENTION: INTERACTIONS BY FLUCRESCENCE REDISTRIBUTION.
| FILE REFERENCE: 3759-0126P
| CURRENT APPLICATION NUMBER: US/10/270,223
| CURRENT FILING DATE: 2002-10-11
| SOFTWARE: Patentin version 3.1
| SOFTWARE: Patentin version 3.1
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Pred. No. 7.4e-124;
0; Mismatches 1; Indels 0
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Pred. No. 4e-124;
0; Mismatches 1; Indels 0
                                                                                                                   APPLICANT: BOORN, SARA P.
APPLICANT: BAGILARO, LEN
APPLICANT: THASTRUP, OLE
TITLE CO INVENTION: NOVEL FLUORESCENT PROTEINS
FILE REFERENCE: PL0095
CURRENT APPLICATION NUMBER: US/10/296,953
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: 60/212,681
PRIOR APPLICATION NUMBER: 60/212,681
PRIOR FILING DATE: 2000-06-20
PRIOR PILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 60/20,170
PRIOR PILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: PA 2001 00739
PRIOR APPLICATION NUMBER: PA 2001 00739
PRIOR PILING DATE: 2001-05-10
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VEY: 2.1
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; ORGANISM: Aequoria Victoria and Human
US-10-270-223-6
                                                  Sequence 4, Application US/10296953
Publication No. US20040072995A1
GENERAL INFORMATION:
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Best Local Similarity 99.6%;
Matches 238; Conservative
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; ORGANISM: Aequorea victoria
US-10-296-953-4
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                                JS-10-296-953-4
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RESULT 8
US-09-920-922-2
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                                                                                                                                             Length 1132;
                                                                     ; FEATURE:
; OTHER INFORMATION: Fusion between Aequorea victoria and human
US-10-257-909A-32
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Pred. No. 2.8e-123;
0; Mismatches 2; Indels (
                                                                                                                                                                               Indels
                                                                                                                                         Score 1268; DB 14;
Pred. No. 3.8e-123;
0; Mismatches 1;
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Patent No. US20020177189A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS
FILE REFERENCE: 3759-0115P
CURRENT FILING DATE: 2001-06-19
NUMBER OF SEQ ID NOS: 24

SOFTWARE: PatentIn version 3.0

LENGTH: 239
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                              TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-887-784-2
                                                                                                                                           Query Match
Best Local Similarity 99.6
Matches 238; Conservative
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Matches 237; Conservative
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US-10-296-953-2
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US-09-887-784-2
SEQ ID NO 32
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Sequence 2, Application US/10296953 Publication No. US20040072995A1 GENERAL INFORMATION:

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61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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Best Local Similarity 98.7%; Pred. No. 5.7e-123;
Matches 236; Conservative 1; Mismatches 2;
APPLICANT: BJORN, SARA P.
APPLICANT: PAGLIARO, LEN
APPLICANT: THASKINP, OLE
TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS
FILE REPERENCE: PLO095
CURRENT APPLICATION NUMBER: US/10/296,953
CURRENT FILING DATE: 2002-11-26
FRIOR APPLICATION NUMBER: PA 2000 00953
FRIOR APPLICATION NUMBER: 60/212,681
FRIOR APPLICATION NUMBER: 60/212,681
FRIOR APPLICATION NUMBER: 60/200,170
FRIOR APPLICATION NUMBER: 60/200,170
FRIOR APPLICATION NUMBER: 80/210, 170
FRIOR APPLICATION NUMBER: PA 2001 00739
FRIOR APPLICATION NUMBER: PA 2001 00739
FRIOR FILING DATE: 2001-05-10
FRIOR PROME APPLICATION NUMBER: PA 2001 00739
FRIOR FILING DATE: 2001-05-10
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TITLE OF INVENTION: METHOD FOR MUTAGENESIS
FILE REFERENCE: 11283-012001
CURRENT APPLICATION NUMBER: US/09/920,922
CURRENT FILING DATE: 2001-08-02
PRIOR FILING DATE: 2000-04
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: 239
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GENERAL INFORMATION: APPLICANT: Miyawaki, Atsushi
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; ORGANISM: Aequorea victoria
US-10-296-953-2
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US-09-920-922-2
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LVTLLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                      61 LVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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APPLICANT: Tsien, Roger Y.
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
FILE REFERENCE: RECEN1470-1
CURRENT APPLICATION NUMBER: US/09/999,745
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 02/316,920
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US-09-866-538-4

i Sequence 4, Application US/09866538

i Publication No. US20030032088A1

i GENERAL INFORMATION:

APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA

APPLICANT: Campbell, Robert

TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS

FILE REFERENCE: REGENTS30-2

CURRENT APPLICATION NUMBER: US/09/866,538

CURRENT FILEM DATE: 2001-05-24

NUMBER OF SEC ID NOS: 29

SOFTWARE: Patentin version 3.0
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Pred. No. 5.7e-123;
1; Mismatches 2;
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 239
TYPE: PAT
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Best Local Similarity 98.7%;
Matches 236; Conservative
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US-09-999-745-4
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LENGTH: 239
TYPE: PRT
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OTHER INFORMATION: Aequorea victoria green fluorescent protein modified as described OTHER INFORMATION: in specification
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Publication No. US20030049597A1
GENERAL INFORMATION:
APPLICANT: Simon, Sanford M.
APPLICANT: Chen, Yu
TITLE OF INVENTION: Chimeric Fluorescent Enzymes and Uses Thereof
FILE REFERENCE: 600-1-567
CURRENT APPLICATION NUMBER: US/09/797,496B
CURRENT FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 2.2
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                                                              Score 1257; DB 10;
Pred. No. 5.7e-123;
                                                                                                         1; Mismatches
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                                                            Query Match
Best Local Similarity 98.7%;
Matches 236; Conservative
; ORGANISM: Aequorea victoria
US-09-866-538-4
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US-09-797-496B-2
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US-09-794-308-4
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181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDBLYK 239
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CRGANISM: Aequorea victoria
FEATURE:
NAME/KEY: VARIANT
LOCATION: (0)...(0)
CTHER INFORMATION: EGFP
US-10-457-982-3
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Sequence 4, Application US/09865291
Publication No. US20030186229A1
SEGNERAL INFORMATION:
APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TSIEN, ROGER
APPLICANT: TING, Alice
APPLICANT: THANG, JIC
APPLICANT: THANG, JIC
APPLICANT: THANG, JIC
APPLICANT: THANG, JOH
TITLE OF INVENTION: EMISSION RATIOMETRIC INDICATORS OF PHOSPHORYLATION
FILE REFERENCE: REGENISSO
CURRENT APPLICATION NUMBER: US/09/865,291
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.0
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APPLICANT: TSIEN, ROGET
APPLICANT: ZACHARIAS, David
APPLICANT: BAIRD, GOOFO
TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
FILE REFERENCE: REGEN1530
CURRENT APPLICATION NUMBER: US/09/794,308
CURRENT FILLING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 25
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98.7%; Score 1257; DB 10;
Best Local Similarity 98.7%; Pred. No. 5.7e-123;
Matches 236; Conservative 1; Mismatches 2;
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Best Local Similarity 98.7%;
Matches 236; Conservative
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ORGANISM: Aequorea victoria
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US-09-794-308-4
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SEQ ID NO 4
LENGTH: 239
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LENGTH: 239
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61 LVTLLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
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Sequence 13, Application US/10121258

Publication No. US20030059835A1

GENERAL INFORMATION:
APPLICANT: Campbell, Robert

TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME
FILE REPERENCE: UCOB3.1CP2CP1

CURRENT APPLICATION NUMBER: US/10/121,258

CURRENT PILING DATE: 2001-02-04-10

PRIOR FILING DATE: 2001-02-26

PRIOR FILING DATE: 2001-02-26

PRIOR FILING DATE: 2001-05-24
                                                                                                                                                                                                         Sequence 3, Application US/10457982
; Deblication No. US20030212265A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Taien, Roger Y.
APPLICANT: Liopis, Juan
APPLICANT: Liopis, Juan
APPLICANT: Machter, Rebekka M.
APPLICANT: Remington, S. James
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: PLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REPERRES 07257/071001
CURRENT PRILING DATE: 2003-06-09
PRIOR APPLICATION NUMBER: US/09/602,641
PRIOR APPLICATION NUMBER: US/09/602,641
PRIOR APPLICATION NUMBER: 09/172,063
PRIOR APPLICATION NUMBER: 09/172,063
PRIOR APPLICATION NUMBER: 09/172,063
PRIOR RELING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 109/172,063
PRIOR APPLICATION NUMBER: 109/172,063
PRIOR RELING DATE: 1000-06-22
PRIOR APPLICATION NUMBER: 109/172,063
PRIOR RELING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 209/172,063
PRIOR PLING DATE: 2000-06-32
PRIOR APPLICATION NUMBER: 109/172,063
PRIOR PLING DATE: 2000-06-32
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98.7%; Score 1257; DB 12;
Best Local Similarity 98.7%; Pred. No. 5.7e-123;
Matches 236; Conservative 1; Mismatches 2;
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51 LVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                                                                                                             Length 239;
                                                                                    TYPE: PRT (CRANISM: Artificial Sequence FEATURE: ORGANISM: Artificial Sequence FATURE: COTHER INFORMATION: Enhanced Green Fluorescent Protein (EGFP) US-10-121-258-13
                                                                                                                                                                                                           Query Match 98.7%; Score 1257; DB 14; Length Best Local Similarity 98.7%; Pred. No. 5.7e-123; Matches 236; Conservative 1; Mismatches 2; Indels
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 239
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Search completed: June 21, 2004, 16:09:27 Job time: 34.7778 secs

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GenCore version 5.1.6
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- protein search, using sw model OM protein

Run on:

June 21, 2004, 15:46:00 ; Search time 10.3333 Seconds (without alignments) 2224.817 Million cell updates/sec

1273 1 MVSKGEELFTGVVPILVELD......VLLGFVTAAGITLGMDELYK 239 US-09-887-784-64L Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283366 segs, 96191526 residues Searched:

Fotal number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
1: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

iron-sulfur cofact DNA-directed DNA p protective surface protective surface cellulase (EC 3.2. photosystem IÎ chi oligoendopeptidase DNA-directed DNA p synaptogamin o-p65 hypothetical prote dihydrolipoamide d DNA-binding protei proprotein convert hypothetical prote leucine-tRNA ligas IgA Fc receptor pr DNA topoisomerase hypothetical prote hypothetical prote leucine-tRNA ligas leucyl-tRNA synthe tRNA (uracil-5-)-m leucine tRNA synth inter-alpha-trypsi hypothetical prote eucine-tRNA ligas green-fluorescent Description SUMMARIES D71614 E70390 JDVLHH JC4078 F64102 S29043 G81355 SYECL JB5564 JC5576 A99552 JH0414 B86615 T400794 H72228 H64102 E82590 AC0582 **JQ1514** Query Match Length DB 860 889 281 461 84.5 84.5 Result No. 

| IgA Fc receptor pr | thioredoxin reduct | hypothetical prote | hypothetical prote | imidazoleglycerol- | ferrichrome-bindin | hypothetical prote | alpha-amylase homo | lipoxygenase (EC 1 | water-stress-induc | DNA-directed DNA p | hypothetical prote | synergohymenotropi | photosystem II chl | photosystem II CP4 | cytovillin homolog |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| FCSOAG             | C97279             | T42323             | C64468             | E84941             | H97144             | T27856             | T39539             | T11852             | S53488             | A36028             | B71094             | S68225             | S42647             | AD2342             | A45620             |
| -                  | 7                  | 7                  | ~                  | 7                  | ~                  | ~                  | ~                  | ~                  | ~                  | н                  | 7                  | ~                  | ~                  | ~                  | N                  |
| 1164               | 285                | 836                | 336                | 353                | 355                | 471                | 774                | 865                | 263                | 2222               | 272                | 310                | 459                | 459                | 559                |
| 9.9                | 6.5                | 6.5                | 6.4                | 6.4                | 6.4                | 6.4                | 6.4                | 6.4                | 6.4                | 6.4                | 6.4                | 6.4                | 6.4                | 6.4                | 6.4                |
| 83.5               | 83                 | 83                 | 82                 | 82                 | 82                 | 82                 | 82                 | . 82               | 81.5               | 81.5               | 81                 | 81                 | 81                 | 81                 | 81                 |
| 30                 | 31                 | 32                 | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

|   | RESULT 1<br>JO1514                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
|---|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|   | green-fluorescent protein [validated] - hydromedusa (Aequorea victoria)<br>C.Snecies: Aequorea victoria                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|   | C,Date: 03-Dec-1999 #sequence revision 03-Dec-1999 #text change 23-Mar-2001                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|   | C;Accession: JS0692; JQ1514; PQ0335; S48693; S51330; S51331<br>R;Prasher, D.C.; Eckenrode, V.K.; Ward, W.W.; Prendergast, F.G.; Cormier, M.J.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
|   | Gene 111, 229-233, 1992                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|   | A,Title: Primary structure of the Aequorea victoria green-iluorescent protein.<br>A,Reference number: JQ1514; MUID:92175527; PMID:1347277                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
|   | A;Accession: JS0692<br>A:Molecule type: DNA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|   | A; Residues: 1-107, 'S', 109-238 < PRA1>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
|   | A;Cross-references: GB:M62654; NID:g155662; FIDN:AAA27722.1; FID:g155663<br>A:Accession: J01514                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
|   | A, Molecule type: mRNA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|   | A;Residues: 1-99,'F',101-140,'L',142-218,'V',220-238 <pra2><br/>A:Cross-references: GB:M62653: NID:q155660: PIDN:AAA27721.1: PID:q155661</pra2>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
|   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
|   | A; Molecule type: protein<br>p. Peciding: 46-64 74-122:132-151:154-181:185-200 / PRA3>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| - | R. Inouve, S. J. Tsuli, F. I.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
|   | FEBS Lett. 351, 211-214, 1994                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
|   | A, Title: Evidence for redox forms of the Aequorea green fluorescent protein.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
|   | A; Reference number: 548693; MULD:94364470; PMID:8082767                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
|   | A A A CCESION: S 48693<br>A Gratus realiminary                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
|   | A Sociale Type: Memory A:MOlecule type: mgNA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
|   | A, Residues: 1-24, 'Q', 26-156,'P', 158-171,'K', 173-238 <ino></ino>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|   | A;Cross-references: GB:L29345; NID:g606383; PIDN:AAA58246.1; PID:g606384                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
|   | K; Watkins, J.N.; Campbell, A.K.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|   | Budditted to the brown Data biblary, called 1999<br>A:Reference number: S51330                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
|   | A; Accession: S51330                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|   | A, Molecule type: mRNA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|   | A; Casaladus: 1-13, V.,12-44, V.,26-44, V.,48-125, V.,153-44, V.,48-125, V.,153-421, K.,133-421, K.,133-421, K.,133-421, V.,133-421, K.,133-421, K.,133-421, K.,133-421, K.,133-421, K.,133-431, V.,133-431, V.,13                                                                                                                                      |
|   | A, Experimental source: clone gfp1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
|   | A. MCGESBLON: SSI331<br>b. MCJEVIJE TVOR: MENA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
|   | A; Residues: 124, 'Q', 26-29, 'R', 31-83, 'L', 85-153, 'G', 155-156, 'P', 158-171, 'K', 173-208, 'Q', 'E'                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
|   | A;Cross-references: EMBL:X83960; NID:g634010; PIDN:CAA58790.1; PID:g634011                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
|   | A.Experimental source: clone gipp:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
|   | submitted to the Brookhaven Protein Dank, August 1996                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
|   | A, Reference number: A65692; PDB:10FL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
|   | A; Contents: annotation; $\lambda$ ray crysteralography. 1.9 augustiums, testudes $\lambda$ $(z^{-1})^2$ , $\lambda$ , $(z^{-1})^2$ . A; $(z^{-1$ |
|   | R, Yang, F.; Moss, L.G.; Phillips Jr., G.N.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|   | Nat. Brutening. 14, 14%-1421, 1521, 1588.<br>A.Title: The molecular structure of green fluorescent brotein.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|   | A, Reference number: A58953; MUID:98294543; PMID:9631087                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
|   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |

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Deucyl-RNA synthetase XF2176 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Date: 18-404-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: E82590
R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MID:20365717; PMD:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: E82590
A;Status: preliminary
A;Molecule type: DNA
A;Status: preliminary
A;Molecule type: DNA
A;Status: Tesminary
A;Accessioner: 1887 **CSIN>
A;Status: Tesminary
A;Cross-references: GB:AE004031; GB:AE003849; NID:g9107309; PIDN:AAF84975.1; GSPDB:GN001;
A;Experimental source: strain 9a5c
A;Experimental source: GB:AE004031; GB:AE003849; NID:g9107309; PIDN:AAF84975.1; GSPDB:GN001;
A;Experimental source: Strain 9a5c
B;Experimental source: Strain 9a5c
A;Experimental source: GB:AE004031; GB:AE003849; NID:g9107309; PIDN:AAF84975.1; GSPDB:GN001;
A;Experimental source: Strain 9a5c
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fromes
A;Authors: Ferreira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.C.; Matsukuma, A.Y.; Marcha, M.C.; Pandod, M.A.; Matchins, E.M.F.; Matsukuma, A.Y.; Marcha, M.C.; Palmieri, D.A.; P.G.; Nunes, L.R.; Ollveira, M.A.; de Rosa Jr., V.E.; Cde Sa, R.G.; Santelli, R.O.; Santelli, R.O.; Sawasaki
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462 GVKSPINADPN 472
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A;Contents: annotation; X-ray crystallography, 1.9 angstroms
C;Comment: This protein is excited by the photoprotein aequorin (see PIR:AQJFNV) emittin
C;Comment: The chromophore of this protein is formed by modification of Ser-dehydro-Tyr-C;Genetics:
A;Gene: GFP
A;Introns: 59/3; 167/3
A;Antrons: 59/3; 167/3
C;Superfamily: green-fluorescent protein
C;Keywords: chromoprotein; luminescence
C;Keywords: chromoprotein; luminescence
F;65-67/Cross-link: 5-imidazolinone (Ser-Gly) #status experimental
F;66/Modified site: dehydrotyrosine (Tyr) #status experimental
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Ajature 399, 323-329, 1999

Ajature 399, 323-329, 1999

Ajature 599, 323-329, 1999

Ajaterence number: A72200; MUID:99287316; PMID:10360571

Ajacession: H72228

Ajatures preliminary

Ajacure zype: DNA

Ajacures 1-785 ARN>
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A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein TM1624 - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Decies: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accesion: H72228
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicgarrett, M.W.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 VITESYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERIIFYKDDGNYKTRAEVKFEGDILV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NRIELKGIDFKEDGNILGHKMEYNYNSHNVYIMADKQKNGIKVNPKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 TLLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 RIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADH 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VILLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 SKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
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8.2%; Score 105; DB 2; Length 785;
Best Local Similarity 19.7%; Pred. No. 0.84;
Matches 46; Conservative 32; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                Score 1235; DB 1;
Pred. No. 1.6e-96;
4; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                   97.0%;
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                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 96.6
Matches 230; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182
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Cipate: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 03-Jun-2002
Cipate: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 03-Jun-2002
Cipate: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 03-Jun-2002
Cipate: 18-Aug-1995 #sequence_revision Lot: Clayton, C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 TTGKLPVPWPTLVTLLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----IADKLEKLGV
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(strain Rd KW20)
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C;Superfamily: leucine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
      Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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7.6%; Score 96.5; DE
Best Local Similarity 24.6%; Pred. No. 4.9;
Matches 47; Conservative 26; Mismatches
      leucine-tRNA ligase (EC 6.1.1.4) - Haemopk
N;Alternate names: leucyl-tRNA synthetase
C;Species: Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203 STQSALSKDPN 213
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213 NE 214
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Best Local S:
Matches 53
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A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir M.; Tauhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A;Reference number: A59328
A;Contents: annotation
A;Genetics:
C;Genetics:
A;Gene: XP2.76
C;Superfamily: leucine-tRNA ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lectyl-tRNA synthetase [imported] - Salmonella enterica subsp. enterica serovar Typhi (6 ispecies: Salmonella enterica serovar Typhi (7 ispecies: Salmonella enterica serovar Typhi (7 ispecies: Salmonella typhi (8 ispecies) has also been called Salmonella typhi (9 ispecies) has also been called Salmonella typhi (9 ispecies) has been called Salmonella typhi (9 ispecies) has been called Salmonella typhi (9 ispecies) of item (9 ispecies) Accession: Ac
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DB3917
DB4 topoisomerase IV subunit B BH2140 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 329 TNEQLPV-WVANFVLMAYGTGAVMAVPGHDQRDQEF--ANKYGLPIRQVIALKEPKNQDE 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       386 STWEPDVWRDWYADKTR---EFE---LINSAEFDGLDYQDAFEVLAERFE------ 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        471
                                                                                                                                                                                                                                                                                                                                                                                                    50 TTGKLPVPWPTLVTLLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNY-- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------KTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 MADKQKNG-IKVNFKIRHNIEDGSVQLADHYQQNTPI------GDGPVLLPDN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: GB:AL513382; PIDN:CAD05125.1; PID:g16501899; GSPDB:GN00176
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                                                                                                                                                                                                                                                                      Length 887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 860;
                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                   67;
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                                                                                                                                                                                                                                                                  Match
Total Similarity 22.7%; Pred. No. 7.5;
es 45; Conservative 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 -HYLSTQSALSKDPNEKR 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              483 VAFSGTGSPIKTDPEWRK 500
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A;Gene: STY0699
C;Superfamily: leucine-tRNA ligase
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Best Local Similarity 23.9%;
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A;Residues: 1-860 <PAR>
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                                                                                                                                                                                                                                                                  Query Match
Best Local S:
Matches 45
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C; Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C; Accession: D83917
R; Taxani, H; Nakasone, K; Taxaki, Y; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and c; A; Reference number: A83650; MUD:20512582; PMID:11058132
A; Accession: D83917
A; Accession: D83917
A; Reference number: A83650; MUD:20512582; PMID:11058132
A; Reference number: A83650; MUD:20512582; PMID:205134613; PIDN:BAB05859.1; GSPDB:GNO01
A; Reference number: A83650; MUD:20514613; PIDN:BAB05859.1; GSPDB:GNO01
A; Reference number: A83650; MUD:20514613; PIDN:BAB05859.1; GSPDB:GNO01
A; Reference number: A83650; MUD:20514613; PIDN:BAB05859.1; GSPDB:GNO01
C; Genetics: A83650; MUD:20514613; PIDN:BAB05859.1; GSPDB:GNO01
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C;Date: 13-Nov-1998 #text_change 21-Jul-2000
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Caccesion: D71614
C;Caccesion: D71616
C;Caccesion:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 NFNVETLSERLREAAFLLKGLKIELVDLRDDTKEVFH-YEDGIKAFVEYLNEDKETLHPV 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 VFFNGESNGIEIEFAFQFN--DGYTENVLSFVNNVRTKDG-----GTHELGAKTAMTRAV 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 VQERTIFFKD--DGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYN--YNSH 149
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A,Status: preliminary; nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-2573 (GAR>
A,Cross-references: GB-AE001396; GB:AE001362; NID:93845188; PIDN:AAC71881.1; BA;Experimental source: clone 3D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----QKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: BH2140
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 TLVTLLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQER-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.9%; Score 87.5; DB 2; I
Best Local Similarity 26.2%; Pred. No. 1.2e+02;
Matches 34; Conservative 30; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 DVNGHK----FSVSGEGEGDAT----YGKLTLKFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.9%; Score 87.5; I
Local Similarity 21.9%; Pred. No. 20;
les 53; Conservative 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
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| Qy 210 KDPNEKRDHM 219  Ob 217 WV KDDPNW 246                                                                                                                                                                                                                                                                                                                                                                                                                  | Oy 58 WPTLVTLLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVOERTIFFKDDGNYK 108                                                                                                                                                                                            |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 2.5 TENGENDIN 2.5 SULT 8                                                                                                                                                                                                                                                                                                                                                                                                                                     | 109 TRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIM                                                                                                                                                                                                       |
| E70390<br>iron-sulfur cofactor synthesis protein nifs - Aquifex aeolicus<br>N;contains: L-cysteine sulfurtransferase (EC 2.8.1)<br>C;Species: Aquifex aeolicus<br>C;Species: Aquifex aeolicus                                                                                                                                                                                                                                                                | Db 197 TWEQKHLVPQQHGAYSSKINDRQESRRRRIITATSSRKNDSSRLFGAHN 245 Qy 155 ADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLL-PDNHYL 202                                                                                                                                |
| E70390<br>.; Warren, P.V.; Gasterland, T.; Young, W.G.; Lenox, A.L.;<br>353-358, 1998                                                                                                                                                                                                                                                                                                                                                                        | QY 203 STQSALSKDPNEKR 216  1                                                                                                                                                                                                                             |
| A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: E70390 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Cross-references: GR:AR000720: NID:G2983529; PIDN:AAC07111.1; PID:G2983536; GB:AE00065 | RESULT 10<br>JC4078<br>protective surface antigen D-15 precursor - Haemophilus influenzae (type b)<br>C;Species: Haemophilus influenzae<br>A;Variety: type b                                                                                             |
| al source: strain VF5  y: nitrogen fixation protein nif6  phosphoprotein; pyridoxal phosphate; sulfurtransferase  site: pyridoxal phosphate (Lys) (covalent) #stetus predicted                                                                                                                                                                                                                                                                               |                                                                                                                                                                                                                                                          |
| sice: cys (cysteine persualine intermediate)  h 6.8%; Score 86.5; DB 2; Leng Similarity 25.4%; Pred. No. 11; 49; Conservative 30; Mismatches 91; Inc                                                                                                                                                                                                                                                                                                         | A,Molecule type: DNA<br>A,Residues: 1-797 <fla><br/>A,Cross-references: GB:U13961; NID:g537447; PIDN:AAA85645.1; PID:g537448<br/>A;Experimental source: type b</fla>                                                                                     |
| QY 4 KGEELFTGVVPILVELDGDVNGHKF-SVSGEGEGDATYGKLTLKFICT 50                                                                                                                                                                                                                                                                                                                                                                                                     | C;Neywords: surface antigen C;Keywords: surface antigen F;1-19/Domain: signal sequence #status predicted <sig> F;2-0-797/Product: protective surface antigen D-15 #status predicted <mat></mat></sig>                                                    |
| QY S1 TGKLPVPWPTLVTLLSYGVQCFSRYPDHMKQ-HDFFKSAMPEGYVQERTIFFKDD 104  Db 224 NGKRSGTENVVGILSLAKALEIIVSNFSRYQEQLKKLRDLFENLLLEA-LPDAQIVGKDA 282                                                                                                                                                                                                                                                                                                                   | Query Match 6.8%; Score 86.5; DB 2; Length 797;<br>Best Local Similarity 21.9%; Pred. No. 31;<br>Matches 48; Conservative 30; Mismatches 78; Indels 63; Gaps 11;                                                                                         |
| QY 105 GNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNG 161<br>                                                                                                                                                                                                                                                                                                                                                                                     | Qy 65 LSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTI 99<br>                                                                                                                                                                                                         |
| Qy 162 IKVNFKIRHNIED 174 Db 343 VRFSPGLLNKEEE 355                                                                                                                                                                                                                                                                                                                                                                                                            | QY 100 FFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNS 148                                                                                                                                                                                             |
| RESULT 9 JUVLHH DNA-directed DNA polymerase (EC 2.7.7.7) - heron hepatitis virus C;Species: heron hepatitis virus, HHBV A;Note: hoft Ardea cinerea (gray heron) C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 11-Jun-1999                                                                                                                                                                                                                  | QY         149 HNVYIMADKQK-NGIKVNFKIRHNIEDGGSVQLADHYQQNTPIGDGBVLL 196           bb         :                                                                                                                                                             |
| CyAccession: A30082<br>R:Sprengel, R.; Kaleta, E.F.; Will, H.<br>M:Sprengel, E.; 3832-3839, 1988<br>A;Title: Isolation and characterization of a hepatitis B virus endemic in herons.<br>A;Reference number: A93037; MUID:88333160; PMID:3418788<br>A;Accession: A30082                                                                                                                                                                                      | RESULT 11 F64102 protective surface antigen D-15 - Haemophilus influenzae (strain Rd KW20) C;Species: Haemophilus influenzae C;Species: Haemophilus influenzae C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 18-Sep-1998               |
| A,Residues: 1-788 <spr> A,Cross-references: GB:M22056; NID:g325452; PIDN:AAA45738.1; PID:g325454 C;Superfamily: heparitis virus DNA-directed DNA polymerase C;Keywords: DNA biosynthesis; nucleotidyltransferase</spr>                                                                                                                                                                                                                                       |                                                                                                                                                                                                                                                          |
| Query Match 6.8%; Score 86.5; DB 1; Length 788; Best Local Similarity 19.7%; Pred. No. 30; Matches 40; Conservative 32; Mismatches 66; Indels 65; Gaps 10;                                                                                                                                                                                                                                                                                                   | A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, C.A;title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800 A;Accession: F64102 |

us-09-887-784-641.rpr

| A;Status: nucleic acid sequence not shown; translation not shown<br>A;Rosidues: 1-808 A;Rosidues: 1-808 A;Rosidues: 1-808 A;Rosidues: 1-808 A;Rosidues: GB:142023; TIGR:HI0917<br>C;Superfamily: protective surface antigen D-15<br>C;Reywords: surface antigen                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Qy 136 NILGHKLEYNYNSHNYYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGD 191  Db 320FEHDMYVIVDWHVHAPGDPRADVYSGAYDFFEEIADHYKDH 360  Qy 192 GPVLLPDNHYLSTQSALSKDPN                                                                                    |
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| Query Match 6.8%; Score 86.5; DB 2; Length 808;<br>Best Local Similarity 21.9%; Pred. No. 31;<br>Matches 48; Conservative 30; Mismatches 78; Indels 63; Gaps 11;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 223 G 223                                                                                                                                                                                                                                  |
| Qy         65 LSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTI 99           :     :     :   :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :   :     :   :     :   :     :   :     :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :                                                                           | Db 416 G 416 RESULT 13                                                                                                                                                                                                                     |
| Qy 100 FFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNS 148                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | G81355<br>trNd (uracil-5-)-methyltransferase (BC 2.1.1.35) Cj0831c [imported] - Campylobacter jejur<br>C;Species: Campylobacter jejuni<br>C;Date: 31-Mar_2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002                      |
| Qy 149 HNVYIMADKQK-NGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLL 196                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | C;ACCEBBION: GB1.55<br>R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling<br>C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell<br>Nature 403, 665-668, 2000 |
| Qy 197 PDNHYLSTQSALSKDPNEKRDHWULGFVTAAGITLG 233                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyper A;Reference number: A81250; MUID:20150912; PMID:10688204 A;Accession: G81355 A;Staus: preliminary                                               |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | A;Rosidues: 1-575 <par> A;Rosidues: 1-575 <par> A;Rosidues: 1-575 <par> A;Cross-references: GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB73096.1; PID:g6968277; A;Experimental source: serotype O2, strain NCTC 11168</par></par></par> |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | C;Genetics:<br>A;Gene: trad, C;10831c<br>C;Keywords: methyltransferase, S-adenosylmethionine                                                                                                                                               |
| ange 01-Dec-2000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Query Match 6.8%; Score 86; DB 2; Length 357;<br>Best Local Similarity 24.8%; Pred. No. 12;<br>Matches 30; Conservative 18; Mismatches 39; Indels 34; Gaps 5;                                                                              |
| A;Itte: Molecular clohing and nucleotide sequence of a gene for alkaline cellulase from A;Reference number: \$29043; MUID:91037937; PMID:2230718 A;Recession: \$29043 A;Molecule type: DNA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Qy 80 KQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKG 128                                                                                                                                                                                |
| ; Ashida, T.; Ozaki,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Qy 129 IDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIE 173                                                                                                                                                                                   |
| A; Title: Crystallization and preliminary X-ray analysis of a truncated family A alkaline A; Reference number: PC4404; MUID:98060488; PMID:9399567 A; Accession: PC4404 A; Accession: PC4404 A; Molecule type: protein A; Residues: 228-584 < CSHID: A; Accession: A; Access | Qy 174 D 174<br>                                                                                                                                                                                                                           |
| in beta-D-glucans such as ce                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | RESULT 14<br>SYECL<br>leucine-tRNA ligase (EC 6.1.1.4) [validated] - Escherichia coli (strain K-12)                                                                                                                                        |
| ayer repeat homology; Thermot<br>ion                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | N;Alternate names: leucyl-tRNA synthetase<br>C;Species: Escherichia coli<br>C;Date: 31-Mar-1989 #sequence_revision 21-Nov-1997 #text_change 03-Jun-2002                                                                                    |
| at homology <txa></txa>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | R.Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col. A.; Rose, D.J.; Mul. B.; Shao, Y.                                                                                                               |
| Query Match 6.8%; Score 86.5; DB 2; Length 941; Best Local Similarity 20.3%; Pred. No. 38; Matches 49; Conservative 34; Mismatches 61; Indels 97; Gaps 11;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Aritie: 2//, 1430-1404, 139/<br>Aritie: The complete genome sequence of Escherichia coli K-12.<br>A;Reference number: A64720; MUID:97426617; PMID:9278503<br>A;Accession: H64798                                                           |
| Qy         16 LVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTLLSYGVQCFSRY 75                   :                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | A;Status: nucleic acid sequence not shown; translation not shown<br>A;Molecule type: DNA<br>A;Residues: 1-860 <blat><br/>A;Cross-references: GB:AE000168; GB:U00096; NID:q1786849; PIDN:AAC73743.1; PID:g1786861;</blat>                   |
| 76 PDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDG 135<br>: ::                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | U                                                                                                                                                                                                                                          |

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A;Accession: A30290
A;Molecule Lype: DNA
A;Crosd-references: EMBL:X06331; NID:g41915; PIDN:CAA29642.1; PID:g41916
A;Note: part of this sequence, including the amino end of the mature protein, was confir
C;Genetics:
A;Mop position: 15 min
A;Map position: EC 6.1.1.4 [Validated, MUID:88096562]
A;Punction:
A;Punction:
A;Punction: C 6.1.1.4 [Validated, MUID:88096562]
A;Puthway: protein biosynthesis
C;Superfamily: leucine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis
F;49-52/Region: ATP binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leucine tRNA synthetase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: H90713
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gencalization number: A99629; MUID:21156231; PMID:11258796
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A;Status: prefilminary
A;Molecule type: DNA
A;Residues: 1-860 <HAY>
A;Cress-references: GB:BA000007; PIDN:BAB34103.1; PID:gl3360138; GSPDB:GN00154
A;Experimental source: strain 0157:H7; substrain RIMD 0509952
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6.7%; Score 85.5; DB 2; Length 860;
Best Local Similarity 22.8%; Pred. No. 41;
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C;Superfamily: leucine-tRNA ligase
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GenCore version 5.1.6
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protein search, using sw model • OM protein

June 21, 2004, 15:42:24; Search time 6.44444 Seconds (without alignments) 1931.085 Million cell updates/sec Run on:

US-09-887-784-64L 1273 score: Perfect

1 MVSKGEELFTGVVPILVELD.......VLLGFVTAAGITLGMDELYK 239 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched: 141681

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 08 08 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt 42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STRAMATES

|           | 1      | Description  |           |           |           |           |           | Q87c65 xylella fas |           |          |            |            |            |            | P19424 bacillus sp |            |            |           | σ.        | P07813 escherichia | P97280 mesocricetu |            | -          |            |            | P24506 discopyge o | σ          | 0        | Q8zdf8 yersinia pe |           |            | P57203 buchnera ap |     | m          | Q7vnf0 haemophilus |
|-----------|--------|--------------|-----------|-----------|-----------|-----------|-----------|--------------------|-----------|----------|------------|------------|------------|------------|--------------------|------------|------------|-----------|-----------|--------------------|--------------------|------------|------------|------------|------------|--------------------|------------|----------|--------------------|-----------|------------|--------------------|-----|------------|--------------------|
| SUMMARIES | ç      | ID           | GFP_AEQVI | SYL HAEIN | SYL_XYLFA | SYL_SALTI | SYL_SALTY | SYL_XYLFT          | SYL_SHEON | GRBE RAT | CP51_CANGA | DPOL HPBHE | D152 HAEIN | D151_HAEIN | GUN BACS6          | TRMA CAMJE | D153_HAEIN | SYL_ECO57 | SYL_ECOL6 | SYL_ECOLI          | ITH3 MESAU         | PSBC_CYAPA | AMPA_WIGBR | PEPF MYCPU | VIT4_CAEEL | SY62_DISOM         | YC03_KLEPN | NEC1_RAT | SYL_YERPE          | BAG_STRAG | YD48 METJA | HIS7_BUCAI         |     | AMY2_SCHPO | SYD_HAEDU          |
|           | 9      | 9 :          | П         | Н         |           | 7         | ч         | н                  | Н         | Н        | н          | H          | Н          | н          | Н                  | н          | -          | Н         | -         | ч                  | Н                  | ٦          | ч          | ч          | ч          | -                  | -          | Н        | -                  | ч         |            | ٦                  | Н   | Ч          | н                  |
|           | 1000   | match bength | 238       | 861       | 879       | 860       | 860       | 879                | 859       | 538      | 533        | 788        | 795        | 797        | 941                | 357        | 793        | 860       | 860       | 860                | 886                | 461        | 501        | 613        | 1603       | 439                | 504        | 752      | 860                | 1164      | 336        | 353                | 366 | 774        | 589                |
| ٠         | Query  | March        |           | 7.6       | 7.4       | 7.3       | 7.3       | 7.2                | •         |          | •          | •          | •          | 6.8        | •                  |            | •          | •         |           |                    |                    |            | 9.9        | ٠          | ٠          | ٠                  | •          |          | •                  | ٠         | •          | 6.4                | 6.4 | 6.4        | 6.4                |
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| 34<br>35             | 81.5<br>81                                                                      | 6.4<br>4.4               | 2222<br>682                             | 44        | DPOE YEAST<br>PRC_ECOLI                | LS          |                                      | saccharomyc<br>escherichia                              |
|----------------------|---------------------------------------------------------------------------------|--------------------------|-----------------------------------------|-----------|----------------------------------------|-------------|--------------------------------------|---------------------------------------------------------|
| 37                   | 8186                                                                            | 4.4.                     | 689<br>874                              |           | AC2L HUMAN<br>SLAP BACLI               | AN<br>LI    | Q9nub1<br>P49052                     | homo sapien<br>bacillus li                              |
| 4 4 39               | 80.5<br>80.5<br>80                                                              |                          | 393<br>658<br>737                       |           | TRMB_HELPY ADAS_HUMAN OPT1_DROME       | A P P P     | 025443<br>025443<br>000116<br>P91679 | nomo sapien<br>helicobacte<br>homo sapien<br>drosophila |
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| 4.<br>R              | 79.5                                                                            | . 2                      | 365                                     | н         | 1A25_HUMAN<br>ALIGNMENTS               | AN<br>MENTS | P18462                               | homo sapien                                             |
| P. A.                | T 1<br>EQVI<br>GFP_AEQVI                                                        | STA                      | STANDARD;                               |           | PRT;                                   | 238 AA.     |                                      |                                                         |
| AC<br>DT 01<br>DT 01 | P42212; Q17104; Q27903;<br>01-NOV-1995 (Rel. 32, C.<br>01-NOV-1995 (Rel. 32, L. | 04; Q2<br>(Rel.<br>(Rel. | 127903;<br>32, Created)<br>32, Last sec | eat<br>st | ;<br>Created)<br>Last sequence update) | update)     |                                      |                                                         |

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[3]
SEQUENCE FROM N.A.
MEDILINE=97299832; PubMed=9154981;
Rouwendal G.J.A., Mendes O., Wolbert E.J.H., de Boer A.D.;
Rouwendal G.J.A., in tobacco of the gene encoding green fluorescent protein by modification of its codon usage.";
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Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
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                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=94.85810; PubMed=8137953;
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Green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
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                                                                                                                                                                                                                                  Gene 111:229-233(1992).
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26886 MW;
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                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or seni an email to license@isb-sib.ch).
    CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF MUTANT WITH YELLOW EMMISSION
   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=99238303; Pubmed=10220315;
                                                                                                                                                                                                                                                                             EMBL; M62654; AAA27722.1; -.
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139C; 17-NOV-00.
13FP; 07-JUL-97.
1C4F; 14-JUN-00.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 NRIELKGIDFKEDGNILGHKLEYNYNSHNYYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 VTLLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWVLLGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                             5-imidazolinone (Ser-Gly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EASA6F21FBFB6E05 CRC64;
                                                                                                                                              3-DIDEHYDROTYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1241; DB 1;
Pred. No. 3.3e-95;
1; Mismatches 4;
PDB; ZEMN; 20-AUG-97.
PDB; ZEMO; 20-AUG-97.
InterPro; IPR009017; GFP_like.
InterPro; IPR000786; Green_fl_protein.
Pfam; PF01353; GFP; 1.
                                                                                               ProDom; PD013756; Green_fl_protein; 1.
Luminescence; 3D-structure.
                                                                                                                                                            100 H Z W K
                                                                                                                                                                             SHOOKER
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181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP, MF 00049; -; 1.
InterPro; IPR002302; Leu-tRNAsyntla.
InterPro; IPR002300; tRNA-synt la.
InterPro; IPR003009; ValRA-synt la.
InterPro; IPR001309; ValRS_IDER_Git.
Pfam, PF00133; tRNA-synt l; 1.
PRINTS; PR00985; TRNASYNTHLEU.
TIGRPAMS; TIGRPAMS, TIGRES less bact; 1.
PROSTE; P800178; AA TRNA_LIGASE l; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diphosphate + L-leucyl-tRNA(Leu).
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Ed / KW20 / ATCC 51907;

MBDLINE=95350630; PubMed=7542800;
Pleistochmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Witerback T.R., Hanna W.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Frager C.M., Smith H.O.,
                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 41, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59;
                                                                                                                                                                                                                              Haemophilus influenzae.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.6%; Score 96.5; DB 1; Length 861;
24.6%; Pred. No. 2.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            861 AA; 97750 MW; EB93304F6B4C8FB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "KMSKS" REGION.
ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "HIGH" REGION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52
623
622
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                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=727;
                                                                                                                                                                                                           OR HI092
                                                                     SYL_HAEIN
P43827;
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                     RESULT 2
SYL HABIN
DT 101-NOV
DT 01-NOV
DT 01-NOV
DT 01-NOV
DT 01-NOV
DT 28-FEI
DE LEUCY.
COC PBACTE.
RA RELIBERS

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                                                                     DEEIDLTKQAFVEHGKLVNSDEFDGKNF--DGAFNG------IADKLEKLGV 408
                                                                                                                                                                                                                                                                 409 GKRQVNYRLRDWGVSRQRYWGAPIPMLTLENGDVVPA-----PMEDLPILLPEDVVMD 461
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SYMAINRE-2055717; PubMed=10910347;
SYMAINRE-2055717; PubMed=10910347;
SA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Colutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
Radonicani A.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
R. Garnier M., Goldman G.L., Lopes S.A., Gruber A.,
R. Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Machado M.A., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Mardue M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Deixoto D.B.R., Poereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Deixoro D.B.R., Poereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA G. Silva A.C.K., de Silva A.M., de Sluva A.J.M.,
RA de Silva A.C.K., de Silva A.M., de Sluva A.D.M.,
RA de Silva A.P., Terenzi M.F., Truffi D., Tsai S.N., Tsuhako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeda S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeda S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeda S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeda S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeda S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeda S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeda S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeda S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeda S., Vettore A.L.,
R
104 DGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADK-OKNGI
                                                                                                                                                                                                           163 ---KVNFKIRH-------NIEDGSVQLADHYQQNTPIGDGPVLLPDNHYL-
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-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
LeCCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
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Q9PBG8;
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Nature 413:852-856(2001)
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623
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622 6
860 AA;
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Q8ZQZ6;
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         STITE SOLUTION AND DESCRIPTION OF SOLUTION                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 TTGKLPVPWPTLVTLLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNY-- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----KTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      378 STWEPDVWRDWYADKTR---EFE---LINSAEFDGLDYQDAFEVLAERFE------ 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 MADKQKNG-IKVNFKIRHNIEDGSVQLADHYQQNTPI------GDGPVLLPDN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAILINE-172 / Arcc 700931;
MEDLINE-272 J Arcc 700931;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                      rkusijs; PSO0178; AA_TRNA_Ligase i; i.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Krogh J., Lasten T.T., Holroyd S., Jagels K., Krogh J., Lasten T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; amultiple drug resistant Salmonella enterica serovar Typhi CT18.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2NA Synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
LEUS CX STY0699 OR 72219.
Salmonèlla typhi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
7.4%; Score 94.5; DB 1; Length 879;
Best Local Similarity 22.7%; Pred. No. 3.9;
Matches 45; Conservative 29; Mismatches 67; Indels 5
                                                                                                                                                                                                                                                                                                                                                        "KMSKS" REGION.
ATP (BY SIMILARITY).
9FDCCB992092919E CRC64;
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                                                                                                                                                                                                                                                                                                                             "HIGH" REGION
InterPro; IPR002302; Leu-tRNAsyntla.
InterPro; IPR002300; tRNA-synt la.
InterPro; IPR001412; tRNA-synt linterPro; IPR001412; tRNA-synt linterPro; IPR009008; ValRS lieRS edit.
Pfam; PF00133; tRNA-synt l; l.
PRINTS; PR00985; TRNASYNTHIEU.
TIGREPMS; TIGR00396; leuS bact; l.
PROSITE; PS00178; AA_TRNA_LIGASE_I; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN:=CT18;
MEDLING=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 185:2330-2337(2003)
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640 640 A
879 AA; 99796 MW;
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641
640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYL SAUTI
Q8ZBHS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.38
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                           SITE
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SYL SALTI
SYL SALTI
DO CO BYL SALTI
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DT 10-00
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DT 10-00
DT 10-00
DE Leucy
ON SALM
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ON NCBI
RR SEQUE
RR STRAII
RR BAKER
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This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 TTGKLPVPWPTLVTLLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ::|| | :: | | | :: | | | 314 TGEEIPV-WAANFVLMEXGTGAVMAVPGH-DQRD-YEPASKYGLTIKPVILAADGSEPDL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 RAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371 SEQALTEKGVLFNSGEFDGLAFEAAFNAIADKL------AEKGVGERKVNYRLR 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      419 DWGVSRQRYWGAPIPMVTLEDGTV-----LPTPEDQLPVILPEDVWMDGITSPIKADP 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 H-------NIEDGSVQLADHYQQNTPIGDGPVLLPDNHYL-STQSALSKDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=LTZ / SGSC1412 / ATCC 700720;
MEDLINE=LTZ / SGSC1412 / ATCC 700720;
MEDLINE=LTZ / SGSC1412 / Bubmed=11677609;
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP; MF 00049; -: 1.

InterPro; IPR001302; Leu-tRNAsyntla.

InterPro; IPR001412; tRNA-synt_I.

InterPro; IPR001412; tRNA-synt_I.

InterPro; IPR001402; tRNA-synt_I.

InterPro; IPR001402; tRNA-synt_I.

Pfam; PF00133; tRNA-synt_I.

PRINTS; PR00985; TRNASYNTHLEU.

PROSITE; PS001798; AA TRNA_LIGASE 1; 1.

Aminoacy1-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                             diphosphare + L-leucyl-tRNA(Leu).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-6CT-2003 (Rel. 42, Created)
10-6CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.3%; Score 92.5; DB 1; Length 860; 23.9%; Pred. No. 5.5; ive 21; Mismatches 77; Indels 3:
CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  623 "KMSKS" REGION.
622 ATP (BY SIMILARITY).
96940 MW; 2F95E480BBAB23C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           860 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "HIGH" REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL627267; CAD05125.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE016841; AA069822.1; -.
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Matches 43; Conservative
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Complete proteome.
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Q8EHP4;
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                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           371 SEQALTEKGVLFNSGEFDGLAFEAAFNAIADKL------AEKGVGERKVNYRLR 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212
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MEDLINE=22421313; PubMed=12533478;

MEDLINE=22421313; PubMed=12533478;

MAJAKI C.Y., Furlan L.R., Camargo L.B.A., da Silva A.C.R., Moon D.H.,

MAJAKI C.Y., Furlan L.R., Machado M.A., Ferro M.I.T., da Silva F.R.,

Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,

Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M.,

Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,

Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.B.,

Marino C.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,

dan G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,

da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; MF_00049; -; I.
InterPro; IPR002302; Leu-tRNAsyntla.
InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR003000; tRNA-synt_la.
InterPro; IPR003008; VaINS_IDE_I.
PROM; PF00133; tRNA-synt_l; 1.
PRINTS; PR00985; TRNASNTHLEU.
TIGRPAMS; TIGRPAMS; TIGRDASE; 1.
FROSTE; PS00178; AA_TRNA_LIGASE; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                 SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
LEUS OR PD1230.
Xylella fastidiosa (strain Temeculal / ATCC 700964).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.3%; Score 92.5; DB 1; Length 860; 23.9%; Pred. No. 5.5; ve 21; Mismatches 77; Indels 3:
CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "KMSKS" REGION.
ATP (BY SIMILARITY).
D5003584DFBCCAB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     879 AA
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                         diphosphate + L-leucyl-tRNA(Leu). SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE008725; AAL19599.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96985 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 23.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kanthomonadaceae; Xylella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43; Conservative
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622 6
860 AA;
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Q87C65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 TTGKLPVPWPTLVTLLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNY-- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 ------KIRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 MADKQKNG-IKVNFKIRHNIEDGSVQLADHYQQNTPI-------GDGPVLLPDN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321 TNEOLPV-WVANFVLMAYGTGAVMAVPGHDQRDQEF--ANKYGLPIRQVIALKEPKNQDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAMAP; MF_00049; -; 1.
InterPro; IPR002302; LBU-LRNAByntla.
InterPro; IPR001412; tRNA-synt_1.
InterPro; IPR001412; tRNA-synt_1.
InterPro; IPR001412; tRNA-synt_1.
InterPro; IPR00131; tRNA-synt_1.
Pfam; PF00133; tRNA-synt_1.
PRINTS; PR00985; TRNASYNTHLEU.
TIGRABA; TIGRAS, 1 LBUS bact; 1.
PR051TE; PS00178; AA TRNA LIGASE 1; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57; Gaps
                                                                                                                                                                                                                           J. Bacteriol. 185:1018-1026 (2003).
-!- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA (Leu) = AMP +
diphosphate + L-leucyl-tRNA (Leu).
-! GYBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS).
LEUS OR SO1174.
Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sassaki F.T., Sena J.A. Ge Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G., Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C., Kitajima J.P.,
                                                                                                                              "Comparative analyses of the complete genome sequences of Pierce' disease and citrus variegated chlorosis strains of Xylella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; Shewanella.
NCBI_TaxID=70863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "HIGH" REGION.
"KMSKS" REGION.
ATP (BY SIMILARITY).
4C2EE01B8FDC497E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 6.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.2%; Score 91.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE012557; AA029080.1; ALT_INIT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 22.79
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55
641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      879 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313 GPRDLKMLCAEEDQSRMCWVTAIRLLKYGMQLYQNYMHPSQARSACSSQSVSPMRSVSEN 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 GHKLEYNYNSH--------INVIMADKQKN------GIKVNF---- 166
                                                                                                                                                                                                                                    Kasus-Jacobi A., Perdereau D., Auzan C., Clauser E., van Obberghen E., Mauvais-Jarvis F., Girard J., Burnol A.-F.; "Identification of the rat adapter Grb14 as an inhibitor of insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 GKLTLKFICT-TGKLPVPWPTLVTLLSYGVQCFSRY--PDHMKQHDFFKSAMPEGYVQER
                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                            actions.",
J. Biol. Chem. 273:26026-26035(1998).

J. Biol. Chem. 273:26026-26035(1998).

-!- FUNCTION: Interacts with the cytoplasmic domain of the autophosphosphorylated insulin receptor which is then inhibited. The interaction is mediated by the SH2 domain.

-!- SUBGNIT: Binds to the anywrin repeat region of TNKL via its N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                 terminus (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic, associated with the Golgi and endosomes (By similarity).
-!- PTM: Phosphorylated on serine residues (By similarity).
-!- SIMILARITY: Contains 1 PH domain.
-!- SIMILARITY: Contains 1 Ras-associating domain.
-!- SIMILARITY: Contains 1 Ras-associating domain.
-!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Belongs to the GRB7/10/14 family.
Growth factor receptor-bound protein 14 (GRB14 adapter protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Match 7.0%; Score 88.5; DB 1; Length 538; Local Similarity 19.4%; Pred. No. 6.7; tes 41; Conservative 33; Mismatches 70; Indels 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     533 SH2.
60592 MW; CEBC9037E7868EEF CRC64;
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                                                                                                                                                                                                                  MEDLINE=98421528; PubMed=9748281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001849; PH.
InterPro; IPR001859; RA_domain.
InterPro; IPR001859; RA_domain.
InterPro; IPR000180; RHZ.
InterPro; PF00788; RA; I.
Pfam; PF00788; RA; I.
Pfam; PF007017; SHZ; I.
PRINTS; PR00401; SHZ; I.
SWART; SW00233; PH; I.
SWART; SW00231; PH; I.
SWART; SW00252; SHZ; I.
PR0SITE; PSS0003; PH_DOMAIN; I.
PROSITE; PSS0001; SHZ; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF076619; AAC61478.1; -
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                                               Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                437 5
538 AA;
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                                                                                                                                                                  FROM N.A.
                                                                                                                     NCBI TaxID=10116;
                                                                                                                                                                                              STRAIN=Wistar
                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 CFSRYPDH-MKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277 ELAAFIDECKNSTTSEAELATMEKRGVAT-GLYAIHPI--TGKQVPIWAANFVLMNYGTG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                334 AVMSVPGHDQRDYEFAK----KYHLPIEAVIKPAEGDLDISEAAYTEKGILFNSGEFDGL 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 DFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRH------NIEDGSVQLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 ELDGDVNGHKFSVSGEGE-----GDATYGKLTLKFICTTGKLPVPWPTLVTLLSYGVQ 70
               FRAIN=WR-1;

MEDLINE=22297686; PubMed=12368813;

MEDLINE=22297686; PubMed=12368813;

Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,

Meyer T., Taapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,

DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,

Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,

Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,

Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,

Feldblyum T. V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;

"Genome sequence of the dissimilatory metal ion-reducing bacterium

Shewanella oneidensis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEAM; PF00133; tRNA-synt 1; 1.
PRINTS; PR00985; TRNASYNTHLEU.
TIGRPAM9; TIGR00396; leug. dect; 1.
PROSTIE; PS00178; AA TRNA LIGASE I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                       Nat. Biotechnol. 20:1118-1123 (2002).
-!- CATALYTIC ACTIVITY: ATP + L.-leucine + tRNA(Leu) = AMP +
diphosphate + L.-leucyl-tRNA(Leu).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "KMSKS" REGION.
ATP (BY SIMILARITY).
C78D6209DFB6CA17 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.0%; Score 89.5; DB 1;
24.1%; Pred. No. 9.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 DHYQQNTPIGDGPVLLPDNHYL-STQSALSKD 211
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(Rel. 38, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  538 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "HIGH" REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMAP; MF_00049; -; 1.
InterPro; IPR002302; Leu-tRNAsyntla.
InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE015561; AAN54244.1; -. TIGR; SO1174; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96827 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52
622
621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 621 6
859 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
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15-JUL-1999
28-FEB-2003
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GRBE RAT
ID GRBE RAT
AC 088900;
DT 15-JUL-199
DT 15-JUL-199
T 28-FEB-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches

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Gaps

67;

431 LHRSQPWFHHRISRDEAQQLITRQGPVDGVFLVRDSQSNPRTFVLSMSHGQKIKHFQIIP 490

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Pred. No. 9.8;

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
DPOL_HPBHE
                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=2001-L5;
MEDLINE=96161286; PubMed=8593007;
MEDLINE=96161286; PubMed=8593007;
Geber A., Hitchcock C.A., Swartz J.E., Pullen F.S., Marsden K.E.,
Kwon-Chung K.J., Bennett J.E.;
"Delection of the Candida glabrata ERG3 and ERG11 genes: effect on cell
viablity, cell growth, sterol composition, and antifungal
susceptibility.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY).
                                                                                                                                                                        PEDS CANDON STANDARD; PRI; 533 AA.
PEDS CANDON STANDARD; PRI; 533 AA.
PEDS CANDON CANDON STANDARD; CLEATED STANDARD; COTT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last amotation update)
10-OCT-2003 (Rel. 34, Last amotation update)
10-OCT-2003 (Rel. 34, Last amotation Candida)
10-OCT-2004 (Rel. 34, Last amotation Candida)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: Obtusifoliol + 3 O(2) + 3 NADPH = 4-alpha-methyl-5-alpha-ergosta-8,14,24(28)-trien-3-beta-ol + formate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME P450; 1.
Electron transport; Oxidoreductase; Monooxygenase; Membrane; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burgener-Kairuz P., Zuber J.P., Jaunin P., Buchman T.G., Bille J.,
Rossier M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lanosterol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Torulopsis (Candida) glabrata in clinical specimens by species-specific nested PCR amplification of a cytochrome P-450 lanosterol-alpha-demethylase (LiA1) gene fragment."; J. Clin. Microbiol. 32:1902-1907(1994).

-i-FUNCTION: Catalyzes C14-demethylation of lanosterol which is critical for ergosterol biosynthesis. It transforms lanoster into 4.4'-dimethyl cholesta-8,14,24-triene-3-beta-ol (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Rapid detection and identification of Candida albicans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           472 IRON (HEME AXIAL LIGAND)
64 I -> M (IN REF. 2).
473 I -> T (IN REF. 2).
61305 MW; A0506C17507E6EF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antimicrob. Agents Chemother. 39:2708-2717(1995).
                   ----KIRHNIEDGS-----VQLADHYQQN 186
                                                          491 VEDDGEVFHTLDDGHTKFTDLIQLVEFYQLN 521
                                                                                                                                                               533 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PATHWAY: Ergosterol biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR001128; Cytochrome P450.
Pfam; PF00067; p450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ATCC 2001;
MEDLINE=95081364; PubMed=7989540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L40389; AAB02329.1; -. EMBL; S75389; AAB32679.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 60-473 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sterol biosynthesis; NADP.
                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              533 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=5478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
                                                                                                                                                               CANGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
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                                                                                                                                            CP51_CANGA
                                                                                                                    RESULT
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DB 1; Length 533;

6.8%; Score 86.5;

Query Match

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                                           õ
                                                                                                                                                                    (09 GHEFIFNAKLADVSAEAAYSHLT------TPV-----FGKGVIYDCPNHRLM 149
                                                                                                                                                                                                                                                       80 KQHDFFKSAM-PEGYV-----QERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDF 131
                                                                                                                                                                                                                                                                                                                         207
                                                                                                                                                                                                                                                                                                                                                                                                                                          208 TASRSILGKEMRDKIDTDFAYLYSDLDKGFTPINF-VFPNLPLEHYRKRDHAQQAIS--- 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 WPTLVTLLSYGVOCFSRYPDHMKQH----DFFKSAMPEGYVQERT----IFFKDDGNYK 108
                                                                                                                                                                                                                                                                                                                                                                                              132 KEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 WPKSISYLPVHSGVKPKYPEFQQNHESLVNDYLNKLFEAGILYKRVSKHLVTFK--GPYF 196
                                                                                                             25 GHKRSVS---GEGEGDATYGKLTLKFICTTGKLPVPWPTLVTLLSYGVQCFSRYPDH--M 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD000814; DNApol viral_C; 1.
Transferase; RNA-directed DNA polymerase; PNA-directed DNA polymerase; Hydrolase; Nuclease; Endonuclease; DNA replication; DNA-binding.
SEQUENCE 788 AA; 90070 MW; FB44F38F75EADF44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPOL_HPBHE STANDARD; PRT; 788 AA.
P13346;
01-JAN-1990 (Rel. 13, Created)
10-JAN-1990 (Rel. 13, Last sequence update)
11-GCT-2001 (Rel. 40, Last annotation update)
P protein [Includes: DNA-directed DNA polymerase (EC 2.7.7.7); RNA-directed DNA polymerase (EC 2.7.7.7); RNA-directed DNA polymerase (EC 2.7.7.9);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sprengel R., Kaleta B.F., Will H., "Isolation and characterization of a hepatitis B virus endemic in
                                           49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.
NCBI_TaxID=28300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                           80;
21.8%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.8%; Score 86.5; L
19.7%; Pred. No. 16;
tive 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192 GPVLLPDNHYLSTQSALSKDPNEKRD 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 -----GTYMSLIKERREKND 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A30082; JDVLHH.
InterPro; IPR001462; DNApol_viral_C.
InterPro; IPR000201; DNApol_viral_N.
InterPro; IPR000477; RVTGe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00336; DNA_pol_viral_C; 1.
Pfam; PF00242; DNA_pol_viral_N; 1.
Pfam; PF00078; rvt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=88333160; Pubmed=3418788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M22056; AAA45738.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Virol. 62:3832-3839(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 19.7% hes 40; Conservative
                                           45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heron hepatitis b virus.
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                                                                                                             543 RNLYIQSMKFKGNGIKTN------DFDFSFGWNYNSLNRGYFPTKGVKASLG-GRVTI 593
65 LSYGVQCFSRYPDHMKQHDF------RTSAMPEGYVQE-----RTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Outer membrane protein D1S is conserved among Haemophilus influenzae species and may represent a universal protective antigen against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Flack F.S., Loosmore S., Chong P., Thomas W.R.; The sequencing of the 80-kDa D15 protective surface antigen of Haemophilus influenzae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protective surface antigen D15 precursor (80 kDa D15 antigen)
CD-15-Ag) (Outer membrane protein D15).
Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 POTENTIAL.
797 PROTECTIVE SURFACE ANTIGEN D15.
87675 MW; 2F93DE538696AF1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invasive disease.";
Infect. Immun. 65:3701-3707 (1997).
-!- SUBCELLULAR COATION: Outer membrane.
-!- SIMILARITY: Belongs to the surface antigen D15 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                             197 P--DNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLG 233
                                                                                                                                                                                                           594 PGSDNKYYKLSADVQGFYPLDRDHLWVVSAKASAGYANG 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Minna / Serotype B, and Eagan / Serotype B; MEDLINE=97427952; PubMed=9284140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ed. No. 16;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.8%; Score 86.5; 21.9%; Pred. No. 16
                                                                                                                                                                                                                                                                                                                           797
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Interpro, IPR000184; Bac_surfAg_D15.
Pfam; PP01103; Bac_surface Ag; I.
Antigen; Outer membrane; Sīgnal.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-Serotype B;
MEDLINE-95255676; PubMed=7737523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U60832; AAB61974.1;
EMBL; U60833; AAB61976.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48; Conservative
                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene 156:97-99(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             797 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                             HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klein M.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                              P46024
                                                                                                                                                                                                                                                                                                   D151_HAEIN
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Matches
                                                                                                                                                                                                                                                                                  RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           486
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                                                                                                                     --- QNTPIGDGPVLL-PDNHYL 202
                            ----RAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIM 154
                                                                                                                                                                  ----NGRKISY---HSTRDGSHRLSGRTSDPTSRGALAGGDSTPIGPGSTAAHPSTHHV 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : | | : | | : | | : | IGYGTESGISYQASVKQDNFLGTGAAVSIAGTKNDYGTSVNLGYTEPYFTKDGVSLGGNV
                                                                     TWEQKHLVPQQHGAYSSKINDRQESRRRRİITATSSRKNDSSRI------FGAHN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95350630; PubMed=7542800; Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Puhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protective surface antigen D15 precursor (80 kDa D15 antigen)
(D-15-Ag) (Outer membrane protein D15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.8%; Score 86.5; DB 1; Length 795; 21.9%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTECTIVE SURFACE ANTIGEN D15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the surface antigen D15 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----FKSAMPEGYVQE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interro, irrova.v. Pedilos Brance, Promplete proteome. Antigen; Outer membrane, Signal; Complete proteome. Potigen; Outer membrane, Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                     155 ADKQKNGIKVNFKIRHNIEDGSVQLADHYQ-----
                                                                                                                                                                                                                                                                                                                                                                             795 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 LSYGVQCFSRYPDHMKQHDF------
                                                                                                                                                                                                               203 STQ-----SALSKDPNEKR 216
                                                                                                                                                                                                                                       : |:|:| |
298 DRRRRQKGQGVLQAISREPSETR 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000184; Bac_surfAg_D15.
                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemophilus influenzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48;
                                                                                                                                                                                                                                                                                                                                                                             D152 HAEIN
                                                                                                                                                                  246
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FFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNI---LGH------KLEYNYNS 148
                                                            HNVYIMADKQK-NGIKVNFKIRHNIEDGSVQLADHYQQ------NTPIGDGPVLL 196
                                                                                         543 RNLYIQSMKFKGNGIKTN-----DFDFSFGWNYNSLNRGYFPTKGVKASLG-GRVTI 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the Buropean Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                           FFENYDNSKSDISSNYKRITYGSNVTL-GFPVNENNSYYVGLGHTYNKISNFALEYN---
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91077937; PubMed=2230718; Okamoto K.; Mikata S., Kawai S., Ito S., Okamoto K.; Ozaki K., Shikata S., Kawai S., Ito S., Okamoto K.; Molecular cloning and nucleotide sequence of a gene for alkaline cellulase from Bacillus sp. KSM-635."; J. Gen. Microbiol. 136:1327-1334(1990).

-I. CATALYTIC ACTIVITY: Endobydrolysis of 1,4-beta-D-glucosidic linkages in cellulose, lichenin and cereal beta-D-glucons.

-I. SIMILARITY: Belongs to cellulase family A (family 5 of glycosyl
                                                                                                                                                                                                                                                                    ol-wov-1990 (Rel. 16, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Endoglucanase precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)
(Alkaline cellulase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00659; GLYCOSYL HYDROL_F5; 1.
PROSITE; PS01072; SLH_DOMAÎN; 2.
Cellulose degradation; Hydrolase; Glycosidase; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hydrolases).
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RES NUCLEOPHILE (BY SIMILARITY).

104628 MW; BEAZAC3B169BFADA CRC64;
                                                                                                                                                                                                                                                                                                                                             Bacillus sp. (strain KSM-635).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus,
                                                                                                                                                     594 PGSDNKYYKLSADVOGFYPLDRDHLWVVSAKASAGYANG 632
                                                                                                                         P--DNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 86.5; D
; Pred. No. 19;
34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENDOGLUCANASE.
SLH 1.
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PDB; 1G02; 31_DEC_02.

Interpro; 1PR005086; CBM 17_28.

Interpro; 1PR008979; Gal_bind like.

Interpro; 1PR001847; Glyco_hydro_5.

Interpro; 1PR001119; Sl.H.

Pfam; PP00150; callulase; 1.

Pfam; PP00159; SLH; 3.
                                                                                                                                                                                                                                                               01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last seq
10-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M27420; AAA22304.1; -.
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Best Local Similarity
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ACT_SITE
SEQUENCE
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Gaps

61; Indels 97;

49; Conservative

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN=NCTC 11168;

MEDINE=20150912; PubMed=10688204;

MEDINE=20150912; PubMed=10688204;

March B.W., Mungall K., Ketley J.M., Churcher C.,

Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,

Agels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

Mitchead S., Barrell B.G.;

"The genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervariable sequences.";

"The genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervariable sequences.";

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"The genome sequences.";

"The genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervariable sequences.";

"The genome sequences.";

"The genome sequence of the food-borne pathol-randine at position

"The genome sequences.";

"The genome sequences.";

"The genome sequence of the RNA MSU methyltransferase family. TrmA
                                                                                                                                                                                                                                   320 -----FEHDMYVIVDWH---VHAPGDPRADVYSGAYDFFEEIADHYKDH---- 360
                                                                                                                                                                                                                                                                                                                                      76 PDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDG 135
                                                                                                                                                                                                        136 NILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSV----QLADHYQQNTPIGD 191
                                             240 LVELNG-----QLTLAGE---DGT--------PV---QLRGMSTHGLQWFG-- 271
LVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTLLSYGVQCFSRY 75
                                                                                                                                     192 GPVLLPDNHYLSTQSALSKDPN-----EKRDHMVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campylobacter jejuni.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
NCBI_TaxID=197;
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PROSITE; PS01231; TRMA_2; FALSE NEG.
PROSITE; PS01231; TRMA_2; FALSE NEG.
Transferase; Methyltransferase; tRNA processing; Complete proteome.
DOMAIN 207 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
tRNA (Urscil-5-)-methyltransferase (BC 2.1.1.35) (tRNA(M-5-U54)-methyltransferase) (RUMT).
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InterPro, IPR000051, SAM bind.
InterPro, IPR001566, TrmA.
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                                                                                                                                                                                                               80 KQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKF--EGDTLV------NRIELKG 128
                                                                                                                                                                                                                                                                                                                                                                                     74 LDFADEKICAFMPRLLEYLRQDNKLKEKL-----FGVEFLTTKQE--LSITLLYHKNIE 125
                                                                                                                                                                                                                                                                                                                                   129 IDFKED------GNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIE 173
                                                                                                                                                                                                                                                        14 BKHSFIKKYFKEFYTKDFKLFASKDKHYRTRABLSFYHBNDTLFYAMFDPKSKKKYIIEY 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Outer membrane protein D15 is conserved among Haemophilus influenzae species and may represent a universal protective antigen against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=PAK 12085;
MEDLINE=97427952; PubMed=9284140;
Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
                                                                                                                                                      Gaps
                                                                                                                                                      34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protective surface antigen D15 precursor (80 kDa D15 antigen)
(D-15-Ag) (Outer membrane protein D15).
Haemophilus influencae.
Bacteria, Proteobacteria; Gammaproteobacteria; Pasteurellales;
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51BFDB2036801A14 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79; Indels
BY SIMILARITY.
CEC5328347CEE497 CRC64;
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Best Local Similarity 22.4%; Pred. No. 19;
Matches 49; Conservative 28; Mismatches
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InterPro; IPR000184; Bac surfAg D15.
Pfam; PF01103; Bac surface Ag; I.
Antigen; Outer membrane; Signal.
      315 B' 42276 MW;
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16-OCT-2001 (Rel. 40, Last seq
16-OCT-2001 (Rel. 40, Last ann
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357 AA;
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032629;
      ACT SIFE
SEQUENCE
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                                                                                              Query Match
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D153_HAEIN
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Search completed: June 21, 2004, 15:55:21 Job time : 7.55556 secs montastraea anemonia ma montastraea goniopora t montastraea

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Q8t6u0 Q8i6j8 Q9u6y3 Q8t5f1 Q7z0w4 Q8mu48 Q7z0w6

trachyphyll

clavularia

discosoma s meandrina m

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Q9gpis Q9bly9 Q9u6y8 Q86lv7 Q9gz28 Q86lv8 Q7z168 Q7z168 Q8t6t9

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VTLLSYGVQCFSRYPDHMKQHDFPKSAMPBGYVQBRTIFFKDDGNYKTRAEVKPEGDTLV 121
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Koranyi P., Bernyi M., Burg K.;
T "Occurrence of green fluorescence protein in diazotrophic bacteria
T Azomonas and Azotcobacter.";
LI Azomonas and Azotcobacter.";
Submitted (Nov-2000) to the EMBL/GenBank/DDBJ databases.
BMB1, AF324408; AAN86140.1;
RGO; GO:0006091; P:energy pathways; IEA.
RI ThterPro; IPR0000786; Green fl_protein.
R InterPro; IPR000786; Green fl_protein.
R Pfam; PF01353; GFP; 1.
R Pfam; PF01355; Green fl_protein; 1.
R ProDom; PD013756; Green fl_protein; 1.
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Pseudomonadaceae; Azotobacter.
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Pred. No. 1.5e-96;
2; Mismatches 4; Indels (
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                           Q8MU47
Q9U6Y6
Q962P9
Q7Z0W8
                                                                                                                                                                                                      Q86LV8
Q7Z168
Q8T6T9
Q8T5F0
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Q95VT0
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Q9BLY9
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Q9GZ28
                                0906Y3
08T5F1
07Z0W4
08MU48
07Z0W6
                                                                                          Q8MMA1
Q8T5F2
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                        2816J8
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Best Local Similarity 97.5%;
Matches 232; Conservative
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                                                                                                                                                                                                                                                                                                                                                   Green fluorescence protein.
2289GFP,
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Azotobacter vinelandii.
NCBI_TaxID=354;
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                                                          June 21, 2004, 15:45:30 ; Search time 30.6667 Seconds
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1 MVSKGEBLFTGVVPILVBLD......VLLGFVTAAGITLGMDBLYK
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Q17105
Q17106
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08ghe4
         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                       1017041 segs, 315518202 residues
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                                          - protein search, using sw model
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Q8WTC6
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sp_unclassified:*
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sp_archeap:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NRIELKGTDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
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                                                                                                                                                                                                Koranyi P., Berenyi M., Burg K.; Cocurrence of green fluorescence protein in diazotrophic bacteria Azomonas and Azotobacter."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Azotobacter vinelandii.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azotobacter.
                                                                                                Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.8%; Score 1232; DB 2; Length 238; 97.1%; Pred. No. 4e-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF324406; AAN86138.1; -0.00 (20) GO:0000091; P:energy pathways; IEA. InterPro; IPR009017; GFP 1ke. InterPro; IPR0090786; Green_fl_protein. PPR153; GFP; 1. PRINTS; PR01229; GFLUORESCENT. ProDom; PD013756; Green_fl_protein; 1.
                                                                                                                                                                                                                                                                        reen_fl_protein; 1.
26887 MW; E0E1616BD2AF6188 CRC64;
  Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
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01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25, Green fluorescence protein.
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                                                                                                    Bacteria; Proteobacteria; G.
Pseudomonadaceae; Azomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 97.1
Matches 231, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                         NCBI_TaxID=116849;
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SEQUENCE FROM N.A.
                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                               Azomonas agilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=354;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Q8GHE3;
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61 VTTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                             NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
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                                        NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
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                                                                                                                  HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
                                                                                                                                             181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDIJNE=96305137; PubMed=8707053;
Cormack B.P., Valdivia R.H., Falkow S.;
"FAGC--Dtimized mutants of the green fluorescent protein (GFP).";
Gene 173:33-38(1996).
                                                                                                                                                                                                                                                                                                                                                                                              Aequorsa victoria (Jellyfish).
Ebkaryota; Metazoa; Chidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoraidae; Aequorea.
NCBI_TaxID=6100;
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Brown A.J.P.;
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Last annotation update)
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InterPro; IPR009017; GFP_like.
InterPro; IPR000786; Green_fl_protein.
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                                                                                                                                                                                                                                                                                                                                                            Green fluorescent protein mutant 3.
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Marcabilogy 0:0-0(1996).
EMBL; 773901; AAB18957.1; -.
HSSP, P42212; 1BFP.
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97.18;
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01-FEB-1997 (TrEMBLrel. 02,
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96.7%; Score 1231; DB 2; Length 238;

Query Match

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61 VITESYGVQCFSRYPDHMKQHDFLKSAMPEGYVQERIIFYKDDGNYKTRAEVKFEGDTLV 120
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STRAIN=GFPAm19uv;
STRAIN=GFPAm19uv;
Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea macrodactyla.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF435431; AAL33916.1; -.
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR0009017; GFP_like.
InterPro; IPR000786; Green_fl_protein.
                                                                                                                                                         Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=6100;
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 93.0%; Score 1184; DB 5; Length 238; Best Local Similarity 92.9%; Pred. No. 4.6e-92; Matches 221; Conservative 7; Mismatches 10; Indels
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Watkins J.N., Campbell A.K.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; X83960; CAS58790.1; -.
PIR; JS0692; JQ1514.
HSSP; P42212; 1BFP.
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                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Green fluorescent protein (Fragment).
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Last annotation update)
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InterPro; IPR000917; GFP like.
InterPro; IPR000918; Green_fl_protein.
Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLÜORESCENT.
Prodom; PD013756; Green_fl_protein; 1.
NON TER.
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                                                                                                                                          Aequorea victoria (Jellyfish)
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SEQUENCE
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=6100;
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94.2%; Score 1199; DB 5; Length 238;
Best Local Similarity 93.7%; Pred. No. 2.5e-93;
Matches 223; Conservative 6; Mismatches 9; Indels
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  Pred. No. 4.9e-96;
2; Mismatches 5;
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97.1%;
                        Matches 231; Conservative
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  Best Local Similarity
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Q17105;
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STRAIN=ShG24;
Luo W.X., Zhang J.,
Li S.J., Xia N.S.;
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                                                                                                              OBWTC4;
01-MAR-2002
01-MAR-2002
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                                                                                           Q8WTC4
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                                                                   Q8WTC4
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STRAIN=GFPxm, and GFPdnaxm;
Li S.Y., Zhang J., Yang H.J., Xie X.Y., Li S.W., Qin Y.X., Pang is Li S.J., Xia N.S.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AY013821, AAK02062.1;
EMBL, AY013821, AAK02059.1;
EMBL, AY013821, Pang pathways; IEA.
GO; GG:0006091, P:energy pathways; IEA.
InterFro; IPR009017; GFP_like.
InterFro; IPR000086; Green_fl_protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aequorea macrodactyla.
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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81.5%; Pred. No. 7.4e-83;
iive 20; Mismatches 24; Indels (
                                                                                                Length 238;
                                                                                      Query Match
84.8%; Score 1079; DB 5; Length 2
Best Local Similarity. 81.9%; Pred. No. 3.4e-83;
Matches 195; Conservative 20; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterFro; 1513 GFP; 1.
Prim; Prol135; GFP; 1.
PRINTS; PRO11229; GFLUORESCENT.
PRODOM; PD013756; Green_fl_protein; 1.
PRODOM; P0013756; Green_fl_protein; 1.
PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl_protein; 1.
SEQUENCE 238 AA; 27015 MW; 6B8FD75E88926903 CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Green fluorescent protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                    Chen M.,
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                                                                                                                            Aequorea macrodactyla.
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae, Aequorea.
NCBI_TaxID=147615;
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Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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                                                                                                                                                                                                                                                                                                                 Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 238;
                                                                                                                                                                                                                                                                                                                                                            "Colorful mutants of green fluorescent protein from Aequores
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                                                                                                                                                                                                                                                                                                                                                                                           macrodactyla.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO.0006091; P.energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IRR00786; Green_fl_protein.
Pfam; PF01353; GFF; 1.
PRINTS; PR01229; GFLVORESCENT.
PRODOM; PD013756; Green_fl_protein; 1.
SRQUENCE 238 AA; 26956 MW; 7552IEAF0CEBA73A CRC64;
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Last sequence update)
Last annotation update)
                                        Created)
Last sequence update)
Last annotation update)
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84.1%; Score 1071; DB 5; Sest Local Similarity 82.4%; Pred. No. 1.6e-82;
Matches 196; Conservative 17; Mismatches 25;
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238
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PRT;
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2003 (TrEMBLrel. 25,
Green fluorescent protein.
                                        01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                           Green fluorescent protein.
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PRELIMINARY;
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121 NRIELKGMDFKEDGNILGHKLEYNFNSHNVYIMPDKANNGLKVNFKIRHNIEGGGVQLAD 180
122 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVQLAD 181
                                                               182 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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238 AA; 27031 MW; 5F80A19C19DC584D CRC64;
                                                                                                                                                                                                         01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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Matches 193; Conservative
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QBWTC7;
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Q8WTC9
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Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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                                                                                                                                                            Length 238;
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                                                                                                                                                                                            25; Indels
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                          Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GPLUORESCENT.
ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 26997 MW; 5F80A192173CB84D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green_fl_protein; 1.
SEQUENCE 238 AA; 27047 MW; 5F80A18FA1E7C84D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 83.9%; Score 1068; DB 5; Best Local Similarity 81.1%; Pred. No. 2.9e-82; Matches 193; Conservative 20; Mismatches 25;
                                                                                                                                                            2
                                                                                                                                                          84.0%; Score 1069; DB 5;
81.1%; Pred. No. 2.4e-82;
iive 20; Mismatches 25
        EMBL, AF435427, AAL33312.1;
GO, GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR000786; Green_fl_protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25, Green fluorescent protein.
                                                                                                                                                                           Best Local Similarity 81.19
Matches 193; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   macrodactyla.";
                                                                                                                                                                                                                                                                                                                                                                                                                        182
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                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NRIELKGMDFKEDGNILGHKLEYNFNSHNVYIMPDKANNGLKVNFKIRHNIEGGVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTLLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSKGEELFTGIVPVLIELDGDVHGHKFSVRGEGEGDADYGKLEIKFICTTGKLPVPWPTL 60
HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
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                                                                                                                                                                                                                                                                                                                                                                                                                Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M., Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                           Aequorea macrodactyla.
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aequorea macrodactyla.
Eukaryota; Metazoa; Chidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                              Chen M.,
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Eukaryota, Metazoa; Chidaria, Hydrozoa; Hydroida; Leptomedusae;
Aeguoreidae; Aeguorea.
NCBI_TaxID=147615;
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81.9%; Pred. No. 6.3e-82;
ive 17; Mismatches 26; Indels (
                                                          Luo W.K., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Li S.J., Xia N.S., "Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                                                                                             Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                       25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       macrodactyla.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, PR495493. AAL33917.1; -.
GO, GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR000786; Green_fl_protein.
                                                                                                                                             Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF435430; AAL33915.1; -0.006091; P:energy pathways; IEA.

GO; GO:006091; P:energy pathways; IEA.
InterPro; IPR00907; GFP like.
InterPro; IPR000786; Green fllprotein.
PRINTS; PR01229; GFLUORESCENT.
PRODOM; PO013756; Green fllprotein; 1.
PRODOM; PO13756; Green fllprotein; 1.
SEQUENCE 238 AA; 27002 MW; BD5BA2982264C018 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01229; GFUORESCENT.
ProDon; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 27018 MW; 75521EA5534E573A CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                          Query Match
83.7%; Score 1066; DB 5;
Best Local Similarity 81.1%; Pred. No. 4.3e-82;
Matches 193; Conservative 20; Mismatches 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Orange fluorescent protein
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Pfam; PF01353; GFP;
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[1]
SEQUENCE FROM N.A.
STRAIN=GFPxm191uv;
                                                                                                                                      macrodactyla."
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cyan fluorescent protein (Fragment).
Montastrace, Metazoa, Cnidaria, Ratr coral).
Bukaryota, Metazoa, Cnidaria, Anthozoa, Zoantharia, Scleractinia, Faviina, Faviinae, Montastrace.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Palkowski P.G., Sun Y.;
Falkowski P.G., Sun Y.;
Falkowski P.G., Sun Y.;
Falkowski P.G., Sun Y.;
"Montastraea cavernosa fluorescent protein.";
Submitted (SEP-201) to the EMBL/GenBank/DDBJ databases.
RMBL; AVO56460; AAL17905.1; -..
RMBL; AVO56460; AAL17905.1; -..
R InterPro; IPR000786; APROFILE.
R InterPro; IPR000786; Green_fl_protein.
R Pfam; PF01353; GFP; 1.
R Pfam; PF01353; GFP; 1.
R PRINTS; PR01229; GFLUORESCENT.
R PRINTS; PR012756; Green_fl_protein; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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19.8%; Score 251.5; DB 5;
Best Local Similarity 31.1%; Pred. No. 2.6e-13;
Matches 64; Conservative 43; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                225 AA
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                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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GenCore version 5.1.6
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- protein search, using sw model OM protein Run on:

June 21, 2004, 15:41:49; Search time 47.1111 Seconds (without alignments) 1433.395 Million cell updates/sec

US-09-887-784-64V score: Sequence: Perfect

1586107 seqs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

1586107

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 290an04:\*

1: geneseqp1980s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2001s:\*

6: geneseqp2003ss:\*

7: geneseqp2003bs:\*

8: geneseqp2003bs:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|               |       | dŧ    |        |    | )<br> <br> |                |           |
|---------------|-------|-------|--------|----|------------|----------------|-----------|
| Result<br>No. | Score | Query | Length | DB | ID         | Description    |           |
| -             | 1269  | 99.7  | 239    | 'n | AAE17518   | Aae17518 Enhai | Enhanced  |
| 7             | 1269  | 99.7  | 363    | 9  | ABR40352   |                | ın ami    |
| m             | 1269  | 99.7  | 893    | 4  | AAG65781   | Aag65781 Amino | no aci    |
| 4             | 1269  | 99.7  | 1132   | 4  | AAG65782   | -              | lo aci    |
| ហ             | 1261  | 99.1  | 239    | ഗ  | AAE17517   |                | Enhanced  |
| 9             | 1258  | 98.8  | 239    | m  | AAB22882   | ~              | Enhanced  |
| 7             | 1258  |       | 239    | m  | AAY54349   | Aay54349 Amino | no aci    |
| æ             | 1258  |       | 239    | m  | AAY79584   | EGFP           | sign      |
| σ             | 1258  |       | 239    | 4  | AAB50804   | Jell           | Jellyfish |
| 10            | 1258  |       | 239    | 4  | AAB85900   | Aab85900 A. v  | victor    |
| 11            | 1258  |       | 239    | 4  | AAB31171   |                | Amino aci |
| 12            | 1258  |       | 239    | ß  | AAG66198   |                | A. victor |
| 13            | 1258  |       | 239    | Ŋ  | ABG94444   |                | Protease  |
| 14            | 1258  | 98.   | 239    | ß  | AAE14599   |                | Aequorea  |
| 15            | 1258  |       | 239    | 9  | AAE34958   |                | Aequorea  |
| 16            | 1258  |       | 239    | 9  | AAG79829   | Aag79829 Green | n flu     |
| 17            | 1258  |       | 239    | 9  | ABR83616   | Abr83616 Green | n flu     |
| 18            | 1258  |       | 239    | 9  | ADA38074   |                | Aequorea  |
| 19            | 1258  |       | 239    | 7  | ABU63204   | Abu63204 Aeque | Aequorea  |
| 20            | 1258  |       | 239    | 7  | ADC18358   | Adc18358 EGFP  | EGFP (enh |
| 21            | 1258  |       | 239    | 7  | ABW00914   | Abw00914 Aeque | Aequorea  |
| 22            | 1258  | 98.8  | 239    | 7  | ADE28570   | Ade28570 Enhai | Enhanced  |
| 23            | 1258  | 98.8  | 246    | 7  | ABM79011   | Abm79011 Enhar | Enhanced  |
| 24            | 1258  | 98.8  | 248    | ഗ  | AAG68319   | Aag68319 Jelly | Jellyfish |
| 25            | 1258  | 98.8  | 259    | ß  | AAU99804   |                | Biomembra |

Novel fluorescent protein in in vitro assay for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution, has a green fluorescent protein with F64L and E222G

Claim 9; Page 37; 41pp; English

mutation.

Thastrup O;

Bjorn SP, Pagliaro L, WPI; 2002-098224/13. N-PSDB; AAD28163.

| Wild-type | Biomembra | Biomembra | Biomembra | Biomembra | Biomembra | Green flu | EGFP-MODC | EGFP-MODC | EGFP/ hum | EGFP/ hum | EGFP/ hum | EGFP/ hum | GFP-DEVD- | Caspase-3 | Recombina | EGFP/DRM | HUB1-GFP  | GFP mutan | RUB1-GFP |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|----------|-----------|-----------|----------|
| Aaw97451  | Aau99803  | Aau99802  | Aau99800  | Aau99801  | Aau99807  | Aay50142  | Aab24252  | Aau10888  | Ade28562  | Ade28564  | Ade28568  | Ade28566  | Aab22860  | Aay79638  | Abg94422  | Aay42181 | Abr 83620 | Aay54359  | Abr83621 |
| AAW97451  | AAU99803  | AAU99802  | AAU99800  | AAU99801  | AAU99807  | AAY50142  | AAB24252  | AAU10888  | ADE28562  | ADE28564  | ADE28568  | ADE28566  | AAB22860  | AAY79638  | ABG94422  | AAY42181 | ABR83620  | AAY54359  | ABR83621 |
| 7         | ß         | Ŋ         | ß         | ហ         | S         | ٣         | m         | Ŋ         | 7         | 7         | 7         | 7         | m         | m         | S         | ~        | 9         | m         | 9        |
| 265       | 268       | 270       | 272       | 273       | 280       | 281       | 281       | 281       | 286       | 289       | 290       | 290       | 294       | 294       | 294       | 308      | 320       | 323       | 323      |
| 98.8      | 98.8      | 98.8      | 98.8      | 98.8      | 8.86      | 98.8      | 98.8      | 98.8      | 98.8      | 98.8      | 98.8      |           | 98.8      | 98.8      | 98.8      | 98.8     | 98.8      | 98.8      | 98.8     |
| 1258      | 1258      | 1258      | 1258      | 1258      | 1258      | 1258      | 1258      | 1258      | 1258      | 1258      | 1258      | 1258      | 1258      | 1258      | 1258      | 1258     | 1258      | 1258      | 1258     |
| 56        | 27        | 28        | 29        | 30        | 31        | 32        | 33        | 34        | 35        | 36        | 37        | 38        | 39        | 40        | 41        | 42       | 43        | 44        | 45       |

## ALIGNMENTS

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/note= "Wild type Glu substituted with Gly; This corresponds to position 222 in the wild type protein"
                                                                                                                                                                     /note= "Wild type Phe substituted with Leu; This
corresponds to position 64 in the wild type protein"
Misc-difference 223
                                                                                                  Jellyfish; green fluorescent protein; GFP; protein redistribution; cellular function; genetic reporter; mutant; Stoke's shift; mutein.
                                                                              Enhanced F64L-E222G jellyfish green fluorescent protein mutant.
                                                                                                                                                           Location/Qualifiers
65
                    AAE17518 standard; protein; 239 AA.
                                                                                                                                                                                                                                                                                                       19-JUN-2000; 2000DX-0000953.
20-JUN-2000; 2000US-02126B1P.
10-MAY-2001; 2001DK-0000739.
10-MAY-2001; 2001US-0290170P.
                                                                                                                                                                                                                                                                                    18-JUN-2001; 2001WO-EP006848
                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                          (BIOI-) BIOIMAGE AS
                                                                                                                             Aequorea victoria.
Synthetic.
                                                                                                                                                             Key
Misc-difference
                                                                                                                                                                                                                                             WO200198338-A2
                                                           22-APR-2002
                                                                                                                                                                                                                                                                 27-DEC-2001.
                                       AAE17518;
RESULT 1
AAE17518
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The invention relates to a fluorescent protein derived from green

fluorescent protein (GFP) or its analogue. The GFP containing mutations

at FeAL and E2226 has a bigger compared to other GFP's making it very

cuitable for high throughput screening due to better resolution. The

fluorescent protein is useful in invitro assays for measuring protein

kinase activity or dephosphorylation activity, or for measuring protein

cucistribution. The fluorescent protein tags in transgenic animals, living

and fixed cells; organelle tags, secretion marker and genetic reporter.

The fluorescent protein is also useful as a cell or organelle integrity

marker, a marker for changes in cell morphology, as transfection marker,

and as a marker to be used in combination with fluorescence activated

cell sorting (FACS). The novel proteins can also be used as reporters to

monitor live or dead biomass of organisms, such as fungi. The fluorescent

protein is also useful as markers in transcriptional and translational

fusions for performing transposon vector mutagenesis and as a reporter

for bacterial detection. Transposons encoding the fluorescent protein are

useful for screening prometers and for tagging plasmids and chromosomes.

The fluorescent protein engineered into the genome of a phage is useful

for designing diagnostic tool. The present sequence is a DNA encoding

enhanced F64L-E222G jellyfish green fluorescent protein (GFP) mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVTVLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.7%; Score 1269; DB 5;
larity 99.6%; Pred. No. 9.7e-123;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 238; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 239 AA;
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ABR40352
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The invention relates to a novel cell, comprising three heterologous conjugates (HC), a first HC (HCI) comprising an anchor protein that specifically binds to an internal structure within the cell conjugated to an interact or type A a second HC (HC2) comprising IP of type B conjugated to a first protein of interest, and a third HC (HC3) comprising a second protein of interest conjugated to detectable group. The cell is useful for detecting if a compound disrupts or induces the interaction between two intracellular proteins. The cell is also useful for accompounds that modulate the interaction between two intracellular proteins. The cell is also useful intracellular proteins. The proteins the interaction between two exemplification of the invention

first conjugate comprising anchor protein, second conjugate having type B interactor protein and third conjugate with detectable group.

Disclosure, Page 112-113; 118pp; English

cell for identifying modulators of protein interaction, contains a conjugate comprising anchor protein, second conjugate having type B

2003-430211/40.

N-PSDB; ACC72604

Novel

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                                                                                                                                                                                                                                                                                                                             61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                                                                                                                                                                                                                                                                                                          61 LVTVLSYGVOCFSRXPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL
                                                                                                                                                                                                                                                                          1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDB4; central nervous system; antiinflammatory; cytostatic; nootro
autoimmune; ischemic; osteopathic; GFP; green fluorescent protein;
                                                                                                                                                                                                                                   99.7%; Score 1269; DB 6; Length 363; 99.6%; Pred. No. 1.8e-122; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of HSPDE4A1-E222G fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG65781 standard; protein; 893 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-APR-2000; 2000DK-0000651.
29-MAY-2000; 2000DK-00000849.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-APR-2001; 2001WO-DK000264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JAN-2002 (first entry)
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.6
Matches 238; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BIOI-) BIOIMAGE AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aequorea victoria.
                                                                                                                                                                                                                      Sequence 363 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fusion protein.
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Human; heterologous conjugate; intracellular protein.

Aequoria victoria. WO2003029827-A2.

10-APR-2003

sapiens

Ношо

01-OCF-2001; 2001DK-00001433. 11-OCF-2001; 2001US-0328896P. 01-OCF-2002; 2002WO-DK000651.

(BIOL-) BIOLMAGE AS

Terry BR,

Human amino acid sequence SEQ ID NO: 6.

(first entry)

08-JUL-2003

ABR40352;

ABR40352 standard; protein; 363

Thastrup O, Almholt DC;

Bjorn SP,

Scudder KM,

2001-611727/70.

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Determining if a compound is a dislocator of PDE4 for identifying compounds for treating CNS and inflammatory disease comprises identifying compounds which remove PDE4 spots.
                                                                                                                                                                                                                                                                                                 Example 1; Page 162-167; 160pp; English.
                                                            17-APR-2000; 2000DK-0000651.
29-MAY-2000; 2000DK-00000849.
                               11-APR-2001; 2001WO-DK000264
                                                                                                           (BIOI-) BIOIMAGE AS
                                                                                                                                                                                                       N-PSDB; AA166853
                                                                                                                                                           Praestegaard M;
   25-OCT-2001.
                                                                                                                                         Terry BR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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                                                                                                                                                                                The invention relates to determining, if a compound, is a dislocator of PDE4. The method comprises testing if the compound removes PDE4 spots, which may optionally be induced by a Roliptam-like reference compound, and testing if it inhibits the catalytic activity of the PDE4, where the compound is a dislocator of PDE4, if it removes PDE spots and if it does not inhibit the catalytic activity of PDE4. The method is useful for identifying compounds useful for the treatment of diseases of the central nervous system such as depression and for the treatment of inflammatory disease such as joint inflammation, Crohn's disease, inflammatory bowel compounds as joint inflammation, Crohn's disease, inflammatory bowel compounds as the chronic bronchitis, pulmonary emphysema, endotoxic shock, toxic shock syndrome, systemic lupus erthematosis, psoriasis, bone resorption diseases, reperfusion injury, cancer and HIV the use of a reagent that can mimic or reverse the effect of the compound with affinity for the catalytic site on intracellular distribution of the PDE for the preparation of a medicament. The present sequence represents the amino acid sequence of a HSPDE4A1-E22G fusion
                                                                                        Determining if a compound is a dislocator of PDE4 for identifying compounds for treating CNS and inflammatory disease comprises identifying compounds which remove PDE4 spots.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       655 MVSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVTVLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ruba; central nervous system; antiinflammatory; cytostatic; nootropic; autoimmune; ischemic; osteopathic; GFP; green fluorescent protein; fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 99.7%; Score 1269; DB 4; Length 893; Best Local Similarity 99.6%; Pred. No. 6.9e-122; Matches 238; Conservative 0; Mismatches 1; Indels
Bjorn SP, Thastrup O, Almholt DC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of HSPDE4A4-E222G fusion protein.
                                                                                                                                                       Example 1; Page 156-160; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG65782 standard; protein; 1132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JAN-2002 (first entry)
Scudder KM,
                                             2001-611727/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aequorea victoria.
                                                            N-PSDB; AAI66852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 893 AA;
                Praestegaard M;
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BR,
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The invention relates to determining, if a compound, is a dislocator of PDE4. The method comprises testing if the compound removes PDE4 spots, which may optionally be induced by a Rolipram-like reference compound, and testing if it inhibits the catalytic activity of the PDE4, where the compound is a dislocator of PDE4, if it removes PDE spots and if it does not inhibit the catalytic activity of PDE4. The method is useful for compound useful for the treatment of diseases of the central nervous system such as depression and for the treatment of inflammatory disease such as joint inflammation, Crohn's disease, inflammatory bowel disease, respiratory diseases, chronic obstructive pulmonary disease (COPD), including asthma, chronic bronchitis, pulmonary emphysema, endotoxic shock, toxic shock syndicame, systemic lupus erthemators, psoriasis, bone resorption diseases, reperfusion injury, cancer and HIV infection. The use of a reagent that can mimic or reverse the effect of the compound with affinity for the catalytic site on intracellular distribution of the PDE for the preparation of a medicament. The present sequence represents the amino acid sequence of a HSPDE4A4-E222G fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             954 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 1013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1074 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 1132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.7%; Score 1269; DB 4; Length 1132; 99.6%; Pred. No. 9.9e-122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enhanced F64L jellyfish green fluorescent protein mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1132 AA;
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Matches
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Novel fluorescent protein in in vitro assay for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution, has a green fluorescent protein with F64L and E222G
                                                                          /note= "Wild type Phe substituted with Leu; This corresponds to position 64 in the wild type protein"
Jellyfish; green fluorescent protein; GFP; protein redistribution; cellular function; genetic reporter; mutant; Stoke's shift; mutein.
                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                           Example 1; Page 35; 41pp; English.
                                                                                                                                                                                                                               Thastrup
                                                                                                                                                                     20-JUN-2000; 2000US-021268IP.
10-MAY-2001; 2001DK-00000739.
10-MAY-2001; 2001US-0290170P.
                                                                                                                                           18-JUN-2001; 2001WO-EP006848
                                                                                                                                                               2000DK-00000953
                                                                                                                                                                                                                               Pagliaro L,
                                                                                                                                                                                                            (BIOI -) BIOIMAGE AS
                                                                                                                                                                                                                                                 WPI; 2002-098224/13
                            Aequorea victoria.
                                                                                                                                                                                                                                                           N-PSDB; AAD28162
                                                                 Misc-difference
                                                                                                      WO200198338-A2
                                                                                                                                                              19-JUN-2000;
                                                                                                                         27-DEC-2001
                                                                                                                                                                                                                               Bjorn SP,
                                      Synthetic.
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thorescent protein (GFP) or its analogue. The GFP containing mutations at F64L and E222G has a bigger compared to other GFP's making it very suitable for high throughput screening due to better resolution. The fluorescent protein is useful in invitro assays for measuring protein kinase activity or dephosphorylation activity, or for measuring protein rediscribution. The fluorescent protein is useful in studying cellular functions in living cells; as protein tags in transgenic animals, living and fixed cells; organelle tags, secretion marker and genetic reporter. The fluorescent protein is also useful as a cell or organelle integrity marker, a marker for changes in cell morphology, as transfection marker, and as a marker to be used in combination with fluorescence activated cell sorting (FACS). The novel proteins can also be used as reporters to monitor live or dead biomass of organisms, such as fungi. The fluorescent protein is also useful as markers in transcriptional and translational fusions for performing transposons encoding the fluorescent protein are useful for screening promoters and for tagging plasmids and chromosomes. The fluorescent protein are fluorescent protein engineered into the genome of a phage is useful for designing diagnostic tool. The present sequence is enhanced F64L jellyfish green fluorescent protein (GFP) mutant The invention relates to a fluorescent protein derived from green

Sequence 239 AA;

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61 LVITLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                         61 LVTVLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                   1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                   1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                             Gaps
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0
Length 239;
                                           Indels
                                               5,
csh 99.1%; Score 1261; DB 5; 11 Similarity 99.2%; Pred. No. 6.5e-122; 237; Conservative 0; Mismatches 2;
                    Best Local Similarity
Matches 237; Conserv
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121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180

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concerning the compounds which affect particular biological functions. The methods of the invention utilise fluorescent biodetector functions. The methods of the invention utilise fluorescent biodetector components which, when acted on by a compound of interest, cause an alteration in the cellular distribution of at least the fluorescent conjecty. In one embodiment, the biosensors comprise heat shock proteins (HSPs) fused to a fluorescent protein (e.g., jellyfish green fluorescent protein (GPP), or derivatives thereof). Such biosensors are located in the cytoplasm, but on stress activation translocate to the nucleus. In another embodiment biodetector proteins can be used to detect protease cetivity. Such protease biodetector fusion proteins one or more fluorescent proteins; a recognition signal which is cleaved by the protease, and at least one cellular localisation signal. The latter two components may be components of a single protein which is acted upon by the protease, or may be from heterologous sources. Due to the consonents may be from heterologous sources. Due to the consonents may be acted on by the protease of interest, the fluorescent protein signal attached to the fluorescent protein contains at localisation signal attached to the fluorescent protein enables the fluorescent protein to be directed to a different cellular compartment after cleavage of the protease recognition sequence. The change in distribution of the fluorescent protein can be detected using imaging methods with a high degree of spatial resolution. The methods and imaging methods and 121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNYYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180 Biodetector protein; fusion protein; recognition site; cellular targetting sequence; cellular localisation; fluorescent protein; protease activity detection; toxin detection; cellular stress detection; drug discovery; cell based screening. 181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239 181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 239 The invention relates to systems, methods and reagents for cell-based Automated cell-based characterization of toxin by contacting cells containing luminescent reporter molecules with test substance and Enhanced green fluorescent protein (EGFP), SEQ ID NO:46. Example 11; Fig 29A; 336pp; English. Ä AAB22882 standard; protein; 239 99US-0122152P. 99US-0123399P. 99US-00352171. 25-FEB-2000; 2000WO-US004794. 10-JAN-2001 (first entry) (CEPT-) CEPTOWICS INC analyzing optically. WPI; 2000-594086/56. Aequorea victoria. N-PSDB; AAA93373. WO200050872-A2. Giuliano KA, 26-FEB-1999; 08-MAR-1999; 12-JUL-1999; 31-AUG-2000 Synthetic. AAB22882; 셤 ò

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cellular activities and to screen compounds which modulate these example, may be used for the screening of compounds which modulate apoptosis, while blosensors containing a recognition site for caspase, for apoptosis, while blosensors containing other protease recognition sites may be used for the detection of proteolytic toxins (such as anthrax lethal factor). The method provides improved target validation and candidate compound optimisation by combining many cell screening formats with fluorescence-based molecular reagents and computer-based feature and speed of data analysis and automation, resulting in increased quantity sextraction, data collection and faster evaluation of drug candidates. Sequences AAB22881-B22885 represent fluorescent proteins which may used as components of biosensor fusion proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                  61 LVTVLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biosensors of the invention can be used to investigate a wide range of
                                                                                                                                                                                                                                                                                                                                1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                  Length 239;
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                                                                                                                                                                                                                                                              98.8%; Score 1258; DB 3;
98.7%; Pred. No. 1.3e-121;
iive 1; Mismatches 2;
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98US-00172063
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UNIV OREGON STATE.
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Matches 236; Conservative
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                                                                                                                                                                                                                                 Sequence 239 AA;
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13-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein based on the Aguarea green fluorescent protein (GFP). The emission intensity changes as pH varies between 5 and 10 of the present protein are novel. The functional engineered fluorescent proteins show reversible changes in fluorescence over physiological pH ranges. They can be used for determining the pH of samples and cells. The polynucleotides can also be used to produce transgenic animals. The fluorescent protein pH sensors can be delivered to cells in the form of polynucleotides encoding the protein sensor fused to a targeting signal. The targeting signal directs the expression of the protein sensors to restricted cell locations. This makes it possible to measure the pH of a precisely defined cellular region or organelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LVTVLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                     New functional engineered green fluorescent proteins, used for measuring the pH in biological samples and cells.
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                                                                                                                                              sequence represents a functional engineered fluorescent
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                                                                                                                                                                                                                                                                                                                                                                       Length 239;
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                                                                                                                                                                                                                                                                                                                                                                       98.8%; Score 1258; DB 3; 98.7%; Pred. No. 1.3e-121;
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                                                                                                                  Disclosure; Page 9; 89pp; English
Wachter RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY79584 standard; peptide; 239
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Matches 236; Conservative
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Tsien RY, Llopis J,
                           WPI; 2000-116540/10.
N-PSDB; AAZ45642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGFP signal domain.
                                                                                                                                                                                                                                                                                                                                           Sequence 239 AA;
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us-09-887-784-64v.rag

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The present sequence is a fluorescnet protein used in the construction of a fluorescent protein indicator. The indicator comprises a sensor polypeptide that is responsive to a chemical, biological electrical or physiological parameter, and a fluorescence protein functional group. The sensor polypeptide is operatively inserted into the fluorescent moiety. The fluorescent indicator is useful for detecting the presence of a response inducing member in a sample. The method involves contacting the sample with the indicator and detecting a change in fluorescence, in which a change is indicative of the effect of the parameter on the sensor polypeptide. The novel fluorescent proteins are advantageous due to their reduced size as compared to the FRET (fluorescence resonance energy transfer)-based sensors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel fluorescent proteins comprising a sensor protein inserted into them, useful for measuring the response of a sensor biological, chemical, electrical or physiological parameter in vivo or in vitro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A. victoria green fluorescent protein (GFP) and linker sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 98.8%; Score 1258; DB 4; Length 239; Best Local Similarity 98.7%; Pred. No. 1.3e-121; Matches 236; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 24; 94pp; English.
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                                                                         99US-00316919.
99US-00316920.
17-MAY-2000; 2000WO-US013684
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                                                                                                                                                                                          (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                       rsien RY, Baird GA;
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                                                                         21-MAY-1999;
21-MAY-1999;
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Comprising at least 1 detectable polypeptic signal such as the present comprising at least 1 detectable polypeptic signal such as the present sequence; a second domain (see AAY79588-622) comprising at least 1.

CC comprising at least 1 reactant target sequence. A recombinant nucleic comprising at least 1 reactant target sequence. A recombinant nucleic acid (see AAA27627-43) encoding the PB, an expression vector, and a genetically engineered host cell are also claimed. A claimed method for identifying compounds that modify protease activity in a cell involves contacting a host cell that possesses the recombinant PB with a test compound, and determining the PB distribution in the host cell, where compounds that modify protease activity in a host cell include the protease activity by the test compound. Claimed kits for identifying compounds that modify protease activity in a host cell include the host cell. The PB is useful in high content screens to detect in vivo activation of enzymatic activity, and to identify specific activity based on cleavage of a known recognition motif
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                                                                                                                                              Recombinant nucleic acid encoding a protease biosensor useful for fluorescence based cell and molecular biochemical assays for drug discovery comprising three operably linked nucleic acid sequences.
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calmodulin-binding domain; mutant; mutein.
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                                                                                                                                                                                                                                                                                                            Claim 14; Fig 29A; 218pp; English
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                                                                         N-PSDB; AAA27573
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Query Match

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Synthetic. Aeguorea victoria.

WO200071565-A2

AAB50834;

RESULT 9 AAB50804 30-NOV-2000

WO200168706-A1

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The specification describes a method for assessing the growth rate and death rate of a micro-organism within a predetermined time period in a desired environment. The method comprises introducing at least two method comprises introducing at least two micro-organisms, incubating luminescent and/or fluorescent products into the micro-organisms, incubating the micro-organism within the desired environment, and detecting luminescence and/or fluorescence after a predetermined time period. Use of two different markers within a micro-organism enables the differentiation between growth and death rates. The method is used to assess the growth rate and death rate of a microorganism within a predetermined time period in a desired environment. The present sequence represents a green fluorescent protein (GFP), and is encoded by a plasmid which encodes luminescent and fluorescent proteins, and is used in the method of the invention
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                                                                                                                                                                                                                                            Assessing growth and death rates of a micro-organism in a desired environment, by introducing 2 reporter genes encoding luminescent and fluorescent products and detecting luminescent fluorescence.
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Pred. No. 1.3e-121;
1; Mismatches 2; Indels

    A. victoria green fluorescent protein (EGFP).

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                   99FI-00001296
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Best Local Similarity 98.7%;
Matches 236; Conservative
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N-PSDB; AAC86954.
                                                                                                                                Lilius E, Virta M;
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                                                              (LILI/) LILIUS E. (VIRT/) VIRTA M.
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                   07-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention provides melanin concentrating hormone (MCH) receptor (MCHR) chimeric and fusion proteins. The MCHR chimeric proteins comprise MCHR polypeptide regions from different species. The MCHR fusion protein comprise MCHR polypeptide region and a fluorescent polypeptide region joined directly, or via a linker, to the carboxy side of the MCHR polypeptide region proteins can be expressed by standard recombinant methodology. MCH action promotes feeding (orexigenic) and up regulation of MCH activity stimulates food intake. The present sequence represents a A. victoria green fluorescent protein (GFP) and a linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LVTVLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                                                                                                                                                                                              Fusion proteins comprising melanin concentrating hormone receptor peptides and fluorescent proteins, useful for identifying appetite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Growth rate, death rate, reporter gene, luminescent protein; fluorescent product; luciferase, green fluorescent protein; GFP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence of a green fluorescent protein (GFP).
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                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 14; 71pp; English
                                          14-MAR-2001; 2001WO-US008071
                                                                                        15-MAR-2000; 2000US-0189698P
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                                                                                                                                   (MERI ) MERCK & CO INC
                                                                                                                                                                                                                              WPI; 2001-565791/63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                                     N-PSDB; AAH47304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-APR-2001
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20-SEP-2001
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Aequorea victoria.
Synthetic.
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                    01-DEC-1999;
         29-OCT-1999;
 17-SEP-1999;
                                                                       Giuliano K,
                                                                                                                                                       identifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAY-2002
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                                                                                                                                                                                                                                                                                                                                               VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                                                                                                                                                                                                                                       VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                The invention relates to a gene encoding proteins having cyan-green fluorescence characteristic and having a function of showing stable fluorescence characteristic in acid region. A method for the preparation of a cyan-green fluorescent protein is provided which involves a transforment transformed by a recombinant vector comprising the gene, where the transforment is cultured and the protein is collected from the culture. The present sequence represents the A. victoria green fluorescent protein (EGFP)
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                                                                                                                                                                                                                                                                                                            1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                         1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection; classification; identification; toxin detection; protease; ADP-ribosylating toxin; cytotoxic phospholipase; exfoliative toxin; toxic threat agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK
                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                   Length 239;
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                  Score 1258; DB 5;
Pred. No. 1.3e-121;
                                                                                            A gene encoding cyan-green fluorescent protein.
                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protease biosensor signal sequence #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG94444 standard; protein; 239 AA
                                                                                                             Example; Page 14; 20pp; Japanese.
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98US-0031271.
99US-0123152P.
99US-0133399P.
99US-00352171.
04-AUG-2000; 2000JP-00237165
                    04-AUG-2000; 2000JP-00237165
                                                                                                                                                                                                                                                 98.8%;
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                                        (RIKA ) RIKAGAKU KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                Query Match
Best Local Similarity 98.7
Matches 236; Conservative
                                                            2002-299190/34.
                                                                      N-PSDB; ABL40628
                                                                                                                                                                                                                               Sequence 239 AA;
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26-FEB-1999;
08-MAR-1999;
12-JUL-1999;
31-AUG-1999;
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The invention describes methods of automated detection, classification and identification comprising treating cells containing luminescent reporter molecules (I) in array of locations with a test substance, where (I) are detectors, classifiers or identifiers, imaging cells in each location to obtain luminescent signals and converting optical information into digital data to interpret presence of toxins in the test substance. The method are useful for detection of toxins chosen from proteases, ADP-ribosylating toxins, cytotoxic phospholipases, and exfoliative toxins. Three classes of cell-based luminescent reporter molecules such as detectors, classifiers and identifiers are described and serve as reporters of toxic threat agents. The first two levels of characterisation ensure a rapid readout of toxin class without several complex mixtures of known toxins. This is the amino acid sequence of a protease biosensor related signal sequence used in the cell-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LVTVLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Automated cell-based toxin detection, classification, and/or identification by treating cells involves use of three classes of luminescent reporter molecules such as detectors, classifiers or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1258; DB 5;
Pred. No. 1.3e-121;
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99US-00398965.
99US-00430656.
99US-0168408P.
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                                                                                                                                                                                                                                                                            Kapur R;
                                                                                                                                                                                                                                                                                                                                                          2002-634730/68.
                                                                                                                                                      (GIUL/) GIULIANO K.
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Best Local Similarity
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or more primers that have a nucleotide sequence containing at least one mutation and a phosphorylated 5'-terminus are annealed to a template DNA and then subjected to an elongation reaction using a thermostable high-fidelity DNA polymerase, after which the phosphorylated 5'-terminus and fidelity DNA polymerase, after which the phosphorylated 5'-terminus and fidelity DNA polymerase, after which the phosphorylated 5'-terminus and the elongated terminus are ligated by means of a thermostable DNA ligase to synthesise a circular DNA containing the primers, a digestion in which the step of DNA synthesis is repeated several times to amplify the DNA containing the primers and then, at least DNAs other than the amplified circular DNA synthesis in which, with the several fragments obtained in the step of digestion as megaprimers, the megaprimers are annealed to the circular DNA synthesised above, followed by an elongation reaction performed using the thermostable high-fidelity DNA polymerase. The method is useful for mutagenesis, particularly for introducing certain mutations at certain sites of the nucleotide sequence. The present method is simple, speedy, economical and widely applicable. The present method is simple, speedy, economical and widely applicable. The present sequence is metagenesis in an exemplification of the invention. The EGFP is derived by altering the green fluorescent protein (GFP) sequence of Aequorea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method for mutagenesis that comprises synthesising a mutated strand and a complementary strand by use of megaprimers. The method basically comprises a DNA synthesis in which one
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              certain or random mutations comprises synthesizing a use of megaprimers.
                                           MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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                                                                                                                          Phe64 is replaced by Leu"
                                                                                                                                                                   /note= "GFP Ser65 is replaced by Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Method for mutagenesis, e.g. for introducing at certain sites of the nucleotide sequence, mutated strand and a complementary strand by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 13-14; 31pp; English.
                     Location/Qualifiers
                                                                                                                                                                                                                                                                                           03-AUG-2001; 2001EP-00306650
                                                                                                                                                                                                                                                                                                                                     04-AUG-2000; 2000JP-00237166
                                                                                                                          "GFP
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                                                                                                                            'note=
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              (RIKE ) RIKEN KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAD27910.
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                        Key
Misc-difference
                                                                                                      Misc-difference
                                                                                                                                             Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                 181 DHYQQNTPIGDGPVILPDNHYLSTQSALSKDPNEKRDHWVLLEFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                          Phosphorylation indicator, fluorescent protein; detection; phosphatase; kinase; enhanced green fluorescent protein; BGFP.
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                                                                                                                                                                                                            Aequorea victoria enhanced green fluorescent protein (EGFP).
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                                                                                                              AAE34958 standard; protein; 239
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les 236; Conserv
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Search completed: June 21, 2004, 15:54:09 Job time: 47.1111 secs

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-922-2

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US-09-172-063-21

US-09-172-063-21

US-09-085-305-6

US-09-417-197-129

US-09-417-197-129

US-09-417-197-155

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Maximum Match 100%
Listing first 45 summaries
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; Sequence 3, Application US/09172063
; Patent No. 615016
; GENERAL INFORMATION:
    APPLICANT: History, Actuali
    APPLICANT: Miyawaki, Actuali
    APPLICANT: Miyawaki, Actuali
    APPLICANT: Miyawaki, Actuali
    APPLICANT: More No. 3. James
    TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
    TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
    TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
    FILE REFERENCE: 07257/071001
    CURRENT APPLICATION NUMBER: US/09/172,063
    CURRENT PILING DATE: 1998-10-13
    EARLIER APPLICATION NUMBER: 09/094,359
; BARLIER FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 38
; SOFT NO 3
; TENNOT: 0.0
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Pred. No. 1.3e-126;
1; Mismatches 2;
                           US-08-818-222-4
US-09-417-197-75
US-09-417-197-71
US-09-417-197-119
US-09-513-783A-176
US-09-417-197-141
US-09-417-197-141
US-09-417-197-77
US-09-513-783A-178
US-09-417-197-61
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Best Local Similarity 98.7%;
Matches 236; Conservative
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ORGANISM: Aequorea victoria
; OTHER INFORMATION: EGFP US-09-172-063-3
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121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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Patent No. 6608189
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ORGANISM: Aequorea victoria
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NAME/KEY: VARIANT
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US-09-602-641-3
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Best Local Similarity 98.7%;
Matches 236; Conservative
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Pred. No. 1.3e-126;
1; Mismatches 2; Indels
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                               Sequence 46, Application US/09513783A

Patent No. 6416959

GENBRAL INFORMATION:
APPLICANT: Kapur, Ravi
TITLE OF INVENTION: A System for Cell Based Screening
FILE REFERENCE: 97-022-L1
CURRENT APPLICATION NUMBER: US/09/513,783A
CORRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
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Fatent No. 6469154
GENERAL INFORMATION STATES
APPLICANT: 181en, Roger Y.
TITLE OF INVENTION FLUORESCENT PROTEIN INDICATORS
FILE REPERENCE: 07257/073001
CURRENT APPLICATION NUMBER: US/09/316,919
CURRENT FILING DATE: 1999-05-21
NUMBER OF ESC ID NOS: 63
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1.3e-126;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 98.7%;
Matches 236; Conservative
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Best Local Similarity 98.7%;
Matches 236; Conservative
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US-09-316-919-4
RESULT 2
US-09-513-783A-46
                                                                                                                                                                                                                                                 SEQ ID NO 46
LENGTH: 239
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US-09-316-919-4
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LENGTH: 239
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121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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APPLICANT: Taien, Roger Y.

APPLICANT: Myawati, Ateushi
APPLICANT: Machter, Juan
APPLICANT: Wachter, Rebekka M.

APPLICANT: Wachter, Rebekka M.

APPLICANT: Wachter, Bebekka M.

TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR

TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
CURRENT APPLICATION NUMBER: 02/09/602,641

CURRENT FILING DATE: 2000-06-22

PRIOR PAPLICATION NUMBER: 09/172,063

PRIOR FILING DATE: 1999-10-13

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 239
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Pred. No. 1.3e-126;
1; Mismatches 2;
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Patent No. 6673610
GENERAL INFORMATION:
APPLICANT: Miyawaki, Atsushi
APPLICANT: Sawano, Asako
TITLE OF INVENTON: METHOD FOR MUTAGENESIS
FILE REFERENCE: 11283-012001
CURRENT APPLICATION NUMBER: US/09/920,922
CURRENT FILING DATE: 2001-08-02
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 9
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US-09-364-946-1
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Batent No. 6130313

GENERAL INFORMATION:
APPLICANT: Kain, Steve
APPLICANT: Li, Xianqiang
TITLE OF INVENTION: Rapidly Degrading GFP-Fusion Proteins and Methods
TITLE OF INVENTION: Rapidly Degrading GFP-Fusion Proteins and Methods
FILE REFERENCE: D6100
CURRENT FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: US 60/060,855
EARLIER PILING DATE: 1997-10-02
NUMBER: OF SEQ ID NOS: 3
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CHER INFORMATION: Sequence of the EGFP-MODC422-461 fusion protein.
Patent No. 6130313
US-09-062-102-1
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                                                                                                                                      Query Match 98.8%; Score 1258; DB 4; Length 239; Best Local Similarity 98.7%; Pred. No. 1.3e-126; Matches 236; Conservative 1; Mismatches 2; Indels
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Pred. No. 1.7e-126;
1; Mismatches 2;
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2
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ORGANISM: artificial sequence
                                                     TYPE: PRT
ORGANISM: Aequorea victoria
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Best Local Similarity
                                       LENGTH: 239
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LENGTH: 281
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Sequence 1, Application US/09364946

Patent No. 6306600

GENERAL INFORMATION:
APPLICANT: Kain, Steve
APPLICANT: Kain, Steve
TITLE OF INVENTION: Rapidly Degrading GFP-Fusion Proteins and Methods
TITLE OF INVENTION: of Use
FILE REFERENCE: D6100CIP/D2
CURRENT APPLICATION NUMBER: US/09/364,946
CURRENT PELLING DATE: 1999-07-30
EARLIER APPLICATION NUMBER: US 09/191,233
EARLIER FILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 14
: SEQ ID NO 1

LENGTH: 281
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; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: GFP-DEVD-Annexin II construct

US-09-313-783A-2
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(7)
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Pred. No. 1.7e-126;
1; Mismatches 2;
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Best Local Similarity 98.7%; Pred. No. 1.8e-126;
Matches 236; Conservative 1; Mismatches 2;
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APPLICANT: Giuliano, Kenneth A.
APPLICANT: Giuliano, Kenneth A.
TITLE OF INVENTION: A System for Cell Based Scr.
FILE REFERENCE: 97-022-L1
CURRENT APPLICATION NUMBER: US/09/513,783A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 294
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ORGANISM: artificial sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

Best Local Similarity 98.7%;
Matches 236; Conservative
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US-09-364-946-1
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                                                                                 61 LVITLIYGVQCFSRXPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                  121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVQLA 180
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                                                 LVTVLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT 60
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Patent No. 6150176

GENERAL INFORMATION:

APPLICANT: Taien, Roger Y.

APPLICANT: Miyawaki, Atsushi

APPLICANT: Miyawaki, Atsushi

APPLICANT: Miyawaki, Juan

APPLICANT: Miyawaki, Juan

APPLICANT: Menter, Rebekka M.

APPLICANT: Remington, S. James

TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR

TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR

TITLE OF INVENTION: PASSORING THE PH OF A BIOLOGICAL SAMPLE

FILE REFERENCE: 07257/071001

CURRENT PAPLICATION NUMBER: US/09/172,063

CURRENT FILING DATE: 1998-10-13

BARLIER APPLICATION NUMBER: 09/094,359

BARLIER FILING DATE: 1998-06-09

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.8%; Score 1258; DB 3; Length 323; 98.7%; Pred. No. 2.1e-126; tive 1; Mismatches 2; Indels
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OTHER INFORMATION: GT-EGFP
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Matches 236, Conservative
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Sequence 21, Application US/09602641; Patent Nc. 6608189; GENERAL INFORMATION:

US-09-602-641-21

APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
APPLICANT: Llopis, Juan

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61 LVTVLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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Sequence 6, Application US/09085305;
Patent No. 6191269
GENERAL INFORMATION:
APPLICANT: Pollock, Allan
TITLE OF INVENTION: Selective Induction of Apoptosis in
TITLE OF INVENTION: Malignant Cancer Cells by Delivery of N-Termi
TITLE OF INVENTION: Interleukin-1-Alpha Pro-Piece Polypeptide
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
COTTY: Palo Alto
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APPLICANT: Wachter, Rebekka M.
APPLICANT: Remington, S. James
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
CURRENT FILING DATE: 1000-06-22
PRIOR APPLICATION NUMBER: 09/172,063
PRIOR PILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 323
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Pred. No. 2.1e-126;
1; Mismatches 2; Indels
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APPLICATION NUMBER: US/09/085,305
FILING DATE: 29-MAY-1998
CLASSIFICATION:
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Best Local Similarity 98.7%;
Matches 236; Conservative
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Aequorea victoria
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: VARIANT
CCATION: (0)...(0)
OTHER INFORMATION: GT-EGFP
US-09-602-641-21
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APPLICATION NUMBER:
FILING DATE:
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USA
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COUNTRY: US
ZIP: 94301
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Sequence 127, Application US/09417197
Sequence 127, Application US/09417197
Sequence 127, Application US/09417197
GENERAL INFORMATION:
APPLICANT: Ole THASTRUP, et al.
TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An IT TITLE OF INVENTION: On A Cellular Response
FILE REFERENCE: 3759-0110P
CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patentin version 3.0
SEQ ID NO: 27
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                       181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
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Sequence 48, Application US/09800170

Patent No. 6481667

GENERAL INFORMATION:

TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES

TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES

FILE REPRESENT

CURRENT APPLICATION NUMBER: US/09/800,170

CURRENT FILING DATE: 2001-08-28

PRIOR PILING DATE: 2000-03-06

NUMBER OF SEQ ID NOS: 90

SEQ ID NO 48

LENGTH: 434

TUPE: PRIOR PILING DATE: 2000-03-06

SEQ ID NO 48

LENGTH: 434

TUPE: PRIOR PILING DATE: 2000-03-06

SEQ ID NO 48

LENGTH: 434

TUPE: PRIOR PILING DATE: 2000-03-06

SEQ US-09-800-170-48
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98.7%; Pred. No. 3.4e-126;
tive 1; Mismatches 2;
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Pred. No. 3.3e-126;
1; Mismatches 2;
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Best Local Similarity 98.7%;
Matches 236; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity
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Patent No. 6518021
GENERAL INFORMATION:
APPLICANT: Ole THASTRUP, et al.
TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An TITLE OF INVENTION: On A Cellular Response
FILE REFERENCE: 3759-0110P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT 185
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 364;
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                                                                                                                                                                                                                                                                                                                                                                                                      Score 1258; DB 3;
Pred. No. 2.5e-126;
1; Mismatches 2;
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CURRENT FILING DATE: 1959-10-07
NUMBER P FILING 143
SOFTWARE: PATENTIN VERBION 3.0
                                                                       6510/102US1
                     NAME: Francis, Carol L
REGISTRATION NUMBER: 36,513
REFERENCE/DOCKET NUMBER: 651
TELECOWMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
TELEFAX: 650-327-3231
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

Best Local Similarity 98.7%;
Matches 236; Conservative
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ORGANISM: Artificial Sequence
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
US-09-085-305-6
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US-09-417-197-129
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LENGTH: 379
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                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: GFP-HSP27US-09-513-783A-170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 98.7%; Pred. No. 3.5e-126;
Matches 236; Conservative 1; Mismatches 2; Indels
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US-09-513-783A-170
; Sequence 170, Application US/09513783A
; Patent Nc. 6416559
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
APPLICANT: ARQUIX, RAVI
; TITLE OF INVENTION: A System for Cell Based Screening; TITLE OF INVENTION: A System for Cell Based Screening; CURRENT APPLICATION NUMBER: 115 CURRENT FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 180
; SEC ID NO: 170
; SEQ ID NO: 170
; LENGTH: 459
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
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Search completed: June 21, 2004, 16:04:01 Job time : 12.7778 secs

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US-10-100-957A-46
US-10-10177-390-2
US-10-318-411-3
US-10-318-640-3
US-10-318-861-35
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Sequence 13,

Sequence Sequence Sequence Sequence

ALIGNMENTS

Sequence

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Sequence 4, Appli
Sequence 6, Appli
Sequence 32, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 3, Appli
Sequence 3, Appli
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                   Compugen Ltd
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1 US-10-257-909A-30

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US-10-257-909A-32

US-10-257-909A-32

US-10-29-987-784-2

US-10-29-953-2

US-09-999-745-4
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comput
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                                                                                                                                                                                                                                                                                                                 1163542 seqs, 282313646 residues
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                                                                       protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Pred. No. 7.3e-124;
0; Mismatches 1;
                                                                   APPLICANT: BJORN, Sara et al
TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS
FLEE REFERENCE: 3759-0115P
CURRENT APPLICATION NUMBER: US/09/887,784
CURRENT FILLING DATE: 2001-06-19
WIMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.0
                Sequence 4, Application US/09887784 Patent No. US20020177189A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  ch 18 Similarity 99.6%; 238; Conservative
                                                                                                                                                                                                                                                ORGANISM: Aequoria Victoria
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TYPE: PRT
US-09-887-784-4
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Best Local S:
Matches 238
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US-09-866-538-4 US-09-797-496B-2 US-09-794-308-4 US-09-865-291-4 US-10-457-982-3 US-10-121-258-13

12222

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Sequence 30, Application US/10257909A
Publication No. US20030187056A1
Publication No. US20030187056A1
Publication No. US20030187056A1
Publication No. US20030187056A1
APPLICANT: Bernard R. TERRY et al.
TITLE OF INVENTION: Live cell procedures to identify compounds modulating intracellulating ENTRENCE: 3759-0125P
CURRENT APPLICATION NUMBER: US/10/257,909A
CURRENT FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 30
LENGTH: 893
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Sequence 32, Application US/10257909A

Sequence 32, Application No. US20030187056A1

Publication No. US20030187056A1

GENERAL INFORMATION: Live cell procedures to identify compounds modulating intracellula

TITLE OF INVENTION: Live cell procedures to phosphodiesterase (PDE) enzymes

TITLE OF INVENTION: distribution of phosphodiesterase (PDE) enzymes

TITLE OF INVENTION: UNMBER: US/10/257,909A

CURRENT EPPLICATION NUMBER: 202-10-17

NUMBER OF SEQ ID NOS: 36

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                             61 LVTVLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                          61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                   121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                                                                             121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNYYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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US-10-257-909A-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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Sequence 5, Application US/2030143634A1
Publication No. US20030143634A1
SEQUENCE INFORMATION:
APPLICANT: BIOIMAGE A/S
TITLE OF INVENTION: INTACT LIVING CELLS, AND TO EXTRACT QUANTITATIVE INFORMA-TION RITLE OF INVENTION: INTERACTIONS BY FLUORESCENCE REDISTRIBUTION.
TITLE OF INVENTION: INTERACTIONS BY FLUORESCENCE REDISTRIBUTION.
FILE REFIRENCE: 3759-0126P
CURRENT APPLICATION NUMBER: US/10/270,223
CURRENT APPLICATION NUMBER: US/10/270,223
CURRENT PILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
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Pred. No. 7.3e-124;
0; Mismatches 1;
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Pred. No. 1.3e-123;
0; Mismatches 1;
                                                                                                                       APPLICANT: BJOCAN, SAKA F.
APPLICANT: BAGLIARO, LEN
APPLICANT: THASTRUP, OLE
TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS
FILE REFERENCE: PLOO95
CURRENT APPLICATION NUMBER: US/10/296,953
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: PA 2000 00953
PRIOR FILING DATE: 2000-06-19
PRIOR FILING DATE: 2000-06-19
PRIOR FILING DATE: 2001-05-10
PRIOR FILING DATE: 2001-05-10
PRIOR FILING DATE: 2001-05-10
PRIOR FILING DATE: 2001-05-10
PRIOR FILING DATE: 2001-05-10
NUMBER OF SEQ ID NOS: 24
SSOCTWARE: PALCHIN VET: 2.1
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US-10-270-2:33-6
                                         Sequence 4, Application US/10296953
Publication No. US20040072995A1
GENERAL INFORMATION:
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Best Local Similarity 99.6%;
Matches 238; Conservative
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ORGANISM: Aequorea victoria
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                                                                                                                     APPLICANT: BJORN, SARA P.
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Best Local Similarity
                  -10-296-953-4
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US-10-270-233-6
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                                                                                                                                                          Length 1132;
                                                                                               ; OTHER INFORMATION: Fusion between Aequorea victoria and human
US-10-257-909A-32
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Pred. No. 5e-123;
0; Mismatches 2; Indels
                                                                                                                                                                                                  Indels
                                                                                                                                                      Query Match
99.7%; Score 1269; DB 14;
Best Local Similarity 99.6%; Pred. No. 6.8e-123;
Matches 238; Conservative 0; Mismatches 1;
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TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS
FILE REPERBLES: 3759-0115P
CURRENT APPLICATION NUMBER: US/09/887,784
CURRENT FILING DATE: 2001-06-19
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn vergion 3.0
SEQ ID NO 2
LENGTH: 239
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Best Local Similarity 99.2%;
Matches 237; Conservative
                                      TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-887-784-2
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US-10-296-953-2
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SEQ ID NO 32
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; Sequence 2, Application US/10296953; Publication No. US20040072995A1; GENERAL INFORMATION:

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61 LVTVLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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Pred. No. 5e-123;
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1; Mismatches 2;
APPLICANT: PAGLIARO, LEN
APPLICANT: THASTRUP, OLE
TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS
FILE REFERENCE: PLOO95
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Patent No. US2020083488A1
GENERAL INFORMATION:
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: METHOD FOR MUTAGENESIS;
FILE REPERENCE: 11283-01201
CURRENT APPLICATION NUMBER: US/09/920,922
CURRENT PILING DATE: 2001-08-02;
PRIOR PILICATION NUMBER: UP 2000-237166;
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 2
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                                                                                            FILE TREADER. FUNCATION NUMBER: US/10/296,953
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: PA 2000 00953
PRIOR PELING DATE: 2000-06-19
PRIOR PILING DATE: 2000-06-20
PRIOR PILING DATE: 2000-06-20
PRIOR PILING DATE: 2001-05-10
PRIOR PILING DATE: 2001-05-10
PRIOR FILING DATE: 2001-05-10
PRIOR FILING DATE: 2010-05-10
PRIOR FILING DATE: 2010-05-10
PRIOR FILING DATE: 2010-05-10
SEQINABLE: PACENTIN NUMBER: PA 2011 00739
PRIOR FILING DATE: 2010-05-10
SEQINABLE: PACENTIN VET: 2.1
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Best Local Similarity 99.2%;
Matches 237; Conservative
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; ORGANISM: Aequorea victoria
US-10-296-953-2
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Matches 236; Conservative
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VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVQLA 180
                                                                       61 LVTVLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                                                                                                                                                      Sequence 4, Application US/09999745

Patent No. USJO020157120A1

GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: Taien, Roger Y.
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
FILE REFERENCE: REGEN1470-1
CURRENT APPLICATION NUMBER: US/09/999,745
CURRENT PILING DATE: 1999-06-21
PRIOR APPLICATION NUMBER: 09/316,920
PRIOR APPLICATION NUMBER: 09/316,920
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin version 3.0
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; Publication No. US20030032088A1
; GENERAL INPORMATION:
; APPLICANT: REGENS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TSIEN, ROGER
; APPLICANT: Campbell, Robert
; TITLE REPERENCE: REGENISOR 120
; CURRENT APPLICATION NON-OLIGOMERIZING FLUORESCENT PROTEINS
; FILE REPERENCE: REGENISOR 20
; CURRENT PALLICATION NUMBER: US/09/866,538
; CURRENT PALLICATION NUMBER: US/09/866,538
; CURRENT PALLICATION NUMBER: US/09/866,538
; SOFTWARE: Patentin version 3.0
; SEQ ID NOS: 29
; SEQ ID NOS: 29
; SEQ ID NOS: 29
; TYPE: PRT
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Pred. No. 1e-122;
1; Mismatches 2; Indels
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Best Local Similarity 98.7%;
Matches 236; Conservative
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ORGANISM: Aequorea victoria
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US-09-999-745-4
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US-09-866-538-4
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OTHER INFORMATION: Aequorea victoria green fluorescent protein modified as described OTHER INFORMATION: in specification
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Publication No. US20030049597A1
GENERAL INFORMATION:
APPLICANT: Simon, Sanford M.
APPLICANT: Chen, Yu
TITLE OF INVENTION: Chimeric Fluorescent Enzymes and Uses Thereof
FILE REFERENCE: 600-1-267
CURRENT APPLICATION NUMBER: US/09/797,496B
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 2.
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                                                                                                                              Indels
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. 1e-122;
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; Publication No. US20030170911A1
; GENERAL INFORMATION:
; APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
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                                                                           DB
                                                                                                                           1; Mismatches
                                                                           Score 1258;
Pred. No. 16
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                                                                        Query Match
Best Local Similarity 98.7%;
Matches 236; Conservative
; ORGANISM: Aequorea victoria
US-09-866-538-4
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US-09-797-496B-2
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181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
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NAME/KEY: VARIANT
LOCATION: (0)...(0)
OTHER INFORMATION: EGFP
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LENGTH: 239
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US-10-457-982-3
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Publication No. US2003018622941
Publication No. US2003018622941
GENERAL INFORMATION:
APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TING, Alice
APPLICANT: ZHANG, Jince
APPLICANTION NUMBER: US/09/865,291
CURRENT APPLICATION NUMBER: 2001-05-24
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.0
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APPLICANT: TSIEN, ROGER
APPLICANT: ASCHARIAS, David
APPLICANT: BACHARIAS, David
APPLICANT: BARD, GOOFIFEY
TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
FILE REFERENCE: RECEN1530
CURRENT APPLICATION NUBER: US/09/794,308
CURRENT FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 239
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1; Mismatches 2; Indels
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Best Local Similarity 98.7%;
Matches 236; Conservative 1
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US-09-794-308-4
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US-09-865-291-4
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181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWVLLEFVTAAGITLGMDELYK 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MVSKGBELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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; Publication No. US20030059835A1
; Publication No. US20030059835A1
; GENERAL INFORMATION:
APPLICANT: Taien, Roger
; APPLICANT: Campbell, Robert
; TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
; TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME
; FILE REFERENCE: UCO83.1CP2CP1
; CURRENT APPLICATION NUMBER: US/10/121,258
; CURRENT FILING DATE: 2001-02-04-10
; PRIOR APPLICATION NUMBER: 09/794,308
; PRIOR PILING DATE: 2001-02-26
; PRIOR FILING DATE: 2001-05-24
                                                                                                                                                                                                                                                                      USTILUTED / 982-3

; Sequence 3, Application US/10457982
; Publication No. US2003021226541
; GENERAL INPORMATION:
    APPLICANT: Tsien, Roger Y.
    APPLICANT: Miyawaki, Atsushi
    APPLICANT: Hopis, Juan
    APPLICANT: Hopis, Juan
    APPLICANT: Remington, S. James
    TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
    TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
    FILE REFERENCE 7025/7071001
    CURRENT APPLICATION NUMBER: US/10/457,982
    CURRENT APPLICATION NUMBER: US/2060-602
    PRIOR PILING DATE: 2000-06-22
    PRIOR PILING DATE: 2000-06-22
    PRIOR FILING DATE: 1998-10-13
    NUMBER OF SEQ ID NOS: 38
    SOFTWARE FREUESE REUES FREUES FREUES FREUES FREUES FREUES FREUES FREUES FREUES FREUES FREUES FREUES FREUES FREUES FREUES FREUES FREUES FREUES FREUES FREUES FREUES FREUES FREUES FREUES FREUES FRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.8%; Score 1258; DB 12
98.7%; Pred. No. 1e-122;
iive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Aequorea victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 98.7
Matches 236; Conservative
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121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                        1 MVSKGEELFTGVVPILVELDGDVNGHKRSVSGEGGGATYGKLTLKFLCTTGKLPVPWPT
                                                                                                                                                                 Gaps
                                                                                                                                                                 ..
                                                                                                                                     Query Match 98.8%; Score 1258; DB 14; Length 239; Best Local Similarity 98.7%; Pred. No. 1e-122; Matches 236; Conservative 1; Mismatches 2; Indels 0;
                                                        TYPE: PRT ORGANISM: Artificial Sequence FEATURE: OFFIRE (FEATURE: ) OTHER INFORMATION: Enhanced Green Fluorescent Protein (EGFP) US-10-121-258-13
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 239
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Search completed: June 21, 2004, 16:09:27 Job time : 35.7778 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

June 21, 2004, 15:46:00 ; Search time 10.3333 Seconds (without alignments) 2224.817 Million cell updates/sec Run on:

US-09-887-784-64V 1273 1 MVSKGEELFTGVVPILVELD......VLLGFVTAAGITLGMDELYK 239 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* H 0 E 4 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|               |       | ٠              |                       |    | SUMMAKIES |                    |
|---------------|-------|----------------|-----------------------|----|-----------|--------------------|
| Result<br>No. | Score | Query<br>Match | Query<br>Match Length | DB | ID        | Description        |
|               | 1236  | 97.1           | 238                   | -  | J01514    | green-fluorescent  |
| 7             | 105   | 8.5            | 785                   | ~  | H72228    | hypothetical prote |
| m             | 93.5  | 7.3            | 861                   | ~  | H64102    |                    |
| 4             | 91.5  | 7.2            | 887                   | N  | E82590    | w                  |
| S             | 89.5  | 7.0            | 860                   | ~  | AC0582    |                    |
| y             | 88.5  | 7.0            | 655                   | ~  | D83917    | DNA topoisomerase  |
| 7             | 87.5  | 6.9            | 370                   | N  | E70390    | iron-sulfur cofact |
| œ             | 87.5  | 6.9            | 2573                  | ~  | D71614    | hypothetical prote |
| 0             | 86.5  | 6.8            | 788                   | -  | ЭБУГНН    | DNA-directed DNA p |
| 10            | 86.5  | 6.8            | 797                   | N  | JC4078    | protective surface |
| 11            | 86.5  | 6.8            | 808                   | ~  | F64102    | protective surface |
| 12            | 98    | 6.9            | 357                   | N  | G81355    | tRNA (uracil-5-)-m |
| 13            | 98    | 6.8            | 461                   | N  | T06936    | photosystem II chl |
| 14            | 85.5  | 6.7            | 889                   | N  | JC5576    | inter-alpha-trypsi |
| 15            | 85.5  | 6.7            | 941                   | N  | \$29043   | cellulase (EC 3.2. |
| 16            | 82    | 6.7            | 281                   | N  | AD2052    |                    |
| 17            | 85    | 6.7            | 336                   | ~  | C64468    |                    |
| 18            | 85    | 6.7            | 439                   | N  | JH0414    |                    |
| 19            | 85    | 6.7            | 632                   | N  | T06586    | DNA-binding protei |
| 20            | •     | 9.9            | 613                   | N  | A99552    | oligoendopeptidase |
| 21            | 84.5  | 9.9            | 836                   | Н  | מסגתני    | DNA-directed DNA p |
|               | 84    | 9.9            | 285                   | ~  | C97279    | thioredoxin reduct |
| 23            | 84    | 9.9            | 578                   | ч  | I40794    | dihydrolipoamide d |
| 24            | 84    | 9.9            | 682                   | ~  | D90946    | hypothetical prote |
|               | 84    | ٠.             | 682                   | 7  | H85794    |                    |
|               | 84    | 9.9            | 682                   | ~  | A41798    |                    |
| 27            | 83.5  | 9.9            | 425                   | ~  | C97354    | hypothetical prote |
| 28            | 83.5  | 9.9            | 1134                  | N  | A60234    | IgA Fc receptor pr |
| 59            | 83.5  | 9.9            | 1164                  | -1 | FCSOAG    | IgA Fc receptor pr |

|       | leucine tRNA synth |        | DNA-directed DNA p | imidazoleglycerol- | hypothetical prote | proprotein convert | hypothetical prote | alpha-amylase homo | lipoxygenase (EC 1 | S-layer protein pr | water-stress-induc | neuraminidase, pro | synergohymenotropi | ferrichrome-bindin | hypothetical prote |
|-------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| SYECL | H90713             | D85564 | A36028             | E84941             | T27856             | KXRTC1             | T25012             | T39539             | T11852             | JC4930             | S53488             | G95153             | S68225             | H97144             | B86815             |
| н     | ď                  | ~      | н                  | ~                  | 7                  |                    | ď                  | ~                  | ~                  | ~                  | ~                  | N                  | ~                  | 7                  | 7                  |
| 860   | 860                | 860    | 2222               | 353                | 471                | 752                | 764                | 774                | 865                | 874                | 263                | 740                | 310                | 355                | 529                |
| 6.5   | 6.5                | 6.5    | 6.5                | 6.4                | 6.4                | 6.4                | 6.4                | 6.4                | 6.4                | 6.4                | 6.4                | 6.4                | 6.4                | 6.4                | 6.4                |
| 82.5  | 82.5               | 82.5   | 82.5               | 82                 | 82                 | 82                 | 82                 | 82                 | 82                 | 82                 | 81.5               | 81.5               | 81                 | 81                 | 81                 |
| 30    | 31                 | 32     | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

### ALIGNMENTS

| JO1514 1 JOHN STREET PROTEIN [validated]                        | alidated] - hydromedusa (Aeguorea victoria)                                                                                                                                        |
|-----------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| C;Species: Aequorea victoria<br>C;Date: 03-Dec-1999 #sequenc    | e_revision 03-Dec-1999 #text_change 23-Mar-2001                                                                                                                                    |
| C; Accession: JS0692; JQ1514;<br>R; Prasher, D.C.; Eckenrode,   | C;Accession: JS0692; JQ1514; PQ0335; S48693; S51330; S51331<br>K;Prasher, D.C.; Eckenrode, V.K.; Ward, W.W.; Prendergast, F.G.; Cormier, M.J.                                      |
| A;Title: Primary structure o                                    | dene 111, 227-233, 1932<br>A;Title: Primary structure of the Aequorea victoria green-fluorescent protein.                                                                          |
| A;Reference number: JQ1514; 1<br>A:Accession: JS0692            | MUID:92175527; PMID:1347277                                                                                                                                                        |
| A; Molecule type: DNA                                           | , [ K Q Q J                                                                                                                                                                        |
| A; Cross-references: GB: M6265                                  | A;Cross-references: GB:M62654; NID:g155662; PIDN:AAA27722.1; PID:g155663                                                                                                           |
| A;Accession: JQ1514<br>A:Molecule tvpe: mRNA                    |                                                                                                                                                                                    |
| A; Residues: 1-99, 'F', 101-140                                 | A, Residues: 1-99, 'F', 101-140, 'L', 142-218,'V', 220-238 <pra2></pra2>                                                                                                           |
| A;Accession: P00335                                             | 15; NID:GISSOOS; FIDN:AAAS//21.1; FID:GISSOOI                                                                                                                                      |
| A; Molecule type: protein                                       | -151.154-183.185-200 VPRA3.                                                                                                                                                        |
| R; Inouye, S.; Tsuji, F.I.                                      |                                                                                                                                                                                    |
| FEBS Lett. 351, Z11-Z14, 199<br>A:Title: Evidence for redox     | 4 forms of the Aeguorea green fluorescent protein.                                                                                                                                 |
| A; Reference number: S48693;                                    | A;Reference number: S48693; MUID:94364470; PMID:8082767                                                                                                                            |
| A; Accession: S48693                                            |                                                                                                                                                                                    |
| A, Molecule type: mRNA                                          |                                                                                                                                                                                    |
| A;Residues: 1-24,'Q',26-156,                                    | A;Residues: 1-24, (0, 26, 125, 12), 158-171, KY, 173-238 <ino)></ino)>                                                                                                             |
| A; Cross-references: GB: L2334<br>R: Watkins, J.N.; Campbell, A | o; wir:goodsas; riba:AAASacto.i; rib:goodsat<br>.K.                                                                                                                                |
| submitted to the EMBL Data Library, January 1995                | ibrary, January 1995                                                                                                                                                               |
| A,Reference number: S51330                                      |                                                                                                                                                                                    |
| A; Accession: Solsso                                            |                                                                                                                                                                                    |
| A;Residues: 1-13,'V',15-24,'                                    | A,Residues: 1-13, VV, 15-24, 'Q', 26-44, 'N', 46-153, 'G', 155-156, 'P', 158-171, 'K', 173-227, 'R', ;                                                                             |
| A; Cross-references: EMBL: X83959;                              | 959; NID:g634008; PIDN:CAA58789.1; PID:g634009                                                                                                                                     |
| A, Accession: S51331                                            | 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                                                                                                                                            |
| A; Molecule type: mRNA                                          | A; Molecule type: mRNA                                                                                                                                                             |
| A, Residues: 1-24, 'Q', 26-29,'.                                | K',31-83,'L',85-153,'G',155-156,'F',158-171,'K',173-208,'Q<br>960: NID:g634010: DIDN:CAB58790.1: DID:g634011                                                                       |
| A;Experimental source: clone                                    | gfp2                                                                                                                                                                               |
| R,Yang, F.; Moss, L.G.; Phil                                    | R;Yang, F.; Moss, L.G.; Phillips Jr., G.N.<br>submitted to the Brookhaven Protein Data Bank. August 1996                                                                           |
| A; Reference number: A65692;                                    | PDB:1GFL                                                                                                                                                                           |
| A; Contents: annotation; X-ra                                   | A;Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 'A',2-79,'R',81-99<br>A:Note: engineered semience based on 101514. Cloned and expressed in Escherichia coli |
| R, Yang, F.; Moss, L.G.; Phil                                   | lips Jr., G.N.                                                                                                                                                                     |
| Nat. Biotechnol. 14, 1246-12                                    | Nat. Biotechnol. 14, 1246-1251, 1996                                                                                                                                               |
| A:Title: The molecular struc                                    | thre of green finorescent brocein.                                                                                                                                                 |

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Query Match
Best Local S:
Matches 46
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A; Contents: annotation; X-ray crystallography, 1.9 angstroms
C; Comment: This protein is excited by the photoprotein aequorin (see PIR:AQJFNV) emittin C; Comment: The chromophore of this protein is formed by modification of Ser-dehydro-Tyr-C; Genetics:
G; Genetics:
A; GEP
A; Introns: 69/3; 167/3
C; Superfamily: green-fluorescent protein
C; Superfamily: green-fluorescent (Ser-Giv) #status experimental
F; 65-67/Cross-link: 5-imidazolinone (Ser-Gly) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUD:99287316; PMID:10360571
A;Accession: H7228
A;Accession: H7228
A;Status: preliminary
A;Molecule E;Ype: DNA
A;Residues: 1-785 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-refarences: GB:AE001806, GB:AE000512, NID:g4982196, PIDN:AAD36691.1, PID:g498219
A,Experimental source: strain MSB8
C,Genetics:
A,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein TM1624 - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: H72228
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VITFSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFYKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTVLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 TVLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 RIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVQLADH 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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8.2%; Score 105; DB 2; Length 785;
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                                                            N;Alternate names: leucyl-tRNA synthetase
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 03-Jun-2002
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- Haemophilus influenzae (strain Rd KW20)
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C,Superfamily: leucine-tRNA ligase
C,Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
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       Leucine-tRNA ligase (EC 6.1.1.4)
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01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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Nature 392, 353-358, 1998
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        Silveir
A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da M., † Buhbako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A; Reference number: A59328
A; Contents: annotation
A; Genetics:
A; Genetics:
C; Genetics:
C; Superfamily: leucine-tRNA ligase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 TTGKLPVPWPTLVTVLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNY-- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : | :||::| | :||:||:| | .: | | .: | | : | .: | | : | .. | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 RAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIR 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DWGVSRQRYWGAPIPMVTLEDGTV-----LPTPEDQLPVILPEDVVMDGITSPIKADP 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329 TNEQLPV-WVANFVLMAYGTGAVMAVPGHDQRDQEF--ANKYGLPIRQVIALKEPKNQDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 MADKQKNG-IKVNFKIRHNIEDGSVQLADHYQQNTPI------GDGPVLLPDN
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                                                                                                                                                                                                                                                                                                                       Match 7.2%; Score 91.5; D
Local Similarity 22.2%; Pred. No. 14;
e8 44; Conservative 30; Mismatches
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C,Superfamily: leucine-tRNA ligase
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Matches 42; Conserva
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Matches
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D83917 DNA topoisomerase IV subunit B BH2140 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans

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C; Accession: D83917
R; Takami, H.; Makasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran R; Takami, H.; Nakasone, R.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran R; Takami, H.; Nakasone, R.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Na; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Reference number: A83650; MUID:20512582; PMID:11058132
A; Accession: D83917
A; Accession: D83917
A; Molecule type: DNA
A; Residues: 1-655 <STO>
A; Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB05859.1; GSPDB:GN00
A; Cross-references: GB:AP01174; GB:BA000004; NID:g10174613; PIDN:BAB05859.1; GSPDB:GN00
C; Genetics:
A; Gene: BH2140
C; Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B
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A; Accession: B70390
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: DNA A; Residues: 1-370 < AQF>
A; TCOSS-references: GB:AE000720; NID:g2983529; PIDN:AAC07111.1; PID:g2983536; GB:AE00065*
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 SVVNALSEWLIVEIKRDGWVYEQRFENGGKPSTTLEKKGKTRQTGTTIHFKPDPTVFSTT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --NYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADK----- 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----QKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGFVLLPDNHYLSTQSALSKDP 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Superfamily: nitrogen fixation protein nifS
Kewporda: phosphoprotein; pyridoxal phosphate; sulfurtransferase
1.95/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
1.318/Active site: Cys (cysteine persulfide intermediate) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 TLVTVLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQER-----TIFFKDDG----
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Local Similarity 25.4%; Pred. No. 9.8;
les 49; Conservative 30; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Score 88.5; I. Similarity 21.9%; Pred. No. 17;
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| 00   00   00   00   00   00   00   0                              | SULT 10 4078 4078 4078 4078 4078 4078 4078 407                                                                                                                                                                                                                                                                                                                                                                                                                                         | Query Match  Query Match  G.8%; Score 86.5; DB 2; Length 797;  Best Local Similarity 21.9%; Pred. No. 32;  Matches 48; Conservative 30; Mismatches 78; Indels 63; Gaps 11;  Qy 65 LSYGVQCFSRYPDHWKQHDFFKSAMPEGYVQERTI 99;  1 | Qy 149 HNVYIMADKQK-NGIKUNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLL 196    1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|-------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Qy 51 TGKLPVPWPTLVTVLSYGVQCFSRYPDHMKQ-HDFFKSAMPEGYVQERTIFFKDD 104 | cal protein PFB0460c - malaria parasite ( 1 Plasmodium falciparum 3-Nov-1998 #sequence_revision 13-Nov-1998 on: D71614  M.J.; Tettelin, H.; Carucci, D.J.; Cumm M.; Salzberg, S.; Zhou, L.; Sutton, G.G Dromosome 2 sequence of the human malari canumber: A71600; MUID:99021743; PMID:98 Dreliminary; nucleic acid sequence not s brype: DNA preliminary; nucleic acid sequence not s a: 1-2573 cGAR> eferences: GB:AE001396; GB:AE001362; NID: Brital source: clone 3D7 FB0460c atch | Qy                                                                                                                                                                                                                           | RESULT 9 JUVALITE DIA polymerase (EC 2.7.7.7) - heron hepatitis virus C; Species: heron hepatitis virus, HHBV A;Note: hos: Ardea cinerea (gray heron) C; Accession: A30082 R; Species: A30082 R; Reference number: A3037; MUD:88333160; PMID:3418788 A; Reference number: A3037; MUD:88333160; PMID:3418788 A; Residues: 1-788 <spr> A; Cosserences: GB:MZ2056; NID:G325452; PIDN:AA45738.1; PID:G325454 C; Superfamily: hepatitis virus DNA-directed DNA polymerase C; Superfamily: hepatitis virus DNA-directed DNA polymerase C; Superfamily: hepatitis virus DNA-directed DNA polymerase C; Keywords: DNA biosynthesis; nucleotidyltransferase Query Match Best Local Similarity 19.7%; Pred: No. 32; Matches 40; Conservative 32; Mismatches 66; Indels 65; Gaps 10;</spr> |

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C;Superfamily: photosystem II chlorophyll a-binding protein psbC
C;Keywords: chlorophyll; cyanelle; membrane-associated complex; photosynthesis; photosyst
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C.Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 17-Mar-1999
C.Jaccession: JCS576, PC4486
G.Jaccession: JCS576, PC4486
J. Blochem: 122, 71-82, 1997
J. Blochem: 122, 71-82, 1997
A.Title: Molscular cloning and sequencing of cDNAs encoding three heavy-chain precursors ain inhibitor heavy chain family.
A.Reference number: JCS574; MUID:97420688; PMID:9276673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chains 1, 2 and 3 were
R;Stirewalt, V.L.; Michalowski, C.B.; Luffelhardt, W.; Bohnert, H.J.; Bryant, D.A. submitted to the EmBL Data Library, July 1995
A;Description: Nucleotide sequence of the cyanelle genome from Cyanophora paradoxa. A;Reference number: 215840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           365 LT-KIKYDIQPWQERRAAEYMTHAPLGSLNSVGGVATEINSVNYVSPRSWLS----TS 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 -----QCFSRYPDHMKQHDFFKSAMPE-GYVQERTIFFKDD-------GN 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268 ALMGFIANCFVWFNNTAYPSEFFGPTGPEASQAQAFTFLVRDQRLGANVGSAQGPTGLGK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 VNFKIRHNIEDGSVQLADHYQQNTPIGD----GPVLLPDN--HYLSTQSALSKDPNEKRD 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 YKTRA---EVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIK 163
                                                                                                                             A;Accession: T06936
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-461 <STI>
A;Experimental source: EMBL:U30821; NID:g1016083; PIDN:AAA81279.1; PID:g1016192
A;Experimental source: strain Pringsheim LBS55
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 GHKFSVSGEGEGDATYGKLTLKFICTTGKL-----PVPWPTLVTV-----LSYGV---
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A; Molecule type: mRNA
A; Residues: 1-889 v.NAK>
A; Experimental source: liver
A; Accession: PC4486
A; Accession: PC4486
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
C; Comment: In the plasma three inter-alpha-trypsin inhibitor heavy
that the complexes play important role for panceatic cancer.
C; Superfamily: inter-alpha-trypsin inhibitor component II
F; 236-239, 664-865/Disulfide bonds: #status predicted
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23.8%; Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.8%; Score 86; DB 2; Length 461; 21.8%; Pred. No. 17;
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es 55; Conserva
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Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Genome: cyanelle
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Best Local S:
Matches 55
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R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tRNA (uracil-5-)-methyltransferase (EC 2.1.1.35) Cj0831c [imported] - Campylobacter jeju
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Filtle: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp. Reference number: A81250, MUID:20150912, PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: DNA,
M.Rebidues: 1-37. cPRA.
A,Rebidues: 1-37. cPRA.
A,Cross-references: GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB73096.1; PID:g696827
A,Experimental source: serotype O2, strain NCTC 11168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         556 RNLYIQSMKFKGNGIKTN-----DFDFSFGWNYNSLNRGYFPTKGVKASLG-GRVTI 606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Campylobacter jejuni
;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                          63;
A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-808 <TIGR>
A;Residues: 1-808 <TIGR>
C,Scose-references: GB:L42023; TIGR:HI0917
C;Superfamily: protective surface antigen D-15
C;Reywords: surface antigen
                                                                                                                                                                                                                                                        DB 2; Length 808;
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Pred. No. 12;
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                                                                                                                                                                                                                                                                                                                       78;
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C;Keywords: methyltransferase; S-adenosylmethionine
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                                                                                                                                                                                                                                                                                                                          30; Mismatches
                                                                                                                                                                                                                                                                                             Pred. No. 33;
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24.8%;
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Best Local Similarity 24...
Best Local Similarity 24...
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A;Status: preliminary
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A. Percion:
A. Description:
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$29043
S29043
S29043
S29043
NiAlternate names: endo-1,4-beta-glucanase
C;Species: Bacillus sp.
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 01-Dec-2000
C;Accession: $29043; Pc440, Pc440, Pc540,  P
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A; Residues: 1-941 < CZDA.

A; Cross-references: ENBL: M27420; NID: g142664; PIDN: AAA22304.1; PID: g142665

B; Shirai, T.; Yamane, T.; Hidaka, T.; Kuyama, K.; Suzuki, A.; Ashida, T.; Ozaki, K.; Itc

B; Shirai, T.; Yamane, T.; Hidaka, T.; Kuyama, K.; Suzuki, A.; Ashida, T.; Ozaki, K.; Itc

A; Title: Crystallization and preliminary X-ray analysis of a truncated family A alkaline

A; Reference number: PC4404; MUID: 98060488; PMID: 9399567
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                                                                                240 LVELNG----QLTLAGE---DGT-------PV---QLRGMSTHGLQWFG-- 271
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126 LKGID--FKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHY 183
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k; Pred. No. 49;
34; Mismatches
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Best Local Similarity '20.3%;
Matches 49; Conservative 3.
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A;Residues: 228-584 <SHI>
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GenCore version 5.1.6
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OM protein - protein search, using sw model

June 21, 2004, 15:42:24; Search time 6.44444 Seconds (without alignments) 1931.085 Million cell updates/sec Run on:

US-09-887-784-64V 1273 1 MVSKGEELFIGVVPILVELD......VLLGFVTAAGITLGMDELYK 239 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description   | P42212 aequorea vi P43827 haemophilus Q92845 syleila fas Q82865 syleila fas Q8265 xyleila fas Q87c65 xyleila fas P50859 candida gla P13846 heron hepat P44935 haemophilus P46024 haemophilus Q8604 shewarallus Q860992 campylobact P48104 cyanophora Q88900 rattus norv O32629 haemophilus P97260 mesocricetu P19424 bacillus sp P18947 caenorhabdi Q88900 xattus norv Q88900 xattus norv Q88900 syleilus sp P18947 caenorhabdi Q58726 mesocricetu P19424 bacillus sp P18947 caenorhabdi Q88900 syleilus sp P18948 selencichia P23865 escherichia P23865 escherichia P23865 escherichia P23865 scherichia P2381 secherichia P2793 buchnera ap Q9710 homo sapien P28840 rattus norv O42918 schizosacch                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
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| SUMMARIES     | GFP AEGVI SYL_HAEIN SYL_SALTY SYL_SALTY SYL_SALTY SYL_SALTY SYL_SALTY CPEI_CNGRA DPOL_HPBHE DISJ_HAEIN DISJ_HAEIN SYL_SHEON TRNA_CAMATE PSBC_CYAPA GRBE_RAT DISJ_HAEIN UTTHJ_MESAU GUN_BACSG VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEEL VYT4_CAEE |
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| Length        | 238<br>861<br>861<br>860<br>860<br>860<br>873<br>873<br>873<br>873<br>873<br>873<br>873<br>873<br>873<br>873                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| 당선            | 0.000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
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| P49052 bacillus li<br>Q7vnf0 haemophilus<br>P55621 homo sapien<br>O25443 helicobacte<br>Q9ugn5 homo sapien<br>Q0116 homo sapien<br>Q82df8 yersinia pe<br>P91679 drosophila<br>P03162 duck hepati<br>Q9pkt7 chlamydia m<br>P94126 azorhizobiu<br>Q63416 rattus norv |
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| SIAP BACLI SYD HAEDU SYD HAEDU TRWB HELPY PPOZ HUWAN SYL YERPE OPTL PROME DPOL HPBDU TRXB CHLMU GLANA AZOCA                                                                                                                                                        |
|                                                                                                                                                                                                                                                                    |
| 874<br>1228<br>1228<br>3933<br>6583<br>658<br>860<br>737<br>737<br>836<br>818<br>818                                                                                                                                                                               |
| ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~                                                                                                                                                                                                                             |
| 81.5<br>80.5<br>80.5<br>80.5<br>80.5<br>80.5<br>79.5<br>79.5                                                                                                                                                                                                       |
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#### ALIGNMENTS

X-RAY

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61 VITESYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 VTVLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                  5-imidazolinone (Ser-Gly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26886 MW; EASA6F21FBFB6E05 CRC64;
                                                                                                                                              3-DIDEHYDROTYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1242; DB 1;
Pred. No. 1.7e-95;
1; Mismatches 4;
                 PDB; 1YFP; 28-OCT-98.
PDB; 2EMD; 20-AUG-97.
PDB; 2EMU; 20-AUG-97.
InterPro; IPR009017; GFP_like.
InterPro; IPR00786; Green_fl_protein.
Pf01353; GFP; 1.
                                                                                                 PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl protein; 1.
Luminescence; 3D-structure.
                                                                                                                                                         97.6%;
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100
108
141
219
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211
217
238 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233;
                                                                                                                                                                                                   CONFLICT
CONFLICT
CONFLICT
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VARIANT
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PDB;
PDB;
PDB;
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                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
          CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF MUTANT WITH YELLOW EMMISSION
                  MEDLINE=98455509; PubMed=9782051; Wachter R.M., Elsliger M.A., Kallio K., Hanson G.T., Remington S.J.; "Structural basis of spectral shifts in the yellow-emission variants structure fluorescent protein."; Structure 6:1267-1277(1998).
                                                                                       X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, 1462654; AAA27722.1; -...
EMBL, 162653; AAA27721.1; -...
EMBL, 306691; AAA58246.1; -...
EMBL, 306692; AOA5278.1; -...
PDB, 1139C, 17-NOV-00.
PDB, 113PP, 07-JUJ-97.
PDB, 113PP, 07-JUJ-97.
PDB, 113PP, 12-MA | 08-NOV-96.
PDB, 113PM, 16-JUN-97.
PDB, 113PM, 20-AUG-97.
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88888

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Gaps

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4

Length 238; Indels 61 9 121

122 NRIELKGIDFKEDGNILGHKLEYNYNSHNYYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181 

ò 엄 182 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239

181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;

Pleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Witerback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diphosphate + L-leucyl-tRNA(Leu).
-!- SUBUNT: Monomer (By similarity).
-!- SUBCELLULA LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-S003 (Rel. 41, Last amnotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeukS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59;
                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.3%; Score 93.5; DB 1; Length 861;
24.1%; Pred. No. 4.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59;
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ATP (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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InterPro; IPR002302; Leu-tRNASyntla.
InterPro; IPR001300; tRNA-synt la.
InterPro; IPR001412; tRNA-synt la.
InterPro; IPR001412; tRNA-synt l.
InterPro; IPR0010408; ValR& IleRS_edit.
Pfam; PF00133; tRNA-synt l; 1.
PRINTS; PR00985; TRNASYNTHLEU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGRFAMS; TIGR00396; leus bact; 1. PROSITE; PS00178; AA_TRNA_LIGASE_I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U32774; AAC22581.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 269:496-512(1995)
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623
622
                                                                                                                                                                                                                                                                                                   Haemophilus influenzae.
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                                                                                                                                                                                                                                                                              OR HI092:
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                                                                     SYL_HAEIN
P43827;
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SEQUENCE
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RESULT 2
SYL HARIN
AC P43824
DAC D1-NO
DT O1-NO
DT O1-NO
DT 28-FB
DB Leucy
OS Pacte
OC Pacte
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104 DGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADK-QKNGI 162
                                       365 DEEIDLIKQAFVEHGKLVNSDEFDGKNF--DGAFNG------IADKLEKLGV 408
                                                                                                              409 GKRQVNYRLRDMGVSRQRYWGAPIPMLTLENGDVVPA-----PMEDLPILLPEDVVMD 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAINB-20355717; PubMed=10910347;
STRAINB-20355717; PubMed=10910347;
Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
Alvarenga R., Alves L.M.C., Arraya J.E., Baia G.S., Bapista C.S.,
Barrocs M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
Colauto C.C. Coota F.F., Costa M.C.R., Costa-Neto C.M.,
RA Bueno M.R.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Pacincani A.D., Cristofani M. Dias-Neto E. Docena C., El-Dorry H.,
RA Fraga J.S., Franco M.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Garnier M., Maclina B.E., Laigtet F., Lambais M.R., Leite L.C.C.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins B.A.L., Martins E.M.F., Marsukuma A.Y.,
RA Marques M.V., Martins B.A.L., Martins E.M.F., Marsukuma A.Y.,
RA Mani A.T., Nobrega F.G., Nunce L.R.O., Netto L.E.S.,
Moni A.T., Nobrega F.G., Nunce L.R.O., Netto L.E.S.,
RA Coliveira M.C., de Oliveira R.C., Fellmieri D.A., Perguero J.B.,
RA G. Silva R.B., Roberto P.G., Roditigues V., de Rosa A.J.M.,
RA G. Salva A.M., da Silva F.R., Silva W.A., Jr.,
RA da Silva A.C.R., da Silva R., da Silva R., Silva W.A., Jr.,
RA da Silva A.C.R., da Silva R., Satuball J.C.;
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
Nature 406:151-159(2000).
R. Carliville L. Leucine + tRNA(Leu) = AMP +
RADARANA C. L. Leucine + tRNA(Leu) = AMP +
                                                                                       163 ---KVNFKIRH-------NIEDGSVQLADHYQQNTPIGDGFVLLPDNHYL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diphosphate + L-leucyl-tRNA(Leu).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Leucyl-TRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
                                                                                                                                                                                                                                                                                                                                      879 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE004031; AAF84975.1; ALT_INIT.
                                                                                                                                                                               213
                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                         462 GVKSPINADPN 472
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                                                                                                                                                                               203 STOSALSKOPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kylella fastidiosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Q9PBG8;
                                                                                                                                                                                                                                                                                          RESULT 3
SYL XYLFA
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Nature 413:852-856(2001)
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Q8ZQZ6;
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      SOLUTION TO THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------KTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 MADKQKNG-IKVNFKIRHNIEDGSVQLADHYQQNTPI------GDGPVLLPDN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : | ::||:::| : : | | : : | | : : | | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | :
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SEQUENCE FROM N.A.
STRAIN:TY2 / ATCC 700931;
MEDLINE-22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.21 TNEQLPV-WVANFVLMAYGTGAVMAVPGHDQRDQEF--ANKYGLPIRQVIALKEPKNQDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.78 STWEPDVWRDWYADKTR---EFE---LINSAEFDGLDYODAFEVLABRRFE-----
                    InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_l.
InterPro; IPR001308; ValRS_ILERS_edit.
PRIM: PR00131; tRNA-synt_l. 1, 1.
PRINTS; PR00985; TRNASYNTHLEU.
TIGRPO396; ISS_DATE. 1.
PROSTIE; PS00178; AA_TRNA_LIGASE 1; 1.
Aminoacyl-tRNA synthètase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parkhill J., Dougna G., Dames K.D., Thomson N.R., Pickard D., Wain J. Churchur C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker B., Basham D., Brooks K., Chillingworth T., Connexton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
LEUS ON STY0699 OR T2219.
Salmonella typhi.
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Enterobacteriaceae; Salmonella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.2%; Score 91.5; DB 1; Length 879;
22.2%; Pred. No. 6.7;
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                                                                                                                                                                                                                                                                                                                              "HIGH" REGION.
"KMSKS" REGION.
ATP (BY SIMILARITY).
9FDCCB992092919E CRC64;
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MEDLINE=21534947; PubMed=11677608;
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                                                                                                                                                                                                                                                                                                                                                                                                                              99796 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44; Conservative
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641
640
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879 AA;
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SITE 45
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Q8Z8HS;
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DOR REAL TERMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 RAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIR 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL627267; CAD05125.1; -.
EMBL; AL627267; CAD05125.1; -.
EMBL; AC01641; AAC69822.1; -.
HAWAP; MF_000919; -; 1.
InterPro; IPR002300; LBU-TRNAsyntla.
InterPro; IPR001412; LBNA-synt_1a.
InterPro; IPR001412; LRNA-synt_1.
InterPro; IPR001412; LRNA-synt_1.
InterPro; IPR00908; ValkS; IIERS_edit.
PRINTS; PR00985; TRNASYNTHLEU;
ITGRFAMS; TIGR00396; LBUS_bact, I.
PROSITE; PS00178; AA TRNA_LIGASE I; 1.
Aminoacy1-tRNA synthētase; Protein biosynthesis; Ligase; ATP-binding;
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STRAINE_LT2 / SGSC1.412 / ATCC 700720;

STRAINE_LT2 / SGSC1.412 / ATCC 700720;

MEDLINE_21S34949; PubMed=11677609;

MCDIelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.,

"Complete genome sequence of Salmonella enterica serovar Typhimurium
                              diphosphate + L-leucyl-tRNA(Leu).
-!- SUBCELLUTAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-OcT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 52 "HIGH" REGION.
619 623 "KMSKS" REGION.
622 622 ATP (BY SIMILARITY).
860 AA, 96940 MW, 2F95E480BBAB23C4 CRC64;
L-leucine + tRNA(Leu)
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NCBI_TaxID=5478;
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                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 SEQALTEKGVLFNSGEFDGLAFEAAFNAIADKL------AEKGVGERKVNYRLR 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 TTGKLPVPWPTLVTVLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 H------NIEDGSVQLADHYQQNTPIGDGPVLLPDNHYL-STQSALSKDP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              419 DWGVSRQRYWGAPIPMVTLEDGTV-----LPTPEDQLPVILPEDVVMDGITSPIKADP 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1] SEQUENCE FROM N.A. MEDIAGG 12533478; Monteiro-Vitorello C.B., Monteiro-Vitorello C.B., Monteiro-Vitorello C.B., Monteiro-Vitorello C.B., Monteiro-Vitorello C.B., Monteiro-Vitorello C.B., Monteiro-Vitorello C.B., Monteiro-Vitorello C.B., Monteiro-Vitorello C.B., Monteiro-Vitorello C.B., Monteiro-Vitorello C.B., Monteiro-Vitorello C.B., Monteiro-Vitorello C.B., Monteiro-Vitorello C.B., Monteiro-Vitorello C.B., Monteiro-Vitorello C.B., Siqueira M.J., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J., Coutinho L.L., Kimura E.T., Ferro E.S., Hararava R., Kuramas E.E., Marino C.L., Gigliott E., Abreu I.L., Alves L.M.C., do Amaral A.M., Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V., da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
                                                                                                                                                                                                                  THAMAP; MF 00049; '. I.L.
InterPro; IPR002302; Leu-tRNAsyntla.
InterPro; IPR002302; Leu-tRNAsyntla.
InterPro; IPR003102; LRNA-synt la.
InterPro; IPR001412; tRNA-synt la.
InterPro; IPR001412; tRNA-synt li.
PFam; PF00133; tRNA-synt li.
PROMITS; PR009085; TRNASYNTHIBU.
PROSTITS; PS00178; AA TRNA_LIGASE li. 1.
PROSTITE; PS00178; AA TRNA_LIGASE li. 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
             diphosphate + L-leucyl-tRNA(Leu).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
LEUS OR PD1230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadacee; Mranthomonadacees, Mylella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 860;
CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77; Indels
                                                                                                                                                                                                                                                                                                                                                                                     42 52 "HIGH" REGION.
619 623 "KMSKG. REGION.
622 622 ATP (BY SIMILARITY).
860 AA, 96985 MW, DS003584DFBCCAB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.0%; Score 89.5; DE 23.3%; Pred. No. 9.6; ative 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 879 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEUS OR PD1230.
Xylella fastidiosa (strain Temeculal
                                                                                                                                                                                        EMBL; AE008725; AAL19599.1; -. StyGene; SG????; leuS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=183190;
                                                                                                                                                                                                                                                                                                                                                                          Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYL XYLFT
Q87C65;
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                    BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321 TNEQLPV-WYANFVLMAYGTGAVMAVPGHDQRDQEF--ANKYGLPIRQVIALKEPKNQDE 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : | | : | | : | | : | | 422 ---ROGRGORRVMYRLR----DWGVSRQRYWGCPIPVIYCPTCGAVPVPENQLPVILPEN 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 MADKQKNG-IKVNFKIRHNIEDGSVQLADHYQQNTPI-------GDGPVLLPDN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||| :|| | |:| :| :| | | |:| | 378 STWEPDVWRDWYADKTR-------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAMAP; MF_00049; -; 1.

InterPro; IPR002302; Leu-tRNAsyntla.

InterPro; IPR001310; tRNA-synt la.

InterPro; IPR001401; tRNA-synt li.

InterPro; IPR001401; tRNA-synt li.

PRIMTS; PR00985; TRNA-synt li.

PRIMTS; PR00985; TRNA-synt li.

IGRAMS; TIGRO396; leuS bact; l.

PROSITE; PS00178; AA_TRNA_LIGASE l; l.

Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 ------KTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYI
                                                                                                                                                                                                                                                         J. Bacteriol. 185:1018-1026(2003).
-!- CATALYTIC ACTIVITY: AFP + L-leucine + tRNA(Leu) = AMP + diphosphate + L-leucyl-tRNA(Leu).
-! GATELLULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57; Gaps
Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sassaki F.T., Sena J.A.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Sterol 14-
                                                                                                                                                "Comparative analyses of the complete genome sequences of Pierce' disease and citrus variegated chlorosis strains of Xylella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CP51 CANGA STANDARD; PRT; 533 AA.
P50859; Q02312;
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2003 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
22ycohrome P450 51 (EC 1.14.13.70) (CYPLI) (P450-LIA1) (Sterol 14 alpha-demethylase) (Lanosterol 14-alpha demethylase) (P450-14DM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryotā; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                           de Souza A.A., Truffi D., Taukumo F., Yanai G.M., Zaros L.G.,
Civerolo B.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
Kitajima J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       637 641 "KMSKS" REGION.
640 640 ATP (BY SIMILARITY).
879 AA; 99823 MW; 4C2EE01B8FDC497E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 22.2%; Pred. No. 12;
nes 44; Conservative 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.0%; Score 88.5; I 22.2%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "HIGH" REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE012557; AA029080.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 -HYLSTQSALSKDPNEKR 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              475 VAFSGTGSPIKTDPEWRK 492
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641
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HAEIN
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P44935;
              HPBHE
                                           d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.)9 GHEFIFNAKLADVSAEAAYSHLT-----TPV-----FGKGVIYDCPNHRLM 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.3.2 KEDGNII.GHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2)8 TASRSLLGKEMRDKLDTDFAYLYSDLDKGFTPINF-VFPNLPLEHYRKRDHAQQAIS--- 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79
                            STRAIN=2001-L5;
MEDLINE=96461286; PubMed=8593007;
MEDLINE=96461286; PubMed=8593007;
Geber A., Hitchcock C.A., Swartz J.E., Pullen F.S., Marsden K.E.,
Kwon-Caung K.J., Bennett J.E.;
"Deletion of the Candida glabrata ERG3 and ERG11 genes: effect on cell
viability, cell growth, sterol composition, and antifungal
gusceptibility.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GHKFSVS---GEGEGDATYGKLTLKFICTTGKLPVPWPTLVTVLSYGVQCFSRYPDH--M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 KQHDFFKSAM-PEGYV-----QERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              472 IRON (HEME AXIAL LIGAND) (BY SIMILARITY)
64 I -> M (IN REF. 2).
473 I -> T (IN REF. 2).
61305 MW; A0506C17507E6EF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001128; Cytochrome_P450.
Pfam; 2P60067; p450; 1.
PRINTS; PR00385; P450.
PROSITE: P500086; CYTOCHROME_P450; 1.
Electron transport; Oxidoreductase; Monooxygenase; Membrane; Heme;
                                                                                                                                                                                                                                       "Rapid detection and identification of Candida albicans and Torulogsis (Candida) glabrata in clinical specimens by species-specific nested for amplification of a cytochrome P-450 lanosersol-alpha-demethylase (LiA1) gene fragment."; J. Clin. Microbiol. 32:1902-1907(1994).
-!- PUNCTION: Garalyzes C14-demethylation of lanosterol which is critical for ergosterol biosynthesis. It transforms lanosterol inco 4,4' dimethyl cholesta-8,14,24-triene-3-beta-ol (By
                                                                                                                                                                             STRAIN=ATCC 2001;
MEDLINE-95081364; PubMed=7989540;
Burgener-Kairuz P., Zuber J.P., Jaunin P., Buchman T.G., Bille J.,
                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: Obtusifoliol + 3 O(2) + 3 NADPH = 4-alpha-methyl-5-alpha-ergosta-8,14,24(28)-trien-3-beta-ol + formate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.8%; Score 86.5; DB 1; Length 533;
21.8%; Pred. No. 9.6;
Live 32; Mismatches 80; Indels 4:
                                                                                                                                                                                                                                                                                                                                                                                                         NAOP(+) + 3 H(2)0.
PATHWAY: Ergosterol biosynthesis.
SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                  Antimicrob. Agents Chemother. 39:2708-2717(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 GPVLLPDNHYLSTQSALSKDPNEKRD 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GTYMSLIKERREKND 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; 540389; AAB02329.1; -. EMBL; 575389; AAB32679.1; -.
                                                                                                                                                               SEQUENCE OF 60-473 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sterol biosynthesis; NADP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 21.8
es 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             533 AA;
              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                  similarity)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 T--------RAEVKFEGDTLVNRIBLKGIDFKEDGNILGHKLEYNYNSHNVYIM 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 ADKQKNGIKVNFKIRHNIEDGSVQLADHYQ------QNTPIGDGPVLL-PDNHYL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probom; PD000814; DNApol viral_C; 1.
Transferace; RNA-directed DNA polymerase; Hydrolase; Nuclease; Endonuclease; DNA replication; DNA-binding.
SEQUENCE 788 AA; 90070 NW; FB44F38F75EADF44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 ----NGRKISY---HSTRDGSHRLSGRTSDPTSRGALAGGDSTPIGFGSTAAHPSTHHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 WPKSISYLPVHSGVKPKYPEFQQNHESLVNDYLNKLFEAGILYKRVSKHLVTFK--GPYF
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16-OCT-2001 (Rel. 40, Last annotation update)
P protein [Includes: DNA-directed DNA polymerase (EC 2.7.7.7); RNA-directed DNA polymerase (EC 2.7.7.7); RNA-directed DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=88333160; PubMed=3418788;
Sprengel R., Kales E.F., Will H.;
"Isolation and characterization of a hepatitis B virus endemic in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65;
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                                                                                                                                                                                                                                                                 Heron hepatitis b virus.
Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'
788 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
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01-NOV-1995 (Rel. 32, Last sequence update)
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InterPro; PR001462; DNApol_viral_C.
InterPro; IPR000201; DNApol_viral_N.
InterPro; IPR000477; RVTse.
Pfam; PF00342; DNA_pol_viral_C; 1.
Pfam; PF00242; DNA_pol_viral_K; 1.
Pfam; PF00078; rvt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 STQ-----SALSKDPNEKR 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1990 (Rel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Virol. 62:3832-3839(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M22056; AAA45738.1; -.
   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phosphomonoester.
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=28300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (N)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
D152 HAEIN
ID D152 HA
AC P44935;
DT 01-NOV-
DT 01-NOV-
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(D-15-Ag) (Outer membrane protein D15).
                                                                                                                                                                                                                                                                                                      invasive disease."
                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                        NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYL SHEON
Q8EHP4;
10-OCT-2003
10-OCT-2003
                                                                                                                                                                                                                                                              Klein M.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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SYL_SHEON
 DA LA LA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 FPKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNI---LGH-----KLEYNYNS 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 HNVYIMADKQK-NGIKVNFKIRHNIEDGSVQLADHYQQ------NTPIGDGPVLL 196
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                                                                                                                                                                                                                                                                                                     "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 LSYGVQCFSRYPDHMKQHDF-----RTI
                                                                                                                                        STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;
Fleischmann R.D., Addms M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Witerback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehn C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63;
                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protective surface antigen D15 precursor (80 kDa D15 antigen)
             Protective surface antigen D15 precursor (80 kDa D15 antigen)
(D-15-Ag) (Outer membrane protein D15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000184; Bac_surfAg_D15.
Pfam; PF01103; Bac_surface Ag; 1.
Antigan; Outer membrane; Signal; Complete proteome.
1 19 POTENTIAL.
CHAIN 20 795 PROTECTIVE SURFACE ANTIGEN D15.
SEQUENCE 795 AA; 87478 MW; B85691FC22E6ED44 CRC64;
                                                                                                                                                                                                                                                                                                                              Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SIMILARITY: Belongs to the surface antigen D15 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           594 PGSDNKYYKLSADVQGFYPLDRDHLWVVSAKASAGYANG 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 P--DNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLG 233
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          797 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.8%; Score 86.5; D
21.9%; Pred. No. 15;
vative 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U32773; AAC22575.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48; Conservative
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                                                       Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                            SEQUENCE FROM N.A.
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D151 HABIN
ID D151 HABIN
AC P46024;
DT 01-NOV-1995
DT 16-OCT-2001
DE Protective s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 FFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNI---LGH-----KLEYNYNS 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            543 RNLYIQSMKFKGNGIKTN-----DFDFSFGWNYNSLNRGYFPTKGVKASLG-GRVTI 593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Outer membrane protein D15 is conserved among Haemophilus influenzae species and may represent a universal protective antigen against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 LSYGVOCFSRYPDHMKQHDF-----RTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           427 IGYGTESGISYQASVKQDNFLGTGAAVSIAGTKNDYGTSVNLGYTEPYFTKDGVSLGGNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                          SEQUENCE FROM N.A.
STRALM-Seroctype B;
MEDLINE-SEZ55676; PubMed=7737523;
Flack F.S., Loosmore S., Chong P., Thomas W.R.;
Flack F.S., Loosmore S., Chong P., Thomas W.R.;
Haesquencing of the 80-kDa D15 protective surface antigen of Haemophius influenzae.";
Gene 156:97-9911995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63;
                         Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 797;
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20 797 PROTECTIVE SURFACE ANTIGEN D15.
797 AA, 87675 MW; 2F93DE538696AF1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Infect. Immun. 65:3701-3707(1997).
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SIMILARITY: Belongs to the surface antigen D15 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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MEDLINE=97427952; PubMed=9284140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.8%; Score 86.5; DB 1;
21.9%; Pred. No. 15;
trive 30; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 42, Created)
(Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               859 AA
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EMBL; U60832; AAB61974.1; -.
EMBL; U60833; AAB61976.1; -.
PIR; JC47078; JC47078.
Interpro; IPR000184; Bac_gurfag_D15.
Pfam; PF01103; Bac_gurface_Ag; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 21.9*
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
Haemophilus influenzae.
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SEQUENCE FROM N.A. STRAIN=NCTC 11168;
                                                                                                                         TRMA OR CJ0831C.
                                                                                                                                                                               NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                                                                                                                                               subfamily.
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                           CAMJE
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELAAFIDECKNSTTSEAELATMEKRGVAT-GLYAIHPI--TGKQVPIWAANFVLMNYGTG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.1 CFSRYPDH-MKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 AVMSVPGHDQRDYEFAK----KYHLPIEAVIKPAEGDLDISEAAYTEKGILFNSGEFDGL 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---NIEDGSVQLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 8 ELDGDVNGHKFSVSGEGE-----GDATYGKLTLKFICTTGKLPVPWPTLVTVLSYGVQ 70
                                                                                                        MEDLINE=2297686; PubMed=12368813; MEDLINE=2297686; PubMed=12368813; MEDLINE=22297686; Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Heidelberg J.F., Paulsen I.T., Nelson K.E., March B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Musthebvan J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; "Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00133; tRNA-synt 1; 1.
PRINTS; PR00985; TRNASYNTHLEU.
TIGRFAMs; TIGR00396; leus, etc.; 1.
PROSITE; PS00178; AA TRNA_LIGASE 1; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                        Nat. Biotechnol. 20:1118-1123 (2002).
-!- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA (Leu) = AMP +
diphosphate + L-leucyl-tRNA (Leu).
-! GYBJCELLULAR LOCATION: Cytoplasmic.
-! SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37;
                                       Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "KMSKS" REGION.
ATP (BY SIMILARITY).
C78D6209DFB6CA17 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 DHYQQNTPIGDGPVLLPDNHYL-STQSALSKD 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 86.5; I
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "HIGH" REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP; MF_00049; -; 1.
InterPro; IPR002302; Leu-tRNAsyntla.
InterPro; IPR002300; TRNA-synt_la.
InterPro; IPR001310; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_l.
InterPro; IPR009008; ValRS_IleRS_edit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE015561; AAN54244.1; -. TIGR; SO1174; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96827 MW;
                                                   Alteromonadaceae; Shewanella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I Similarity 23.6%; 50; Conservative 3
                                                                                                                                                                                                                                                              Shewanella oneidensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52
622
621
                         Shewanella oneidensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              618 6
621 6
859 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome.
                                                                                            SEQUENCE FROM N.A.
                                                                   NCBI_TaxID=70863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 KQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKF--EGDTLV-----NRIELKG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -I- FUNCTION: Catalyzes the formation of 5-methyl-uridine at position 54 (M-5-U54) in all tRNA (By similarity).
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-homocysteine + tRNA containing thymine.
-!- SIMILARITY: Belongs to the RNA M5U methyltransferase family. TrmA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 EKHSFIKKYPKEFYTKDFKLFASKDKHYRTRAELSFYHENDTLFYAMFDPKSKKKYIIEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 IDFKED------GNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20150912; PubMed=10688204; Retley J.M., Churcher C., Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C., Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M., Whitehead S., Barrell B.G.; The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PSO1230; TRMA_1; 1.
PROSITE; PSO1231; TRMA_2; FALSE_NEG.
Transferase; Methyltransferase; tRNA processing; Complete proteome.
207 213 S-ADENOSYLMETHIONINE BINDING (BY
                                                                                                                                                                                                                                                                               Campylobacter jejuni.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
                                                                                                   28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
tRNA (Uracil-5-)-methyltransferase (EC 2.1.1.35) (tRNA(M-5-U54)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY. CEC5328347CEE497 CRC64;
357 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.8%; Pred. No. 6.5; ive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.8%; Score 86;
24.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reveals hypervariable sequences.";
Nature 403:665-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMAP; MF 01011; -; 1.
InterPro; IPR000051; SAM bind.
InterPro; IPR001566; TrmA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL139076; CAB73096.1; -. PIR; G81355; G81355.
                                                                  28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315 B
42276 MW;
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                                                                                                                                                                                                             methyltransferase) (RŪMT)
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315 3
357 AA;
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PSBC\_CYAPA

RESULT 13

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                        GRB14.
                                                                                                                                   RESULT 14
                                                                                                                                                           GRBE
                                                                요
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation-the European Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a alicense agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibbsib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 ------QCFSRYPDHMKQHDFFKSAMPE-GYVQERTIFFKDD-------GN 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 ALMGFIANCFVWFNNTAYPSEFFGPTGPEASQAQAFTFLVRDQRLGANVGSAQGPTGLGK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 YKTRA---EVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIK 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 VNFKIRHNIEDGSVQLADHYQQNTPIGD----GPVLLPDN--HYLSTQSALSKDPNEKRD 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 GHKFSVSGEGEGDATYGKLTLKFICTTGKL-----PVPWPTLVTV-----LSYGV--- 69
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-UTEX LB 555 / Pringsheim;
Loeffelhardt W., Stirewalt V.L., Michalowski C.B., Annarella M.,
Loeffelhardt W., Stirewalt V.L., Michalowski C.B., Annarella M.,
Earley J.Y., Schluchter W.M., Chung S., Newmann-Spallart C.,
Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.;
"The complete sequence of the cyanelle genome of Cyanophora paradoxa:
the genetic complexity of a primitive plastid.";
[In) Schenk H.B.A., Herrmann R., Jeon K.W., Mueller N.E.,
                                                                                                                                                                                                                                                                                                                                                                   "Nucleotide sequence of the cyanelle DNA from Cyanophora paradoxa."; Plant Mol. Biol. Rep. 13:327-332(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- FUNCTION: The 43 kDa protein (p6) is a component of the core of photosystem II. It is a chlorophyll binding protein.
-i- SUBCELLULAR LOCATION: Integral membrane protein. Cyanelle
                                                              01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Photosystem II 44 kDa reaction center protein (P6 protein) (CP43).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00421; PSII; 1.
TIGRFAMs; TIGR01153; psbC; 1.
Photosynthesis; Photosystem II; Thylakoid; Chlorophyll; Cyanelle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotism and Symbiosis, pp.40-48, Springer-Verlag, Heidelberg (1997).
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=UTEX LB 555 / Pringsheim;
Stirewalt V.L., Michalowski C.B., Loeffelhardt W., Bohnert H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.8%; Score 86; DB 1; Length 461;
                                                                                                                                                                                                      Eukaryota; Glaucocystophyceae; Cyanophoraceae; Cyanophora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         461 AA; 50402 MW; 62664E239E13B9C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to the psbB / psbC family
  461 AA
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  PRT;
                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR005869; Photo44.
InterPro; IPR000932; PSIIprot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, U30821; AAA81279.1; -. PIR; T06936; T06936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 21.8%
es 55; Conservative
STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thylakoid membrane.
                                             (Rel. 33, (Rel. 33,
                                                                                                                                                           Cyanophora paradoxa.
                                                                                                                                                                                                                           NCBI_TaxID=2762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schwemmler W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane
                                           01-FEB-1996
PSBC_CYAPA
                                                                                                                                                                                   Cyanelle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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Kasus-Jacobi A., Perdedreau D., Antaan C., Clauser E., van Obberghen E.,
Mauvais-Jarvis F., Girard J., Burnol A.-F.;
"Identification of the rat adapter Grb14 as an inhibitor of insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   July 1980. Chem. 273:26026-26035(1998).

-!- FUNCTION: Interacts with the cytoplasmic domain of the autophosphorylated insulin receptor which is then inhibited. The interaction is mediated by the SH2 domain.

-!- SUBUNIT: Binds to the ankyrin repeat region of TNKL via its N-terminus (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic, associated with the Golgi and endosomes (By similarity).

-!- PTM: Phosphorylated on serine residues (By similarity).

-!- SIMILARITY: Contains 1 PH domain.
-!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Belongs to the GRB7/10/14 family.
                                                                                                                                                                                                                                                                                                        15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Growth factor receptor-bound protein 14 (GRB14 adapter protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CEBC9037E7868EEF CRC64;
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PH.
                                                                                                                                                                                                                                          538 AA
                                                                                                                                                                                                                                              PRT;
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SMART; SM00214; RA; 1.
SMART; SM00214; RA; 1.
SMART; SM00252; SH2; 1.
A PROSITE; PS50003; PH DOMAIN; 1.
R PROSITE; PS50001; RA; 1.
PPOSITE; PS50001; SH2; 1.
PPOSITE; PS50001; SH2; 1.
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ProDom; PD000093; SH2; 1.
218 HMVLLGFVTAAG 229
                                                                 418 HFV-LGFFLFIG 428
                                                                                                                                                                                                                                          STANDARD;
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InterPro; IPR000159; RA
InterPro; IPR000980; SHZ
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Pfam; PF00788; RA; 1.
Pfam; PF00017; SH2; 1.
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Score 85.5; DB 1; Length 538; Pred. No. 12;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313 GPRDLKMLCAEEDQSRNCWVTAIRLLKYGMQLYQNYMHPSQARSACSSQSVSPMRSVSEN 372
                                                                                                             139 GHKLEYNYNSH------GIKVNF---- 166
                                                                                                                                                                        |: : :: | | | | | | 431 LHRSQPWFHHRISRDEAQQLITRQGPVDGVFLVRDSQSNPRTFVLSMSHGQKIKHFQIIP 490
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                            41 GKLTLKFICT-TGKLPVPWPTLVTVLSYGVQCFSRY--PDHMKQHDFFKSAMPEGYVQER
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Gaps
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67;
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Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Last sequence update)
Protective surface antigen D15 precursor (80 kDa D15 antigen)
(D-15-Ag) (Outer membrane protein D15).
Bacteria: protein
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PROTECTIVE SURFACE ANTIGEN D15.
; 51BFDB2036801A14 CRC64;
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-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SIMILARITY: Belongs to the surface antigen D15 family.
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Indels
 70;
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Best Local Similarity 22.4%; Pred. No. 19;
Matches 49; Conservative 28; Mismatches
 Mismatches
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InterPro; PR000184; Bac_surfAg_D15.
Pfan; PF01103; Bac surface Ag; 1.
Antigen; Outer membrane; SIgnal.....
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Infect. Immun. 65:3701-3707(1997).
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MEDLINE=97427952; PubMed=9284140;
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Pseudomonadaceae; Azotobacter.
NCBI_TaxID=354;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Green fluorescence protein.
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    Azotobacter vinelandii
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                          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                    OM protein - protein search, using sw model
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Q8GHE4
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_mammal:*
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sp_bacteriap:*
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sp_bacteria:*
sp_fungi:*
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sp_human:*
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PRINTS, PR01229, GFLUORESCENT.
ProDom, PD013756; Green_fl_pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonadaceae; Azotobacter
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Conservative
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01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25, Green fluorescence protein.
                                                                                                                          Pseudomonadaceae; Azomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Azotobacter vinelandii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
es 231; Conserv
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                                                                                        Azomonas agilis.
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                                                                                                                  Bacteria;
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                                                                            121 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
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  61 VTTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                  NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
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                                                                                                                                          182 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
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Histopiology 0:0-0:(1996).

Histopiology 0:0-0:(1996).

Histopiology 1: Preneway pathways; IEA.

InterPro; IPR009017; GFP like.

InterPro; IPR00786; Green_fl_protein.
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Cormack B.P., Valdivia R.H., Falkow S.;
"FACS-optimized mutants of the green fluorescent protein (GFP).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aequorea victoria (Jellyfish).
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=6100;
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Brown A.J.P.;
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Pred. No. 1.7e-96;
2; Mismatches 5; Indels
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26840 Mw; A28622809A9DEA60 CRC64;
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01-MAF.-2003 (TrEMBLrel. 23, Created)
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PRINTS; PR01229; GFLUORESCENT.
Probom; PD013756; Green fl prc
SEQUENCE 238 AA; 26840 MW;
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01-FEB-1997
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VIVLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cocurrence of green fluorescence protein in diazotrophic bacteria "Occurrence of green fluorescence protein in diazotrophic bacteria Azomonas and Azotobacter.";
Submitted (NOV-2000) to HEBEL/GenBank/DDBJ databases.
EMBL; AF324405; AAN86137.1; -.
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IPR0090786; Green_fl_protein.
PF01353; GFP; 1.
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Koranyi P., Berenyi M., Burg K.;
"Occurrence of green fluorescence protein in diazotrophic bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                           Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
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26887 MW; E0E1616BD2AF6188 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green_fl_protein; 1.
SEQUENCE 238 AA; 26902 MW; 15FE9B9C5B4F6B89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
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97.1%; Pred. No. 2.5e-96;
iive 2; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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61 VITFSYGVQCFSRYPDHMKQHDFLKSAMPEGYVQERIIFYKDDGNYKTRAEVKFEGDTLV 120
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STRAIN=GFPAM19uv;
Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M., Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aeguoreidae; Aeguorea.
NCBI_TaxID=6100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aequorea macrodactyla.
Bukaryota; Metazoa; Chidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 93.1%; Score 1185; DB 5; Length 238; Best Local Similarity 92.9%; Pred. No. 2.8e-92; Matches 221; Conservative 7; Mismatches 10; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watkins J.N., Campbell A.K.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; X83960; CAAS8790.1; -.
PIR; JS0692; JQ1514.
HSSP; P42212; 1BFP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              macrodactyla.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AR495431; AAL33916.1;
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009101; GFP like.
InterPro; IPR000786; Green_fl_protein.
Fign; PF0153; GFP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 AA; 26867 MW; BD4648262D8EABD4 CRC64;
                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IPR000786; Green_fl_protein.
Pfam; PF01353; GFP; 1.
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                                                                                                                                                                                                                                          Aequorea victoria (Jellyfish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
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                                                                                                                                                                      1 MSKGBELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLILTFICTTGKLPVPWPTL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
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                                                                                                                  2 VSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
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                                          Gaps
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Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=6100;
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                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; X83959; CAA58789.1; -.
PIR; 305692; JQ1514.
HSSP; P42212; 1GFL.
GO, GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IPR000786; Green_fl_protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
97.1%; Pred. No. 3e-96;
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ProDom; PD013756; Green fl protein; 1.
NON TER 238 238
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01-OCT-2003 (TrEMBLrel. 25, Last ann
Green fluorescent protein (Fragment)
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                                  Matches 231; Conservative
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Best Local Similarity
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OBWTC4
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Bukaryvta; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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                                                                                                                               84.8%; Score 1080; DB 5; Length 238; 81.9%; Pred. No. 2.2e-83; ive 20; Mismatches 23; Indels (
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                            ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 27015 MW; 6B8FD75E88926903 CRC64;
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae, Aequorea.
NCBI_TaxID=147615;
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF495-433; AAL33918.1; -.
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR00911; GFP like.
InterPro; IPR000786; Green_fl_protein.
Pfan; PF01353; GFP; 1.
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Bukaryota; Metazoa; Chidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 238;
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF435427; AAL33912.1; -
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP_11ke.
InterPro; IPR0090786; Green_fl_protein.
Pfam; PR01329; GFPP; 1.
PRINTS; PR01229; GFLUORESCENT.
PRODOM; P013756; Green_fl_protein; 1.
SEQUENCE 238 AA; 26997 WW; SF80A192173CB84D CRC64;
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Submitted (OCT-2013) to the EMBL/GenBank/DDBJ databases.
EMBL; AF43-429; AAL3314.1;
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR000786; Green_fl_protein.
Pfam; PF01353; GFP; II
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ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 27047 MW; 5F80A18FA1E7C84D CRC64;
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Last sequence update)
Last annotation update)
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84.1%; Score 1070; DB 5;
Best Local Similarity 81.1%; Pred. No. 1.5e-82;
Matches 193; Conservative 20; Mismatches 25;
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84.0%; Score 1069; DB 5;
Best Local Similarity 81.1%; Pred. No. 1.8e-82;
Matches 193; Conservative 20; Mismatches 25;
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Li S.J., Xia N.S.;
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SEQUENCE FROM N.A.
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DT 01-MA
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121 NRIELKGMDFKEDGNILGHKLEYNFNSHNYYIMPDKANNGLKYNFKIRHNIEGGGVQLAD 180
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Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
MCBI_TaxID=147615;
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF433429. AAL33913.1;
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR000786; Green_fl_protein.
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PRINTS; PR01229; GFLUORESCENT.
Probom; PD013756; Green fl_protein; 1.
SEQUENCE 238 AA; 27031 MW; SF80A19C19DC584D CRC64;
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84.0%; Score 1069; DB 5;
Best Local Similarity 81.1%; Pred. No. 1.8e-82;
Matches 193; Conservative 20; Mismatches 25;
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Eukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Leptomedusae,
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Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
                                                                  Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Li S.J., Xia N.S.; "Colorful mutants of green fluorescent protein from Aequorea
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83.7%; Score 1065; DB 5; Length 238;
Best Local Similarity 81.9%; Pred. No. 4e-82;
Matches 195; Conservative 17; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25; Indels
                                                                                                                                            macrodactyla.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF435430; AAL33915.1; -.
GO; GO: 0000691; P:energy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR00786; Green_fl_protein.
Pfam; 3P01333; GFP; 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF415432; AAL33917.1; -. GO, GO:0006091; P:energy pathways; IEA. InterPro; IPR009017; GFP like. InterPro; IPR009076; Green_fl_protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 27018 MW; 75521EA5534E573A CRC64;
                                                                                                                                                                                                                                                                                                                   PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl protein; 1.
SEQUENJE 238 AA; 27002 WW; BD5BA2982264C018 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                  83.8%; Score 1067; DB 5;
81.1%; Pred. No. 2.7e-82;
iive 20; Mismatches 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Orange fluorescent protein
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 81.1'
Matches 193, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aequoreidae; Aequorea.
NCBI_TaxID=147615;
[1]
SEQUENCE FROM N.A.
STRAIN=GFPxm191uv;
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Submitted (OCT-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 NRIELKGMDFKEDGNILGHKLEYNFNSHNVYIMPDKANNGLKVNFKIRHNIEGGGVQLAD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYOONTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSKGBELFTGVVPILVELDGDVHGHKFSVRGEGEGDADYGKLEIKFICTTGKLPVPWFTL
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Bukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
Faviina; Faviidae; Montastraea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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19.8%; Score 252.5; DB 5;
Best Local Similarity 31.1%; Pred. No. 2e-13;
Matches 64; Conservative 43; Mismatches 82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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01-DEC-2001
01-DEC-2001
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SEQUENCE
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Q95UA7
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61

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                  Copyright
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OM protein - protein search, using sw model

June 21, 2004, 15:41:49; Search time 47.1111 Seconds (without alignments) 1433.395 Million cell updates/sec Run on:

US-09-887-784-222A

1 MVSKGEELFTGVVPILVELD......VLaGFVTAAGITLGMDELYK 239 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1586107 seqs, 282547505 residues Searched:

Total number of hits satisfying chosen parameters:

1586107

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% .
Maximum Match 100%
Listing first 45 summaries

A_Geneseq_29Jan04:* 1: genesern1000~ Database

geneseqp1980s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2001s:*
geneseqp2002s:*
geneseqp2003bs:*
geneseqp2003bs:* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

		de			SUMMARIES	
	Score	Query	Query Match Length	DB	ID	Description
-1	1269	9.66	239	เร	AAE17518	Aae17518 Enhanced
~	1269	99.6	363	9	ABR40352	Abr40352 Human ami
٣	1269	99.6	893	4	AAG65781	Aag65781 Amino aci
4	1269	99.6	1132	4	AAG65782	Aag65782 Amino aci
Ŋ	1261	99.0	239	Ŋ	AAE17517	Age17517 Enhanced
9	1258	98.7	239	٣	AAB22882	Aab22882 Enhanced
7	1258	98.7	239	m	AAY54349	Aay54349 Amino aci
80	1258	98.7	239	m	AAY79584	
6	1258	98.7	239	4	AAB50804	Aab50804 Jellyfish
10	1258	98.7	239	4	AAB85900	Aab85900 A. victor
11	1258	98.7	239	4	AAB31171	Aab31171 Amino aci
12	1258	98.7	239	S	AAG66198	Aag66198 A. victor
13	1258	98.7	239	S	ABG94444	Abg94444 Protease
14	1258	98.7	239	ß	AAE14599	Aae14599 Aequorea
15	1258	98.7	239	9	AAE34958	
16	1258	98.7	239	9	AAG79829	Aag79829 Green flu
17	1258	98.7	239	9	ABR83616	Abr83616 Green flu
18	1258	98.7	239	9	ADA38074	. Ada38074 Aequorea
19	1258	98.7	239	7	ABU63204	Abu63204 Aequorea
20	1258	98.7	239	7	ADC18358	
21	1258	98.7	239	7	ABW00914	Abw00914 Aequorea
22	1258	98.7	239	7	ADE28570	Ade28570 Enhanced
23	1258	98.7	246	7	ABM79011	
24	S	98.7	248	ហ	AAG68319	Aag68319 Jellyfish
25	1258	98.7	259	ß	AAU99804	Aau99804 Biomembra

Claim 9; Page 37; 41pp; English.

mutation.

Wild-type Biomembra Biomembra Biomembra	Biomembra Biomembra Green flu	EGFP-MODC EGFP-MODC EGFP/ hum	17.78	Caspase-3 Recombina EGFP/DRM	HUB1-GFP GFP mutan RUB1-GFP
Aaw97451 Aau99803 Aau99802 Aau99800	Aau99801 Aau99807 Aay50142	Aab24252 Aau10888 Ade28562	Ade28568 Ade28568 Ade28566 Aab22860	Aay79638 Abg94422 Aay42181	Abr83620 Aay54359 Abr83621
AAW97451 AAU99803 AAU99802 AAU99800	AAU99801 AAU99807 AAY50142	AAB24252 AAU10888 ADE28562 ADE28564	ADE28568 ADE28566 AAB22860	AAY79638 ABG94422 AAY42181	ABR83620 AAY54359 ABR83621
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265 268 270 272	273 280 281	281 281 286	2990 290 294	294 308	320 323 323
98.7 98.7 98.7	98.7 7.86 7.86 7.86	98.7.7.89	98.7 98.7 98.7	98.7 98.7 98.7	98.7 98.7 98.7
1258 1258 1258 1258	1258 1258 1258	1258	1258 1258 1258 1258	1258 1258 1258	1258 1258 1258
26 27 28 29	310		3 3 3 4 6 9 6 9 6 9 6 9 9 9 9 9 9 9 9 9 9 9 9	0 4 4 0 1 2	4 4 4 6 4 3

#### ALIGNMENTS

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Novel fluorescent protein in in vitro assay for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution, has a green fluorescent protein with F64L and E222G
                                                                                                                                                                                                                                                                /note= "Wild type Glu substituted with Gly; This corresponds to position 222 in the wild type protein"
                                                                                                                                                                                                               /note= "Wild type Phe substituted with Leu; This
corresponds to position 64 in the wild type protein"
Misc-difference 223
                                                                                                                          Jellyfish, green fluorescent protein, GPP, protein redistribution, cellular function, genetic reporter; mutant, Stoke's shift, mutein.
                                                                                                 Enhanced F64L-E222G jellyfish green fluorescent protein mutant
                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thastrup O;
                         AAE17518 standard; protein; 239 AA.
                                                                                                                                                                                                                                                                                                                                                                                19-JUN-2000; 2000DK-0000953.
20-JUN-2000; 2000US-0212681P.
10-MAY-2001; 2001DK-00000739.
10-MAY-2001; 2001US-0290170P.
                                                                                                                                                                                                                                                                                                                                                        18-JUN-2001; 2001WO-EP006848
                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pagliaro L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-098224/13.
N-PSDB; AAD28163.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (BIOI -) BIOIMAGE AS.
                                                                                                                                                                 Aequorea victoria.
                                                                                                                                                                                                     Key
Misc-difference 65
                                                                                                                                                                                                                                                                                                        WO200198338-A2
                                                                         22-APR-2002
                                                                                                                                                                                                                                                                                                                                 27-DEC-2001
                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bjorn SP,
                                                AAE17518;
RESULT 1
AAE17518
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fluorescent protein (GFP) or its analogue. The GFP containing mutations at F64L and E222G has a bigger compared to other GFP's making it very suitable for high throughput screening due to better resolution. The fluorescent protein is useful in invitro assays for measuring protein kinase activity or dephosphorylation activity, or for measuring protein kinase activity or dephosphorylation activity, or for measuring protein cafferibution. The fluorescent protein is useful in studying cellular functions in living cells; as protein tags in transgenic animals, living and fixed cells; organelle tags, secretion marker and genetic reporter. The fluorescent protein is also useful as a cell or organelle integrity and as a marker for changes in cell morphology, as transfection marker, and as a marker to changes in cell morphology, stransfection marker, and as a marker to be used in combination with fluorescence activated cell sorting (FACS). The novel proteins can also be used as reporters to monitor live or dead biomass of organisms, such as fungi. The fluorescent fusions for performing transposon vector mutagenesis and as a reporter fusions for performing transposons encoding the fluorescent protein are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for screening promoters and for tagging plasmids and chromosomes. The fluorescent protein engineered into the genome of a phage is useful for designing diagnostic tool. The present sequence is a DNA encoding enhanced F64L-E222G jellyfish green fluorescent protein (GFP) mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MVSKGEBLFTGVVPILVBLDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPMPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MVSKGEELFTGVVP1LVELDGDVNGHKFSVSGEGEGDATYGKLTLKF1CTTGKLPVPWPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 239;
               invention relates to a fluorescent protein derived from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1269; DB 5;
Pred. No. 4.6e-122;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human amino acid sequence SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABR40352 standard; protein; 363 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.68;
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11-OCT-2001; 2001US-0328896P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2002; 2002WO-DK000651
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Best Local Similarity
Marches 238; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 239 AA;
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Novel cell for identifying modulators of protein interaction, contains a first conjugate comprising anchor protein, second conjugate having type B interactor protein and third conjugate with detectable group.
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                                                                                                                                                       The invention relates to a novel cell, comprising three heterologous conjugates (HC), a first HC (HCI) comprising an anchor protein that specifically binds to an internal structure within the cell conjugated tan interactor protein (TP) of type A, a second HC (HC2) comprising IP of type B conjugated to a first protein of interest, and a third HC (HC3) comprising a second protein of interest conjugated to detectable group. The cell is useful for detecting if a compound disrupts or induces the interaction between two intracellular proteins. The cell is also useful for screening compounds that modulate the interaction between two intracellular proteins. The present sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDE4; central nervous system; antiinflammatory; cytostatic; nootropic; autoimmune; ischemic; osteopathic; GFP; green fluorescent protein; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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                                                                                                                                                                                                                                                                                                                                                                                             Score 1269; DB 6;
Pred. No. 8.6e-122;
0; Mismatches 1;
                                                                                                                              Disclosure; Page 112-113; 118pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG65781 standard; protein; 893 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-APR-2000; 2000DK-0000651.
29-MAY-2000; 2000DK-0000849.
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                                                                                                                                                                                                                                                                                                                                                                                                 99.6%;
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Matches 238; Conservative
             2003-430211/40
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                             N-PSDB; ACC72604
                                                                                                                                                                                                                                                                                                                                                                  Sequence 363 AA;
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Thastrup O, Almholt DC;

Bjorn SP,

Scudder KM,

Praestegaard M;

BR,

(BIOI-) BIOIMAGE AS

WPI; 2001-611727/70. N-PSDB; AAI66853.

11-APR-2001; 2001WO-DK000264. 17-APR-2000; 2000DK-00000651. 29-MAY-2000; 2000DK-00000849.

25-OCT-2001.

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The invention relates to determining, if a compound, is a dislocator of PDE4. The method comprises testing if the compound removes PDE4 spots, which may optionally be induced by a Rolipram-like reference compound, and testing if it inhibits the catalytic activity of the PDE4, where the compound is a dislocator of PDE4, if it removes PDE spots and if it does not inhibit the catalytic activity of PDE4. The method is useful for identifying compounds useful for the treatment of diseases of the central nervous system such as depression and for the treatment of inflammatory disease, respiratory diseases, chronic obstructive pulmonary disease.

(COPD), including asthma, chronic bronchitis, pulmonary disease conductoric shock, toxic shock syndrome, systemic lupus erthematosis, postiasis, bone resorption diseases, reperfusion injury, cancer and HIV infection. The use of a reagent that can mimic or reverse the effect of the compound with affinity for the catalytic site on intracellular distribution of the PDE for the preparation of a medicament. The present sequence represents the amino acid sequence of a HSPDE4A1-E22G fusion
                                                                                                                                          Determining if a compound is a dislocator of PDE4 for identifying compounds for treating CNS and inflammatory disease comprises identifying compounds which remove PDE4 spots.
Bjorn SP, Thastrup O, Almholt DC;
                                                                                                                                                                                                                                           Example 1; Page 156-160; 160pp; English.
Scudder KM,
                                                                     WPI; 2001-611727/70
                                                                                                 N-PSDB; AAI66852
                         Praestegaard M;
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Sequence 893 AA;

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LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                               1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                 Gaps
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 Score 1269; DB 4; Length 893;
Pred. No. 3.2e-121;
0; Mismatches 1; Indels
Query Match
Best Local Similarity 99.6%;
Matches 238; Conservative (
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Amino acid sequence of HSPDE4A4-E222G fusion protein. AAG65782 standard; protein; 1132 AA 07-JAN-2002 (first entry) AAG65782; RESULT

PDE4; central nervous system; antiinflammatory; cytostatic; nootropic; autoimmune; ischemic; osteopathic; GFP; green fluorescent protein; fusion protein.

Aequorea victoria. Homo sapiens

WO200179526-A2

Enhanced F64L jellyfish green fluorescent protein mutant.

22-APR-2002 (first entry)

XEXEXEX

AAE17517 standard; protein; 239 AA

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The invention relates to determining, if a compound, is a dislocator of PDE4. The method comprises testing if the compound removes PDE4 spots, which may optionally be induced by a Rollpram-like reference compound, and testing if it inhibits the catalytic activity of the PDE4, where the compounds useful fit it inhibits the catalytic activity of PDE4. The method is useful for identifying compounds useful for the treatment of diseases of the central nervous system such as. depression and for the treatment of inflammatory disease such as joint inflammation, Crohn's disease, inflammatory bowel disease, respiratory diseases, chronic obstructive pulmonary disease.

(COPD), including asthma, chronic bronchitis, pulmonary emphysema, endotoxic shock, toxic shock syndrome, systemic lupus erthematosis, psoriasis, bone resorption diseases, reperfusion injury, cancer and HIV includiound with affinity for the catalytic site on intracellular distribution of the PDE for the preparation of a medicament. The present sequence represents the amino acid sequence of a HSPDE4A4-E222G fusion
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                                                                                                                                                                                                                                                                                         Determining if a compound is a dislocator of PDE4 for identifying compounds for treating CNS and inflammatory disease comprises identifying compounds which remove PDE4 spots.
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                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 162-167; 160pp; English.
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Matches 238; Conservative
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181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLAGFVTAAGITLGMDELYK 239

AAB22882 standard; protein; 239 AA

AAB22882

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The invention relates to a fluorescent protein derived from green fluorescent protein (GFP) or its analogue. The GFP containing mutations at F64% and E2226 has a bigger compared to other GFP's making it very suitable for high throughput screening due to better resolution. The fluorescent protein is useful in invitro assays for measuring protein kinase activity or dephosphorylation activity, or for measuring protein cedistribution. The fluorescent protein is useful in studying cellular functions in living cells; as protein tags in transgenic animals, living and fixed cells; organelle tags, secretion marker and genetic reporter. The fluorescent protein is also useful as a cell or organelle integrity marker, a marker to be used in combination with fluorescence activated cell sorting (FACS). The novel proteins can also be used as reporters to monitor live or dead biomass of organisms, such as fungi. The fluorescent protein is also useful as markers in transcriptional and translational fusions for performing transposon vector mutagenesis and as a reporter consecut protein is also useful as markers in transcriptional and translational fusions for performing transposons encoding the fluorescent protein are useful for escenting plasmids and chromosomes. The fluorescent protein engineered into the genome of a phage is useful consulational engineered into the genome of a chance for it is also useful as ensured for tagging plasmids and chromosomes. The fluorescent protein engineered into the genome of a phage is useful confident.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel fluorescent protein in in vitro assay for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution, has a green fluorescent protein with F64L and E222G
                                                                                                                                                                                /note= "Wild type Phe substituted with Leu; This corresponds to position 64 in the wild type protein"
Jellyfish; green fluorescent protein; GFP; protein redistribution; cellular function; genetic reporter; mutant; Stoke's shift; mutein.
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                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thastrup 0;
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20-JUN-2000; 2000US-021268IP.
10-MAX-2001; 2001DK-0000739.
10-MAX-2001; 2001US-0290170P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BIOI-) BIOIMAGE AS
                                                                  Aequorsa victoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAD28162
                                                                                                                                                             Misc-difference
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                                                                                                                                                                                                                                                                                                   27-DEC-2001.
                                                                                             Synthetic.
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The invention relates to systems, methods and reagents for cell-based screening or detection of compounds which affect particular biological functions. The methods of the invention utilise fluorescent biodetector concerns. The methods of the invention utilise fluorescent biodetector molecules which, when acted on by a compound of interest, cause an alteration in the cellular distribution of at least the fluorescent concerns. The cytoplasm, but on stress activation translocate to the nucleus. In concern concerns but on stress activation translocate to the nucleus. In canother embodiment biodetector proteins can be used to detect protesse activity. Such protease biodetector fusion proteins comprise one or more fluorescent proteins, a recognition signal which is cleaved by the components may be components of a single protein signal relater two components may be from heterologous sources. Due to the because or may be from heterologous sources. Due to the collular collular localisation signal, the biodetector protein is localised to a particular region of the cell. Once acted on by the protease of interest, the localisation signal, the biodetector protein is localised to a particular region of the cell. Once acted on by the protease of interest, the fluorescent protein is cleaved from the localisation sequence of a second localisation signal attached to the fluorescent protein enables the fluorescent protein of the protease recognition sequence. The compartment after cleavage of the protease recognition can be detected using imaging methods with a high degree of spatial resolution. The methods and
                                                                                                                                                      Biodetector protein; fusion protein; recognition site; cellular targetting sequence; cellular localisation; fluorescent protein; protease activity detection; toxin detection; cellular stress detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Automated cell-based characterization of toxin by contacting cells containing luminescent reporter molecules with test substance and analyzing optically.
                                                                                                            Enhanced green fluorescent protein (EGFP), SEQ ID NO:46.
                                                                                                                                                                                                                          drug discovery; cell based screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 11; Fig 29A; 336pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0122152P.
99US-0123399P.
99US-00352171.
                                                                                                                                                                                                                                                                                                                                                                                                                                25-FEB-2000; 2000WO-US004794.
                                                                    10-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Giuliano KA, Kapur R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CELL-) CELLOMICS INC.
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                                                                                                                                                                                                                                                                          Aequorea victoria
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                                                                                                                                                                                                                                                                                                                                           WO200050872-A2.
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08-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                      31-AUG-2000.
                                                                                                                                                                                                                                                                                               Synthetic.
6.1 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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Length 239; Indels

Score 1261; DB 5; Pred. No. 3.1e-121; 0; Mismatches 2;

99.0%;

237; Conservative

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Local Similarity

Query Match Best Loca Matches .

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biosensors of the invention can be used to investigate a wide range of cellular activities and to screen compounds which modulate these extivities. Biosensors containing a recognition site for caspase, for example, may be used for the screening of compounds which modulate apoptosis, while biosensors containing other protease recognition sites may be used for the detection of proteolytic toxins (such as anthrax lethal factor). The method provides improved target validation and candidate compound optimisation by combining many cell screening formats with fluorescence-based molecular reagents and computer-based feature extraction, data analysis and automation, resulting in increased quantity and speed of data collection and faster evaluation of drug candidates. Sequences AAB22881-B22885 represent fluorescent proteins which may used as components of biosensor fusion proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                               61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of the mutant green fluorescent protein EGFP
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                                                                                                                                                                                                                                                                                       Length 239;
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                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                    Score 1258; DB 3;
Pred. No. 6.3e-121;
1; Mismatches 2;
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98US-00172063
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UNIV OREGON STATE.
                                                                                                                                                                                                                                                                                                                        236; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                     Sequence 239 AA;
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13-OCT-1998;
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protein based on the Aequorea green fluorescent protein (GFP). The emission intensity changes as pH varies between 5 and 10 of the present protein are novel. The functional engineered fluorescent proteins show reversible changes in fluorescence over physiological pH ranges. They can be used for determining the pH of samples and cells. The polymucleotides can also be used to produce transgenic animals. The polymucleotides pH sensors can be delivered to cells in the form of polymucleotides encoding the protein sensor fused to a targeting signal. The targeting signal incots the expression of the protein sensors to restricted cell locations. This makes it possible to measure the pH of a precisely defined cellular region or organelle
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                                                                     New functional engineered green fluorescent proteins, used for measuring the pH in biological samples and cells.
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                                                                                                                                           sequence represents a functional engineered fluorescent
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                                                                                                                                                                                                                                                                                                                                                                                              98.7%; Score 1258; DB 3;
98.7%; Pred. No. 6.3e-121;
iive 1; Mismatches 2;
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                                                                                                                          Disclosure; Page 9; 89pp; English
Wachter RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY79584 standard; peptide; 239
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99US-0136078P.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 236; Conservative
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Tsien RY, Llopis J,
                            WPI; 2000-116540/10.
N-PSDB; AAZ45642.
                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGFP signal domain
                                                                                                                                                                                                                                                                                                                                                                  Sequence 239 AA;
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26-MAY-1999;
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17-MAY-2000; 2000WO-US013684.
                                                                                                                       (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                        Baird GA;
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                                                   21-MAY-1999;
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                                                                                                                                                                                                                                          The present sequence is that of the EGFP signal domain, which can be included in novel recombinant protease biosensors (PBS) of the invention. The present segments a farst domain (see AAY79579-87) comprising at least 1 detectable polypeptide signal such as the present sequence; a second domain (see AAY79588-622) comprising at least 1 protease recognition site; and a third domain (see AAY7963-37) comprising at least 1 reactant target sequence. A recombinant nucleic acid (see AAA27627-43) encoding the PB, an expression vector, and a cand (see AAA27627-43) encoding the PB, an expression vector, and a candentically engineered host cell are also claimed. A claimed method for identifying compounds that modify protease activity in a cell involves contacting a host cell that possesses the recombinant PB with a test compound, and determining the PB distribution in the host cell, where changes in the distribution of the PB are correlated with modification of protease activity by the test compound. Claimed kits for identifying compounds that modify protease activity in a host cell include the compounds that modify protease activity in a host cell include the compounds that modify protease activity in a host cell include the compounds that modify protease activity in a host cell include the host call include the compounds that modify protease activity in a host cell include the host call include the compounds that modify protease activity in a lost cell include the compounds that incleic acid, or the recombinant PB, or the vector, or the host cell. The PB is useful in high content screens to detect in vivo activity to a claim of activity by activity by activity by activity by activity by activity by activity by activity by activity by activity by activity by activity by activity by activity by activity by activity by activity by activity by activity by activity by activity by activity by activity by activity by activity by activity by activity by activity by activity by activity by activity by activity by activity by activ
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                                                                                                Recombinant nucleic acid encoding a protease biosensor useful for fluorescence based cell and molecular biochemical assays for drug discovery comprising three operably linked nucleic acid sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.7%; Score 1258; DB 3;
98.7%; Pred. No. 6.3e-121;
iive 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cleavage of a known recognition motif
                                                                                                                                                                                                    Claim 14; Fig 29A; 218pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB50804 standard; protein; 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jellyfish GFP mutant EGFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236; Conservative
                                 WPI; 2000-365644/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                          N-PSDB; AAA27573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 239 AA;
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Matches
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The present sequence is a fluorescnet protein used in the construction of a fluorescent protein indicator. The indicator comprises a sensor polypeptide that is responsive to a chemical, biological, electrical or physpiological parameter, and a fluorescence protein functional group. The sensor polypeptide is operatively inserted into the fluorescent moiety. The fluorescent indicator is useful for detecting the presence of a response inducing member in a sample. The method involves contacting the sample with the indicator and detecting a change in fluorescence, in which a change is indicative of the effect of the parameter on the sensor polypeptide. The novel fluorescent proteins are advantageous due to their transfer)-based sensors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VNRIELKGIDFKEDGNILGHKEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                                                                                                                                                                                                                                                 Novel fluorescent proteins comprising a sensor protein inserted into them, useful for measuring the response of a sensor biological, chemical, electrical or physiological parameter in vivo or in vitro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLAGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWVLBFVTAAGITLGMDELYK 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MVSKGEBLFTGVVPILVBLDGDVNGHKRSVSGEGEGBATYGKLTKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A. victoria green fluorescent protein (GPP) and linker sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 1258; Score 1258; DB 4; Length 239; Local Similarity 98.7%; Pred. No. 6.3e-121; les 236; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB85900 standard; protein; 239 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 24; 94pp; English.
99US-00316919.
99US-00316920.
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                                                                                                                                                                                                                 The invention provides melanin concentrating hormone (MCH) receptor (MCHR) chimeric and fusion proteins. The MCHR chimeric proteins comprise MCHR polypeptide regions from different species. The MCHR fusion protein comprise MCHR polypeptide region and a fluorescent polypeptide region joined directly, or via a linker, to the carboxy side of the MCHR polypeptide region. The MCHR fusion proteins can be expressed by standard recombinant methodology. MCH action promotes feeding (orexigenic) and up regulation of MCH activity stimulates food intake. The present sequence represents a A. victoria green fluorescent protein (GFP) and a linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                              1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                                                                                                                                                 1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                               Fusion proteins comprising melanin concentrating hormone receptor peptides and fluorescent proteins, useful for identifying appetite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Growth rate, death rate, reporter gene, luminescent protein, fluorescent product, luciferase, green fluorescent protein, GFP.
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                                                                                                                                                                                                                                                                                                                                                                     Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of a green fluorescent protein (GFP).
                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                    98.7%; Score 1258; DB 4;
98.7%; Pred. No. 6.3e-121;
cive 1; Mismatches 2;
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                                                                                                                                                                                            Claim 2; Page 14; 71pp; English.
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                     14-MAR-2001; 2001WO-US008071
                                            15-MAR-2000; 2000US-0189698P
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                                                                                                                                                                                                                                                                                                                                                                                            236; Conservative
                                                                 (MERI ) MERCK & CO INC
                                                                                                               WPI; 2001-565791/63.
                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                           N-PSDB; AAH47304
                                                                                                                                                                                                                                                                                                                                              Sequence 239 AA;
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20-SEP-2001
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                                                                                        Marsh DJ;
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                                                                                                                                                                                                                                                                                                                                                                     Query Match
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death rate of a micro-organism within a predetermined time period in a desired environment. The method comprises introducing at least two reporter genes encoding luminescent and/or fluorescent products into the micro-organisms, incubating the micro-organism within the desired environment, and detecting luminescence and/or fluorescence after a predetermined time period. Use of two different markers within a micro-organism enables the differentiation between growth and death rates. The method is used to assess the growth rate and death rate of a micro-organism within a predetermined time period in a dealred environment. The present sequence represents a green fluorescent protein (GFP), and is encoded by a plasmid which encodes luminescent and fluorescent proteins, and is used in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specification describes a method for assessing the growth rate and
                                                                                                                                                                                                                                                                                                                               Assessing growth and death rates of a micro-organism in a desired environment, by introducing 2 reporter genes encoding luminescent and fluorescent products and detecting luminescent fluorescence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 98.7%; Score 1258; DB 4; Length 239; Best Local Similarity 98.7%; Pred. No. 6.3e-121; Matches 236; Conservative 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 27; 32pp; English
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07-JUN-1999; 99FI-00001296.
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                                                                                                                                                                                                                                  2001-061737/07
                                                                                                                                                                 Lilius E, Virta M;
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                                                             (LILI/) LILIUS E.
(VIRT/) VIRTA M.
                                                                                                                                                                                                                                                                    N-PSDB; AAC86954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 239 AA;
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01-DEC-1999;
          29-OCT-1999;
                                                                      Giuliano K,
                                                                                                                                                     identifiers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
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                                       (GIUL/)
(KAPU/)
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AAE14599
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                                                                                                                                                                                                                                                                                                                                                                                         VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                The invention relates to a gene encoding proteins having cyan-green fluorescence characteristic and having a function of showing stable fluorescence characteristic in acid region. A method for the preparation of a cyan-green fluorescent protein is provided which involves a transformant transformed by a recombinant vector comprising the gene, where the transformed by a recombinant vector comprising the gene, culture. The present sequence represents the A. victoria green fluorescent protein (EGFP)
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                                                                                                                                                                                                                                                                                                                                                                                                              DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLAGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                           LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL
                                                                                                                                                                                                                                                                                                          MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                       1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detection, classification, identification, toxin detection, protease, ADP-ribosylating toxin, cytotoxic phospholipase, exfoliative toxin; toxic threat agent.
                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                               Length 239;
                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                               98.7%; Score 1258; DB 5; 98.7%; Pred. No. 6.3e-121;
                                                                                         gene encoding cyan-green fluorescent protein
                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protease biosensor signal sequence #6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG94444 standard; protein; 239 AA
                                                                                                              Example; Page 14; 20pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-00810983.
98US-00031271.
99US-0123152P.
99US-013329P.
99US-00352171.
04-AUG-2000; 2000JP-00237165
                     04-AUG-2000; 2000JP-00237165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-00513783
                                         (RIKA ) RIKAGAKU KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                        Local Similarity 98.7
les 236; Conservative
                                                             WPI; 2002-299190/34
                                                                        N-PSDE; ABL40628
                                                                                                                                                                                                                             Sequence 239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAE-1999;
12-JUL-1999;
31-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-FEE-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6416959-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-FEE-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG94444;
                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                        121
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                                                                                                                                                                                                                                                                     Matches
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The invention describes methods of automated detection, classification
and identification comprising treating cells containing luminescent
creporter molecules (I) in array of locations with a test substance, where
(I) are detectors, classifiers or identifiers, imaging cells in each
clocation to obtain luminescent signals and converting optical information
into digital data to interpret presence of toxins in the test substance.
The method are useful for detection of toxins chosen from proteases, ADP-
ribosylating toxins, cytotoxic phospholipases, and exfoliative toxins.
Three classes of cell-based luminescent reporter molecules such as
detectors, classifiers and identifiers are described and serve as
reporters of toxic threat agents. The first two levels of
characterisation ensure a rapid readout of toxin class without
sacrificing the ability to detect many new mutant toxins or dissect
several complex mixtures of known toxins. This is the amino acid sequence
of a protease biosensor related signal sequence used in the cell-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLAGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LVITLITYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutagenesis; enhanced green fluorescent protein; EGFP; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPMPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           Automated cell-based toxin detection, classification, and/or identification by treating cells involves use of three classes of luminescent reporter molecules such as detectors, classifiers or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               °,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aequorea victoria enhanced green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1258; DB 5;
Pred. No. 6.3e-121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 10; Fig 29A; 214pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ä
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99US-00398965.
99US-00430656.
99US-0168408P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.7%;
98.7%;
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Best Local Similarity 98.7
Matches 236; Conservative
                                                                                                                                                                                                                                                          Kapur R;
                                                                                                                                                                                                                                                                                                                             2002-634730/68,
                                                                                                                                                 GIULIANO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aequorea victoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 239 AA;
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mutation and a phosphorylated 5'-terminus are annealed to a template DNA mutation and a phosphorylated 5'-terminus are annealed to a template DNA and then subjected to an elongation reaction using a thermostable high-fidelity DNA polymerase, after which the phosphorylated 5'-terminus and then subjected terminus are ligated by means of a thermostable DNA ligase the elongated terminus are ligated by means of a thermostable DNA ligase to synthesise a circular DNA containing the primers, a digestion in which the step of DNA synthesis is repeated several fines to amplify the DNA containing the primers and then, at least DNAs other than the amplified circular DNA are digested into several fragments obtained in the step of DNA synthesis in which, with the several fragments obtained in the step of digestion as megaprimers, the megaprimers are annealed to the circular DNA synthesised above, followed by an elongation reaction performed using the thermostable high-fidelity DNA polymerase. The method is useful for mutagenesis, particularly for introducing centain mutations at certain sites of the nucleotide sequence. The present method is simple, speedy, economical and widely applicable. The present sequence is Aequorea victoria enhanced green fluorescent protein (SGFP) used for mutagenesis in an exemplification of the invention. The EGFP is derived by a latering the green fluorescent protein (GFP) sequence of Aequorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNRIELKGIDFKEDGNILGHKLEYNYNSHNYYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Method for mutagenesis, e.g. for introducing certain or random mutations at certain sites of the nucleotide sequence, comprises synthesizing a mutated strand and a complementary strand by use of megaprimers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method for mutagenesis that comprises synthesising a mutated strand and a complementary strand by use of megaprimers. The method basically comprises a DNA synthesis in which one
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                                            . .3
note= "Wild-type GFP Met-Ser are replaced with Met-Val-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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                                                                                                                          "GFP Phe64 is replaced by Leu"
                                                                                                                                                                     /note= "GFP Ser65 is replaced by Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 13-14; 31pp; English
                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                    03-AUG-2001; 2001EP-00306650
                                                                                                                                                                                                                                                                                                                                               04-AUG-2000; 2000JP-00237166
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                                                                                                                               'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                  Miyawaki A, Sawano A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002-208112/27.
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                                                                                                                                                                                                                                                                                                                                                                                     (RIKE ) RIKEN KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAD27910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 239 AA;
                                        Misc-difference
                                                                                                                                                 Misc-difference
                                                                                                      Misc-difference
                                                                                                                                                                                                               EP1178109-A1
                                                                                                                                                                                                                                                          06-FEB-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNYYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                  181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWVLAGFVTAAGITLGMDELYK 239
DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLAGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                     Phosphorylation indicator, fluorescent protein; detection; phosphatase; kinase; enhanced green fluorescent protein; EGFP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel chimeric phosphorylation indicators, useful for detecting kinase/phosphatase in samples, has donor molecule, phosphorylatable domain, phosphoaminoacid binding domain, and acceptor molecule, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                                                                                                                                                   Aequorea victoria enhanced green fluorescent protein (EGFP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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                                                                                                                            AAE34958 standard; protein; 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAY-2002; 2002WO-US016955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAY-2001; 2001US-00865291.
                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tsien RY, Ting AY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-148474/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 236; Conserv
                                                                                                                                                                                                                                                                                                                           Aequorea victoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               operative linkage.
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                                                                                                                                                                                                                                                                                                                                                               WO200295058-A2
                                                                                                                                                                                                 28-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                   28-NOV-2002
                                                                                                                                                             AAE34958;
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 181
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                                                                                        RESULT 15
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181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 239

Search completed: June 21, 2004, 15:54:13 Job time: 48.1111 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-513-783A-46

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US-09-171-197-129

US-09-417-197-113

US-09-417-197-115

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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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US-09-513-783A-176
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US-09-417-197-143
US-09-417-197-77
US-09-513-783A-178
US-09-513-783A-178
US-09-417-197-53
US-09-417-197-61
US-09-417-197-61
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Pred. No. 4e-128;
1; Mismatches 2
                                                                                                         US-09-417-197-117
                                                                                                                                    ALIGNMENTS
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ORGANISM: Aequorea victoria
FEATURE:
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Best Local Similarity 98.7
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                       NAME/KEY: VARIANT
LOCATION: (0)...(0)
OTHER INFORMATION: EGFP
US-09-172-063-3
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61
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DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLAGFVTAAGITLGMDELYK 239 

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121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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ORGANISM: Aequorea victoria
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Best Local Similarity 98.7
Matches 236; Conservative
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COTHER INFORMATION: EGFP
US-09-602-641-3
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NAME/KEY: VARIANT
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98.7%; Score 1258; DB 4; Length 239;
Best Local Similarity 98.7%; Pred. No. 4e-128;
Matches 236; Conservative 1; Mismatches 2; Indels
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1; Mismatches 2; Indels
                                                                       GENERAL INFORMATION:
APPLICANT: Giuliano, Kenneth A.
APPLICANT: Rapur, Ravi
TITLE OF INVENTION: A System for Cell Based Screening;
FILLE REPRENCE: 97-022-L1
CURRENT APPLICATION NUMBER: US/09/513,783A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 46
LENGTH: 239
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Patent No. 6469154;
GENERAL INFORMATION:
APPLICANT: Taien, Roger Y.
APPLICANT: Baird, Geoffrey,
TITLE OF INVENTION: FLUORESCENT PROTEIN INDICATORS;
FILE REFERENCE: 07257/073001
CURRENT APPLICATION NUMBER: US/09/316,919
CURRENT SILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSEQ for Windows Version 4.0
                                       ; Sequence 46, Application US/09513783A; Patent No. 6416959
                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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Best Local Similarity 98.7%;
Matches 236; Conservative
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US-09-316-919-4
RESULT 2
US-09-513-783A-46
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US-09-316-919-4
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LENGTH: 239
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APPLICANT: Hiyawaki, Atsushi
APPLICANT: Hiyawaki, Atsushi
APPLICANT: Hippis, Juan
APPLICANT: Machter, Bebeka M.
APPLICANT: Wachter, S. James
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REPERENCE: 07257/071001
CURRENT APPLICATION NUMBER: US/09/602,641
CURRENT PILING DATE: 1998-10-13
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 239
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Pred. No. 4e-128;
1; Mismatches 2;
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Patent No. 6673610
GENERAL INFORMATION:
APPLICANT: Miyawaki, Atsushi
APPLICANT: Sawano, Asako
TITLE OF INVENTION: METHOD FOR MUTACENESIS
FILE REFERENCE: 11283-012001
CURRENT APPLICATION NUMBER: US/09/920, 922
CURRENT FILING DATE: 2001-08-02
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 9
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RESULT 8
US-09-513-783A-2
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Patent No. 613033
REGINERAL INFORMATION:
APPLICANT: Li, Xianqiang
TITLE OF INVENTION: Rapidly Degrading GFP-Fusion Proteins and Methods
TITLE OF INVENTION: of Use
FILE REPERENCE: D6100
CURRENT APPLICATION NUMBER: US/09/062,102
CURRENT APPLICATION NUMBER: US 60/060,855
EARLIER APPLICATION NUMBER: US 60/060,855
EARLIER APPLICATION NUMBER: US 60/060,855
EARLIER PILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: Sequence of the EGFP-MODC422-461 fusion protein.
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: artificial sequence
                                                              TYPE: PRT
ORGANISM: Aequorea victoria
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US-09-062-102-1
                  SEQ ID NO 2
LENGTH: 239
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US-09-062-102-1
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                                                                         APPLICANT: Kain, Steve
APPLICANT: Kain, Steve
APPLICANT: Li, Xianqiang
TITLE OF INVENTION: Rapidly Degrading GFP-Fusion Proteins and Methods
TITLE OF INVENTION: of Use
FILE REFERENCE: D6100CIP/D2
CURRENT APPLICATION WUMBER: US/09/364,946
CURRENT FILING DATE: 1999-07-30
EARLIER FILING DATE: 1999-11-13
NUMBER OF SEQ ID NOS: 14
LENGTH: 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Sequence of the EGFP-MODC422-461 fusion protein.
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98.7%; Score 1258; DB 4;
Best Local Similarity 98.7%; Pred. No. 5.5e-128;
Matches 236; Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1258; DB 4;
Pred. No. 5.1e-128;
1; Mismatches 2;
Sequence 1, Application US/09364946
Patent No. 6306600
GENERAL INFORMATION:
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Best Local Similarity 98.7
Matches 236; Conservative
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US-09-364-946-1
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1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT 60
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                                             61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL
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APPLICANT: Myawaki, Atsushi
APPLICANT: Llopis, Juan
APPLICANT: Llopis, Juan
APPLICANT: Mochter, Rebekka M.
APPLICANT: Remington, S. James
APPLICANT: Remington, S. James
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/071001
CURRENT APPLICATION NUMBER: US/09/172,063
CURRENT FILING DATE: 1998-10-13
EARLIER APPLICATION NUMBER: 09/094,359
SAPLIER FILING DATE: 1998-06-09
NUMBER CF SEQ ID NOS: 38
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 21, Application US/09172063; Patent No. 6150176; GENERAL INFORMATION:
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Patent No. 6608189
GENERAL INFORMATION:
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LOCATICN: (0)...(0)
OTHER INFORMATION: GT-EGFP
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Matches 236; Conservative
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US-09-172-063-21
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US-09-602-641-21
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LENGTH: 323
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APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi APPLICANT: Llopis, Juan

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Sequence 6, Application US/09085305
; Sequence 6, Application US/09085305
; Patent No. 6191269
; GENERAL INFORMATION:
; APPLICANT: Pollock, Allan
; APPLICANT: Lovett, David H.
; APPLICANT: Turck, Johanna
; TITLE OF INVENTION: Selective Induction of Apoptosis in
TITLE OF INVENTION: Interleukin-1-Alpha Pro-Piece Polypeptide
; TITLE OF INVENTION: Interleukin-1-Alpha Pro-Piece Polypeptide
; TITLE OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Boaicevic & Reed, LLP
; TREET: 285 Hamilton Ave, Suite 200
; CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT 144
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APPLICANT: Remington, S. James
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MASCURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/071001
CURRENT APPLICATION NUMBER: US/09/602,641
CURRENT FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/172,063
PRIOR APPLICATION NUMBER: 09/172,063
PRIOR PRILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 323
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Pred. No. 6.38-128;
1; Mismatches 2; Indels (
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,305
FILING DATE: 29-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 98.7%;
Best Local Similarity 98.7%;
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Aequorea victoria FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (0)...(0); OTHER INFORMATION: GT-EGFP US-09-602-641-21
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: VARIANT
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Sequence 127, Application US/09417197
Sequence 127, Application US/09417197
Patent No. 6518021
GENERAL INFORMATION:
APPLICANT: Ole THASTRUP, et al.
APPLICANT: Ole THASTRUP, et al.
TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An ITILE OF INVENTION: On A Cellular Response
FILE REFERENCE: 3759-0110P
CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patentin version 3.0
SEQ ID NO 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 LVTTLIYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 315
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                                           321 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 379
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APPLICANT: Kinsella, Todd
TITLE OF INVENTION: 1N VIVO PRODUCTION OF CYCLIC PEPTIDES
TILE FERENCE: A-66614-1/DJB/RNS/RMK
CURRENT PILING DATE: 2001-08-28
CURRENT PILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: US 60/187,130
PRIOR FILING DATE: 2000-03-06
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.7%; Score 1258; DB 4;
98.7%; Pred. No. 1e-127;
tive 1; Mismatches 2;
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Pred. No. 9.9e-128;
1; Mismatches 2;
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                                                                                                                                                                              Sequence 48, Application US/09800170 Patent No. 6481667
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ORGANISM: Synechocystis PCC6803
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Best Local Similarity 98.7%;
Matches 236; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity
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US-09-417-197-127
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APPLICANT: Ole THASTRUP, et al.
TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An TITLE OF INVENTION: On A Cellular Response
FILE REFERENCE: 3759-0110P
CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                                                                                                                       Length 364;
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                                                                                                                                                                                                                                                                                                                                                                    Score 1258; DB 3;
Pred. No. 7.6e-128;
                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                     NAME: Francis, Carol L
REGISTRATION NUMBER: 36,513
REFERENCE/DOCKET NUMBER: 6510/102US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
TELEFAX: 650-327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 129, Application US/09417197
Patent No. 6518021
                                                                                                                                                                                                                                                                                                                                                                       98.78;
98.78;
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ORGANISM: Artificial Sequence
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 98.7
Matches 236; Conservative
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US-09-085-305-6
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Matches 236; Conserv
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US-09-417-197-129
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LENGTH: 379
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61 LVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                                                                            LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                                                                                                                             181 DHYQONTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLAGFVTAAGITLGMDELYK 239
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1 MVSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT 60
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US-09-513-783A-170
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                                                                                                                                                                                                                                                                                                                              RESULT 15
US-09-513-783A-170
| US-09-513-783A-170
| Sequence 170, Application US/09513783A
| Patent No. 6416959
| GENERAL INFORMATION:
| APPLICANT: Giuliano, Kenneth A. APPLICANT: Giuliano, Kenneth A. APPLICANT: Giuliano, Kenneth A. TITLE OF INVENTION: A System for Cell Based Screening;
| TITLE OF INVENTION: A System for Cell Based Screening;
| FILE REFERENCE: 90.022-L1
| CURRENT APPLICATION NUMBER: US/09/513,783A
| CURRENT FILING DATE: 2000-02-25
| SOFTWARE: PatentIn Ver. 2.0
| SEG ID NO 170
| SEG ID NO 170
| TYPE: RRT
| OVGANISA: Artificial Sequence
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Search completed: June 21, 2004, 16:04:05 Job time: 13.7778 secs

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US-10-221-461-7 US-10-10-257A-46 US-10-10-318-411-3 US-10-318-411-3 US-10-318-61-11 US-10-314-861-31 US-10-314-861-37 US-10-314-861-37 US-10-314-861-37 US-10-314-861-39 US-10-314-861-39 US-10-314-861-39 US-10-314-861-29 US-10-314-861-29 US-10-318-411-11 US-10-318-411-13 US-10-318-411-13 US-10-318-411-13 US-10-318-411-13 US-10-318-411-13 US-10-318-411-13 US-10-318-411-13 US-10-318-411-13 US-10-318-411-13 US-10-318-411-13 US-10-318-411-13 US-10-318-411-13 US-10-318-411-13 US-10-318-411-13 US-10-318-411-5 US-10-318-411-5 US-10-318-411-5 US-10-318-411-5 US-10-318-411-5 US-10-318-411-5

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ALIGNMENTS

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Pred. No. 2.6e-124;
0; Mismatches 1;
Sequence 4, Application US/09887784

Patent No. US20020177189A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS
FILE REFERENCE: 3759-0115P

CURRENT FILING DATE: 2001-06-19

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PatentIn version 3.0
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al Similarity 99.6%;
238; Conservative
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Best Local Similarity
Matches 238; Conserv
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US-09-866-538-4 US-09-797-496B-2 US-09-794-308-4 US-09-865-291-4 US-10-121-258-13

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18-10-257-909A-30

Sequence 30, Application US/10257909A

Sequence 30, Application US/10257909A

Publication World Sequence 30, Application US/10257909A

Publication World Sequence 30, US20030187056A1

GENERAL INFORMATION:

APPLICANT: Bernard R. TERRY et al.

TITLE OF INVENTION: Live cell procedures to identify compounds modulating intracellul?

TITLE OF INVENTION: distribution of phosphodiesterase (PDE) enzymes

FILE REFRENCE: 3759-0125P

CURRENT APPLICATION NUMBER: US/10/257,909A

CURRENT FILING DATE: 2002-10-17

NUMBER OF SEQ ID NOS: 36

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 30

LENGTH: 893
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Publication No. US20030187056A1
GENERAL INFORMATION.
APPLICANT: Bernard R. TERRY et al.
TITLE OF INVENTION: Live cell procedures to identify compounds modulating intracellulating of INVENTION: Live cell procedures to phosphodiesterase (PDE) enzymes
FILE REFERENCE: 3759-0125P
CURRENT APPLICATION NUMBER: US/10/257,909A
CURRENT FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: BIOITINGS A/S

TITLE OF INVENTION: AN IMPROVED METHOD TO DETECT INTERACTIONS BETWEEN CELLULAR COMPON

TITLE OF INVENTION: INTERACTIONS ELLS, AND TO EXTRACT QUANTITATIVE INFORMA-TION RE

TITLE OF INVENTION: INTERACTIONS BY FLUORESCENCE REDISTRIBUTION.

FILE REFERENCE: 3759-0126P

CURRENT APPLICATION UNDEBE: US/10/270,223

CURRENT FILING DAIE: 2002-10-11

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin version 3.1

SEQ ID NO 6

LENGTH: 363
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Pred. No. 4.7e-124;
0; Mismatches 1;
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Pred. No. 2.6e-124;
0; Mismatches 1;
                                                                                                             GENERAL INFORMATION:
APPLICANT: BJORN, SARA P.
APPLICANT: BJORN, SARA P.
APPLICANT: PAGLIARO, LEN
TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS
FILTE OF INVENTION: NOVEL FLUORESCENT PROTEINS
FILE OF INVENTION: NOVEL FLUORESCENT PROTEINS
CURRENT APPLICATION NUMBER: US/10/296,953
CURRENT APPLICATION NUMBER: DO2-11-26
PRIOR APPLICATION NUMBER: 60/212,681
PRIOR APPLICATION NUMBER: 60/212,681
PRIOR APPLICATION NUMBER: 60/220,170
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2001-05-10
PRIOR FILING DATE: 2001-05-10
PRIOR FILING DATE: 2001-05-10
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 4
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; ORGANISM: Aequoria Victoria and Human
US-10-270-223-6
                                              ; Sequence 4, Application US/10296953; Publication No. US20040072995A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 5, Application US/10270223
; Publication No. US20030143634A1
; GENERAL INFORMATION:
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99.6%;
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Best Local Similarity 99.6%;
Matches 238; Conservative
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ORGANISM: Aequorea victoria
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Best Local Similarity 99.6'
Matches 238; Conservative
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US-10-270-223-6
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APPLICANT: BJORN, SARA P.
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                                                                                                                                                               Length 1132;
                                                                                               ; OTHER INFORMATION: Fusion between Aequorea victoria and human US-10-257-909A-32
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Pred. No. 1.8e-123;
0; Mismatches 2;
                                                                                                                                                             Score 1269; DB 14;
Pred. No. 2.4e-123;
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Patent No. US20020177189A1;
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS;
FILE REPERBURE: 3759-0115P;
CURRENT APPLICATION NUMBER: US/09/887,784;
CURRENT FILING DATE: 2001-06-19
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2;
LENGTH: 239
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US-10-296-953-2
Sequence 2, Application US/10296953
Publication No. US20040072995A1
GENERAL INFORMATION:
                   LENGTH: 1132
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 99.6%;
Matches 238; Conservative
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Best Local Similarity 99.2%;
Matches 237; Conservative (
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US-09-887-784-2
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US-09-887-784-2
SEQ ID NO 32
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Best Local Similarity 98.7%; Pred. No. 3.6e-123;
Matches 236; Conservative 1; Mismatches 2;
APPLICANT: PAGLIARO, LEN
APPLICANT: THASTRUP, OLE
TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS
FILE REFERENCE: PLOO95
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US-09-920-922-2
Sequence 2, Application US/09920922
Sequence 2, Application US/09920922
Sequence 2, US20020083488A1
GENERAL INFORMATION:
APPLICANT: Miyawaki, Atsushi
APPLICANT: Sawano, Asako
TITLE OF INVENTION: METHOD FOR MUTAGENESIS
FILE REFERENCE: 11283-012001
CURRENT APPLICATION NUMBER: US/09/920, 922
CURRENT PELING DATE: 2001-08-02
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 239
                                                                                                     CURRENT APPLICATION NUMBER: US/10/296,953
CURRENT FILING DATE: 2002-11-26
PRIOR PILING DATE: 2002-11-26
PRIOR PLING DATE: 2000-06-19
PRIOR PLING DATE: 2000-06-20
PRIOR PLING DATE: 2000-06-20
PRIOR PLING DATE: 2001-05-10
PRIOR PLING DATE: 2001-05-10
PRIOR PLING DATE: 2001-05-10
PRIOR FILING DATE: 2001-05-10
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN OFF: 21
SOFTWARE: PATENTIN OFF: 239
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, ORGANISM: Aequorea victoria
US-10-296-953-2
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US-09-920-922-2
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ORGANISM: Aequorea victoria
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     ; ORGANISM: A:
US-09-866-538-4
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                   61 LVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                  VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                                                                                           Sequence 4, Application US/0999745;
Patent No. US20020137120A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: Taien, Roger Y.
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
FILE REFERENCE: REGEN1470-1
CURRENT APPLICATION NUMBER: US/09/999,745
CURRENT FILING DATE: 1001-10-23
PRIOR PELICATION NUMBER: 109/316,920
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 67
SEOFFWARE: Patentin version 3.0
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; Sequence 4, Application US/09866538;
; Publication No. US20030032088A1
; GENERAL INFORMATION:
; APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TSIEN, ROGER
; APPLICANT: Campbell, Robert
; TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
; FILE REFERENCE: REGENTS30-2
; CURRENT APPLICATION NUMBER: US/09/866,538
; CURRENT FILING DATE: 2011-05-24
; UNMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.0
; LENGTH: 239
; TYPE: PATENCE: REGION NOS: 29
; SEQ ID NO 4
; LENGTH: 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1258; DB 9; Length 239;
Pred. No. 3.6e-123;
1; Mismatches 2; Indels
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98.7%;
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ORGANIEM: Aequorea victoria

US-09-999-745-4
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Matches 236; Conservative
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US-09-866-538-4
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US-09-999-745-4
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Best Local S
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OTHER INFORMATION: Aequorea victoria green fluorescent protein modified as described OTHER INFORMATION: in specification
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; Sequence 2, Application US/09797496B
; Publication No. US20030049597A1
; GENERAL INPOWARTON:
; APPLICANT: Simon, Sanford M.
; TITLE OF INVENTION: Chimeric Pluorescent Enzymes and Uses Thereof
; TITLE OF INVENTION: Chimeric Pluorescent Enzymes and Uses Thereof
; TITLE NEFERRNCE: 600-1-267
; CURRENT FILING DATE: 2002-05-24
; UNRBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2.
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Length 239;
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Score 1258; DB 10;
Pred. No. 3.6e-123;
1; Mismatches 2;
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vuery Match
Best Local Similarity 98.7%;
Matches 236; Conservative
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   181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLAGFVTAAGITLGMDELYK 239
                                               181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 239
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Fublication No. US2030059835A1
GENERAL INFORMATION:
APPLICANT: Taien, Roger
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME
TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME
TITLE OF INVENTION: PROTEIN VARIANTS AND
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
PRIOR FILING DATE: 2001-02-26
PRIOR FILING DATE: 2001-05-24
                                                                                                                                                                                                                                       Sequence 3, Application US/10457982
; Publication No. US20030212265A1
; GENERAL INFORMATION:
    APPLICANT: Taien, Roger Y.
    APPLICANT: Miyawaki, Atsushi
    APPLICANT: Miyawaki, Atsushi
    APPLICANT: Miyawaki, Atsushi
    APPLICANT: Machier, Rebekka M.
    APPLICANT: Machier, Rebekka M.
    APPLICANT: Machier, Rebekka M.
    APPLICANT: Machier, S. James
    TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
    TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
    TILE REFERENCE: 07257/071001
    CURRENT APPLICATION NUMBER: US/10/457,982
    CURRENT FILING DATE: 2003-06-09
    PRIOR APPLICATION NUMBER: US/09/602,641
    PRIOR PELING DATE: 1998-10-13
    PRIOR PELING DATE: 1998-10-13
    NUMBER OF SEQ ID NOS: 38
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 3
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ORGANISM: Aequorea victoria
FEATURE:
NAME/LY VARIANT
LOCATION: (0) ... (0)
OTHER INFORMATION: EGFP
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Matches 236; Conservative
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; Sequence 4, Application US/09865291
; Publication No. US20030186229A1
; GENERAL INFORMATION:
    APPLICANT: RECENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TING, Alice
; APPLICANT: TING, Alice
; APPLICANT: TING, Alice
; APPLICANT: TING, Alice
; APPLICANT: TING, Alice
; APPLICANT: TING, Alice
; APPLICANT: TING, Alice
; APPLICANT: TING, Alice
; TILLE OF INVENTION EMISSION RATIOMETRIC INDICATORS OF PHOSPHORYLATION
; FILE REFERENCE: RECENTIS 0
; CURRENT FILING DATE: 201-05-24
; NUMBER OF SEQ ID NOS: 42
; SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 239;
                               APPLICANT: ZACHARIAS, David
APPLICANT: BAIRD, Geoffrey
TITLE OF INVITON: NON-OLIGOMERIZING FLUORESCENT PROTEINS
TITLE OF INVITON: NON-OLIGOMERIZING FLUORESCENT PROTEINS
TITLE REPRENCE: REGENIS30
CURRENT APPLICATION NUMBER: US/09/794,308
CURRENT FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 25
SOFWARE: PALENLIN VERSION 3.0
SEQ ID NO 4
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Pred. No. 3.6e-123;
1; Mismatches 2;
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Best Local Similarity 98.7%;
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Aequorea victoria
US-09-794-308-4
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Matches 236; Conservative
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                                                                                        Query Match 98.7%; Score 1258; DB 14; Length 239; Best Local Similarity 98.7%; Pred. No. 3.6e-123; Matches 236; Conservative 1; Mismatches 2; Indels 0
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FRATURE: ORGANISM: Enhanced Green Fluorescent Protein (EGFP) US-10-121-258-13
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Search completed: June 21, 2004, 16:09:30 Job time : 35.7778 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

June 21, 2004, 15:46:00 ; Search time 10.3333 Seconds Run on:

(without alignments)
2224.817 Million cell updates/sec

1274 1 WVSKGEELFTGVVPILVELD......VLaGFVTAAGITLGMDELYK 239 US-09-887-784-222A Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

283366 segs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

nitrogenase (EC 1. DNA-directed DNA p IgA Fc receptor pr IgA Fc receptor pr

JDVLD A60234 FCSOAG

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## ALIGNMENTS

RESULT 1
ovins. greenies victoria G.Snecies: Aemiorea victoria
C. December 03-December 4 sequence revision 03-Dec-1999 #text change 23-Mar-2001
C:ACCEBBION: USU694; UQL114; PQU335; S48893; S31330; S31331 R;Prasher, D.C.; Eckenrode, V.K.; Ward, W.W.; Prendergast, F.G.; Cormier, M.J.
Gene 111, 223-233, 1992 Afile: Primary structure of the Aequorea victoria green-fluorescent protein. A.Deferance number. 101514. MITD.99175577. DMTD.1147277
A:Molecule type: DNA
A;Residues: 1-107,'S',109-238 <pra1> A;Cross-references: GB:M62654; NID:q155662; PIDN:AAA27722.1; PID:q155663</pra1>
A;Accession: JQ1514 A:Molecule type: mRNA
A;Residues: 1-99,'F',101-140,'L',142-218,'V',220-238 <pra2> A;Cross-references: GB:M62653; NID:g155660; PIDN:AAA27721.1; PID:g155661</pra2>
A:Accession: PQ0335 A:Molecule tyme: profein
A; Residues: 46-64; 74-122;132-151;154-183;185-200 <pra3></pra3>
R;Inouye, S.; TBuji, F.I. FBBS Lett. 351. 211-214. 1994
A, Title: Evidence for redox forms of the Aequorea green fluorescent protein.
A; Reference Tumber: S48693; MULD:943644/U; FMLD:8082/6/ A: Accession: S48693
A; Status: preliminary
A;Molecule type: mkNA A;Residues: 1-24,'Q',26-156,'P',158-171,'K',173-238 <ino></ino>
A; Cross-references: GB: L29345; NID: 9606383; PIDN: AAA58246.1; PID: 9606384
RIMMAKINE, O.N.; CHRIDDELL, A.N. Submitted to the EMBL Data Library, January 1995
A, Reference number: S51330
A;Accession: S51330
A;Residues: 1-13,'V',15-24,'Q',26-44,'N',46-153,'G',155-156,'P',158-171,'K',173-227,'R',;
A;Cross-reterences: EMBL:X83959; NID:g634008; PIDN:CAA58789.1; P1D:g634009 A;Experimental source: clone gfpl
A; Accession: S51331
A;Residues: 124, 'Q', 26-29, 'R', 31-83, 'L', 85-153, 'G', 155-156, 'P', 158-171, 'K', 173-208, 'Q', 'A
A;Cross-references: EMBL:X83960; NID:g634010; PIDN:CAA58790.1; PID:g634011 A:Experimental source: clone afb2
R.Yang. F.; Moss, L.G.; Phillips Jr., G.N. submitted to the Brookhaven Protein Data Bank. August 1996
A;Reference number: A65692; PDB:1GFL
A;Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 74,72-79,78, 81-93. A;Note: engineered sequence based on JQ1514, cloned and expressed in Escherichia coli
R;Yang, F.; Moss, L.G.; Phillips Jr., G.N. Nat. Biotechnol. 14, 1246-1251, 1996
A;Title: The molecular structure of green fluorescent protein. A;Reference number: A58953; MUID:98294543; PMID:9631087

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PDHMKQHDFFKSAMPEGYV------QERTIFFKDDGNYKTRAEVKFEGDTLVNRIE 125
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                                                                                                                             leucine-tRNA ligase (EC 6.1.1.4)
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A)Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A, Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A, Reference number: A72200; MUID:99287316; PMID:10360571

A, Accession: H7228

A, Accession: H7228

A, Residues: Draiminary

A, Residues: 1-785 < ARN>

A, Residues: 1-785 < ARN>

A, Residues: 1-785 < ARN>

A, Experimental source: strain MSB8

C, Genetics:
A;Contents: annotation; X-ray crystallography, 1.9 angstroms
C;Comment: This protein is excited by the photoprotein aequorin (see PIR:AQJFNV) emittin
C;Comment: The chromophore of this protein is formed by modification of Ser-dehydro-Tyr-G;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Introns: 69/3; 167/3
A;Introns: 69/3; 167/3
A;Introns: 69/3; 167/3
A;Introns: 69/3; 167/3
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H72228
H72228
H72229
H72229
H72229
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Dates: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Dates: 11-Jun-19228
K;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hiclgarrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 TILSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 RIBLKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVQLADH
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.larity 19.7%; Pred. No. 0.75;
Conservative 32; Mismatches 71; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1236; DB 1;
Pred. No. 5.1e-96;
4; Mismatches 4;
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15 NEGRFSFEGTVPGVVQAD----
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Best Local Similarity 96.6%;
Matches 230; Conservative
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Best Local Similarity
Matches 46; Conserv
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Nighternate names: leucyl-tRNA synthetase
Nighternate names: leucyl-tRNA synthetase
C.Species: Haemophilus influenzae
A.Schaceston: Haemophilus influenzae Rd.
A.Stitle: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A.Reference number: Haemophilus influenzae Rd.
A.Reference number: Haemophilus influenzae Rd.
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                                                                                                                                                                                                                                                                                                                       A,Accession: H64102
A,Status: nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-861 <TIGR>
A,Cross-references: GB:U32774; GB:L42023; NID:g1573942; PIDN:AAC22581.1; PID:g1573943; C,Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-binding protein PD2 - garden pea
C.Species: Pisum sativum (garden pea)
C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C.Accession: T06586
R.Sato, N.; Kazuno, A.A.; Ohta, N.; Ohshima, K.
Submitted to the EMBL Date Library, June 1996
A.Description: Identification of a novel family of DNA-binding proteins with A.Reference number: Z1774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mENA
A;Residues: 1-632 <SAT>
A;Cross-references: EMBL:X98740; NID:e995229; PIDN:CAA67292.1; PID:e275185
A;Experimental source: CV. Alaska
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- Haemophilus influenzae (strain Rd KW20)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Gene: leuS
C,Superfamily: leucine-tRNA ligase
C,Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
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llarity 23.3%; Pred. No. 12;
Conservative 26; Mismatches
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Local Similarity 24.1%; Pred. No. 14;
les 46; Conservative 26; Mismatches
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Sun Jun

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A; Accession: 140794
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-578 «KRU»
A; Residues: 1-578 «KRU»
A; Residues: 1-578 «KRU»
A; Residues: 1-578 «KRU»
A; Description: catalyzes the oxidation of dihydrolipoamide to lipoamide using NAD
A; Pathway: acetoin dehydrogenese enzyme system
A; Pathway: acetoin dehydrogenese enzyme system
C; Superfamily: Alcaligenes dihydrolipoamide dehydrogenase; dihydrolipoamide dehydrogenase
C; Keywords: FAD; flavoprotein; lipoamide, NAD; oxidoreductase; redox-active disulfide
F; 5-77/Domain: lipoyl/biotin-binding houcleotide-binding fold
F; 117-145/Region: beta-alpha-beta RAD nucleotide-binding fold
F; 119-56/Domain: dihydrolipoamide dehydrogenase homology «DLD»
F; 287-315/Region: beta-alpha-beta NAD nucleotide-binding fold
F; 153-158/Disulfide bonds: redox-active #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and ç A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: D83917
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A;Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB05859.1; GSPDB:GN001
A;Experimental source: strain C-125
                                                                                                                                   A,Title: Biochemical and molecular characterization of the Clostridium magnum acetoin del
A,Reference number: 140789; MUID:94266715; PMID:8206840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA topoisomerase IV subunit B BH2140 [imported] - Bacillus halodurans (strain C-125)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 IELKGIDFKEDG----NILGHKLEYNYNSHNVYIMADKQKN--GIKVNFKIRHNIEDGSVQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 TLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNR 123
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C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: D83917
   C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 TGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK-----FICTTGKLPVPWPTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 LADHYQQNT----PIGD--GPVLLPDNHYLSTQSALSKD----PNEKRDHMVLAGFV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.0%; Score 89; DB 1; Length 578; 22.9%; Pred. No. 13; Live 43; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                     Kruger, N.; Oppermann, F.B.; Lorenzl, H.; Steinbuchel, A.
Bacteriol. 176, 3614-3630, 1994
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C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 6.9%; Score 88.5; DB 2; 1 Similarity 21.9%; Pred. No. 17; 53; Conservative 37; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 DVNGHK---FSVSGEGEGDAT---YGKLTLKFI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                306 SLGCKVSIIEMLPHILPPMDREISEI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.0%;
Best Local Similarity 22.9%,
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PELASVGLT 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          226 ---TAAGIT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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Best Local S:
Matches 53,
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R; Simpson, A.JG.; Reinard, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.P.; Camardo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H se.Neto, E.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H se.Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000
A, Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junquaira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E. Ayuthors: Martins, E.M.; Madeira, A.M.; M. A.Y.; Menck, C.P.M.; Miracca, E.C.; Miyaki, C.Y.; F. Gollyosira, M.C.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Antiques, V.; Rosa, A.J. de M.; de Oliveira, M.C.; de Sa, R.G.; Santelli, R.V.; Sawasak A, Authors: A.C.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, W.A.; Verference number: A59328

A; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-887 <SIM>
A;Cross-references: GB:AE004031; GB:AE003849; NID:g9107309; PIDN:AAF84975.1; GSPDB:GN001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for Nucleotide Sequer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dihydrolipoamide dehydrogenase (EC 1.8.1.4) [validated] - Clostridium magnum NA. Lernate names: 2-oxoglutarate dehydrogenase complex chain E3; acetoin dehydrogenase hydrogenase complex chain E3; S-complex 50K chain C;Species: Clostridium magnum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        386 STWEPDVWRDWYADKTR---EFE---LINSAEFDGLDYQDAFEVLAERFE-----429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            409 PSSAKVNVLTKDLIVETFPLRSVARTSSGREGSEELKDSGNSLERDTKKLELEQGKNS-E 467
                                                                                                           -----KTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 MADKQKNG-IKVNFKIRHNIEDGSVQLADHYQQNTPI-------GDGPVLLPDN 199
                                                                                                                                                                                                                                                                                                                                                                                                                            Teucyl--rRNA synthetase XF2176 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Species: Xylella fastidiosa C;Species: Xylella fastidiosa C;Species: Shaqs-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 C;Accession: E82590 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucle Nature 406, 151-157, 2000 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MulD::0365717; PMID::0910347 A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 TIGKLPVPWPTLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNY--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.0%; Score 89.5; DB 2; Best Local Similarity 22.2%; Pred. No. 21; Matches 44; Conservative 29; Mismatches 68;
                                                                                                                                                                                                                                           161 GIKVNFKIRHNIEDG-----SVQLADHYQ 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 -HYLSTOSALSKDPNEKR 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: XF2176
C;Superfamily: leucine-tRNA ligase
                                                                     LKGIDFKEDGNILGHKLE
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Genetics:
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A;Status: preliminary
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A36028
DNA-directed DNA polymerase (EC 2.7.7.7) II catalytic chain - yeast (Saccharomyces Cerevi)
N;Alternate names: DNA-directed DNA polymerase II chain A; protein N0825; protein YNL262w, C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Accession: A36028; B56028; S60919; S63235; S65121
R;Morrison, A; Araki, H.; Clark, A.B.; Hamatake, R.K.; Sugino, A.
Ccell 62, 1143-1151, 1990
A;Title: A third essential DNA polymerase in Saccharomyces cerevisiae.
A;Reference number: A36028; MUID:90381771; PMID:2169349
A;Accession: A36028
A;Molecule type: DNA
A;Residues: 1-2222 <MOR>
A;Accession: B36028
A;Molecule type: protein
A;Residues: 1214-1216, X', 1218-1221 <MO2>
A;Residues: 1214-1216, X', 1218-1221 <MO2>
A;Residues: 1214-1216, X', 1218-1221 <MO2>
A;Residues: 1214-1216, X', 1218-1221 <MO2>
A;Residues: 1214-1216, X', 1218-1221 <MO2>
A;Residues: 1214-1216, X', 1218-1221 <MO2>
A;Residues: 1214-1218, Data Library, October 1995
A;Residues: 1214-1218, Data Library, October 1995
A;Reference number: S60909
A;Reference number: S60909
A;Reference number: S60909
A;Reference number: S60909
A;Reference number: S0909
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A;Residues: 1-2222 <SEW>
A;Cross-references: EMBL:Z71538; NID:g1302316; PIDN:CAA96169.1; PID:g1302317; GSPDB:GN00C
A;Experimental source: strain S288C
R;Sen-Gupta, M.; Lyck, R.; Fleig, U.; Niedenthal, R.K.; Hegemann, J.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 RAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIR 169
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A;Title: The sequence of a 24 152 bp segment from the left arm of chromosome A;Ritle: The sequence of a 24 152 bp segment from the left arm of chromosome A;Reference number: 865111; MUID:96310631; PMID:8740425
A;Accession: S65121
A;Atatus: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
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A;Residues: 1-2221 - KSEN>
A;Cross-references: EMBL:X92494; NID:g1045236; PIDN:CAA63235.1; PID:g1045247
R;Sen-Gupta, M.; Lyck, R.; Niedenthal, R.K.; Fleig, U.N.; Hegemann, J.H.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63235
A;Reference number: S63235
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|-------AEKGVGERKVNYRLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78;
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23.3%; Pred. No. 30;
tive 21; Mismatches
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Best Local Similarity 23.3%
Matches 42; Conservative
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Leucyl-tRNA synthetase [imported] - Salmonella enterica subsp. enterica serovar Typhi (6 C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AC0582
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
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                       63 NVTIHKDQSVSVRDEGRGMPTGMHKLGKPTPEVILTVLHAGGKFGQGGYATSGGLHGVGA 122
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                                                                                                                                                                                                  123 SVVNALSEWLIVEIKRDGWVYEQRFENGGKPSTTLEKKGKTRQTGTTIHFKPDPTVFSTT
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                                                                                                               60 TLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQER---
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VRFSFGLLNKEEE 355
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Best Local Similarity 25.43
Matches 49; Conservative
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A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype A;Reference number: A81250; MUD:20150912; PMID:10688204
A;Recession: G81355
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1.357 cPAR>
A;Cross-references: G8.AL139076; G8.AL111168; NID:g6968128; PIDN:CAB73096.1; PID:g696827;
A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Genome: cyanelle
C;Superfamily: photosystem II chlorophyll a-binding protein psbC
C;Keywords: chlorophyll; cyanelle; membrane-associated complex; photosynthesis; photosyst
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C;Species: cyanelle Cyanophora paradoxa
C;Accession: T06936
R;Stirewalt, V.L.; Michalowski, C.B.; Luffelhardt, W.; Bohnert, H.J.; Bryant, D.A.
Bubmitted to the EMBL Data Library, July 1995
A;Bescription: Nucleotide sequence of the cyanelle genome from Cyanophora paradoxa.
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74 LDFADEKICAFMPRLLEYLRQDNXLKEKL-----FGVEFLTTKQE--LSITLLYHKNIE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 KOHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKF--EGDTLV-----NRIELKG 128
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A,Cross-references: EMBL:U30821; NID:g1016083; PIDN:AAA81279.1; PID:g1016192
A,Experimental source: strain Pringsheim LB555
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 EKHSFIKKYFKEFYTKDFKLFASKDKHYRTRAELSFYHENDTLFYAMFDPKSKKKYIIEY
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                                                                                                                                                                                                                                                                            A;Gene: trmA; Cj0831c
C;Keywords: methyltransferase; S-adenosylmethionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Status: preliminary, translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 HMVLAGFV------TAAGITLGMD 235
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C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Accession: D71614
R;Gardner, M.J; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O. Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A7160; MUID:99021743; PMID:9804551
A;Reference number: A7160; Mulo:99021743; PMID:9804551
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: DNA
A,Residues: 1-2573 cGAR>
A,Residues: 1-2573 cGAR>
A,Cross-references: GB.AE001396, GB.AE001362, NID:g3845188; PIDN:AAC71881.1, PID:g384519
A,Experimental source: clone 3D7
C,Genetics:
A,Gene: PFB0460c
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C.Species Campylobacter jejuni
C.Species 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C.Accession: G81355
R.Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
                                          A Cross-references: EMBL:X92494; NID:g1045236; PIDN:CAA63235.1; PID:g1045247
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
GGenetis GD:POL2; DUN2; MIPS:YNL262w
A;Gene: SGD:POL2; DUN2; MIPS:YNL262w
A;Cross-references: SGD:S0005206; MIPS:YNL262w
A;Map position: 14L
C;Superfamily: DNA-directed DNA polymerase II
C;Keywords: DNA binding; nucleotidyltransferase; nucleus; zinc finger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 VQERTIFFKD---DGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYN--YNSH 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 NVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 FFKDDGNYKTR--AEVKFEGDTLVNR------IELKGIDFKEDGNILGHKLEYNYN 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 LKKETILCKDIKSGSNDPMDEISLFKDDMVDDKELK--DFEKSSLKIKNKEVYNFIYNKM 183
                                                                                                                                                                                                                                                                                                                                                                                                                                 66
                                                                                                                                                                                                                                                                                                                                                                                                                                 54 LPVPWP-TLVTTLSYGVQCFSRYPDHM-----KQHDFFKSAMPEGYV----QERTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.9%; Score 87.5; DB 2; Length 2573; Best Local Similarity 26.2%; Pred. No. 1.2e+02; Matches 34; Conservative 30; Mismatches 53; Indels 13
                                                                                                                                                                                                                                                                                                             DB 1; Length 2222;
                                                                                                                                                                                                                                                                                                       ch 6.9%; Score 87.5; DB 1; Length 22 1 Similarity 28.2%; Pred. No. 1e+02; 37; Conservative 14; Mismatches 49; Indels
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1000 SDIFKVFLEGD 1010
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                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 37; Conserva
                  A;Residues: 1-2221 <SEF>
                                                                                                                                                                                                                                                                                                                 Query Match
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Db 487 FFENYDNSKSDTSSNYRTTYGSNVTL-GFPVNENNSYYVGLGHTYNKISNFALEYN-	OY 149 HNVXIMADKQK-NGIKVNFKIRHNIEDGSVOLADHYOQNTPIGDGPVLL.	Search completed: June 21, 2004, 16:01:59 Job time : 10.3333 secs 54	10; K 108 F 196	M 154 - 245 L 202 : 297		66	Haemophilus infl	111,	7.486	3 148
:   Bb 418 HFVLGFFLFIGHLWHAGRARAASGGFEKGLD 448	RESULT 14. JDVLHH DNA-directed DNA polymerase (EC 2.7.7.7) - heron hepatitis virus C;Species: heron hepatitis virus, HHBV A;Note: host Ardea cinerea (gray heron) C;Abate: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 11-Jun-1999 C;Accession: A30082	Rispensel, R.; Kaleta, E.F.; Will, H. J. Virol. 62, 3832-3839, 1988 A.Title: Isolation and characterization of a hepatitis B virus endemic in A; Reference number: A93037; MUID:88333160; PMID:3418788 A; Recession: A30082 A; Molecule type: DNA A; Residues: 1-788 <spr> A; Cross-references: GB:MZ2056; NID:9325452; PIDN:AAA45738.1; PID:9325454 C; Superfamily: hepatitis virus DNA-directed DNA polymerase C; Keywords: DNA biosynthesis; nucleotidyltransferase</spr>	Duery Match Best Local Similarity Matches 40; Conservati 58 WPTLVTTLSYGVQ 139 WPKSISYLPVHSG	197 TWEQKHLVPQQHGAYSSKINDRQ: 155 ADKQKNGIKVNFKIRHNIEDGSVC	Qy 203 STQSALSKDPNEKR 216	JC4078  JC4078  JC4078  Protective Surface antigen D-15 precursor - Haemophilus influenzae (type b) C;Species: Haemophilus influenzae A;Variety: Eype b C;Date: 30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 29-Sep-1999 C;Accession: JC4078 B;Flack F;S: Johanne S: Chong D: Thomas W D	Gene 156, 97-99, 1995 A,Title: The sequencing of the 80-kDa D15 protective surface antigen of Ha A,Title: The sequencing of the 80-kDa D15 protective surface antigen of Ha A,Reference number: UC4078; MUID:95255676; PMID:7737523 A,Accession: JC4078 A,Molecule :ype: DNA A,Residues: 1-797 <fla> A,Residues: 1-797 <fla> A,Residues: 1-797 <fla> A,Experimental source: type b C;Superfamily: protective surface antigen D-15 C;Keywords: surface antigen C;Keywords: surface antigen F;1-19/Domain: signal sequence #status predicted <sig>F;20-797/Product: protective surface antigen D-15 #status predicted <mat></mat></sig></fla></fla></fla>	2; Length 797; 79; Indels 63;	65 LSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQE :	QY 100 FFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNS

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GenCore version 5.1.6
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OM protein - protein search, using sw model

June 21, 2004, 15:42:24; Search time 6.44444 Seconds (without alignments) 1931.085 Million cell updates/sec Run on:

US-09-887-784-222A 1274 1 MVSKGEELFIGVVPILVELD.......VLaGFVTAAGITLGMDELYK 239 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Déscription	P42212 aequorea vi	7			Q8zgz6 salmonella	P21951 saccharomyc	1 homo say	candida	xylella		Q9pp92 campylobact	P48104 cyanophora										Q8ehp4 shewanella		buch	Q8wts6 homo sapien	baci	P00467 clostridium		P27951 streptococc		_		P91679 drosophila
SUMMARIES	ID	GFP AEOVI		SYL XYLFA	SYL_SALTI	SYL_SALTY	DPOE YEAST	AC2L_HUMAN	CP51_CANGA	SYL_XYLFT	VIT4 CAEEL	TRMA_CAMJE	PSBC_CYAPA	YC03_KLEPN	AMPA_WIGBR	DPOL_HPBHE	D152_HABIN	D151_HAEIN	ITH3 MESAU	SYD_HAEDU	PEPF MYCPU	D153_HAEIN	SYL_SHEON	GUN BACS6	HIS7_BUCAI	SET7_HUMAN	SLAP_BACLI		GRBE_RAT	BAG_STRAG	YD48 METJA	PSBC_CHLEU	PRC_ECOLI	OPTI_DROME
	DB	-	H	н	7	7	т	т	П	П	7	٦	Н	Т	٦	1	-	Н	Н	н	• •	• •	• •		•	•	H					-		-
	Length	238	861	879	860	860	2222	689	533	879	1603	357	461	504	501	788	795	797	986	589	613	793	859	941	353	366	874	533	538	1164	336	461	œ	737
	% Query Match	97.5	~		6.9	٠			6.8		٠	6.8	6.8	6.8	6.7	٠	6.7			9.9		•			•		•	9.9			6.4	6.4	6.4	
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	Result No.	1	8	ım	4	ß	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P28840 rattus norv O25443 helicobacte	Q99nbl mus musculu Q42918 schizosacch	O00116 homo sapien Q8xbn8 escherichia	Q8fjy9 escherichia P07813 escherichia	P39321 escherichia P24506 discopyge o	P33563 bacillus su Q92405 aspergillus	
NEC1_RAT TRMB_HELPY	AC2L_MOUSE AMY2_SCHPO	ADAS HUMAN SYL ECO57	SYL_ECOL6	YTFW ECOLI SY62 DISOM	MTBB_BACSU CATB_ASPFU	
					н н	
752	682	658 860	860	1259	501 728	
6.4 4.4	4.4	6.3	6.0	6.3	6.3	
82	81	80.5	80.5	80.5	80	
3.44	36	38	4 4 4 1	4 4 2 8	44 45	

## ALIGNMENTS

RESULT 1

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61 VTTFSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VITLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
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                                                                                                                                                                                                                                                                                              5-imidazolinone (Ser-Gly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26886 MW; EASA6F21FBFB6E05 CRC64;
                                                                                                                                                                                                                                                                                                                     3-DIDEHYDROTYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1242; DB 1;
Pred. No. 5.5e-95;
1; Mismatches 4;
                                                                                                                                           InterPro; IPR009017; GFP like.
InterPro; IPR000786; Green_fl_protein.
                                                                                                                                                                                                                                              ProDom; PD013756; Green fl_protein; 1.
Luminescence; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR01229; GFLUORESCENT
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100
108
141
219
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20-AUG-97.
                                                                                                                                                                                                PF01353; GFP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217
238 AA;
PDB; 1KYR; 1
PDB; 1KYS; 1
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                                                                                                                                                                              NEAT CRYSTALLOGRAPHY (2.0 ANGSTROMS).

X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

REDLINE=99238303; PubMed=10220315;

RISTUCTURAL and spectral response of green fluorescent protein

XT variants to changes in pH.";

RICHOCHMISTRY 38:5295-5301(1999).

RICHOCHMISTRY 38:5295-5301(1999).

C. I-FUNCTION: Energy-transfer acceptor. Its role is to transduce the blue chemiluminescence of the protein aequorin into green

Eluorescent light by energy transfer. Fluorescence in vivo upon receiving energy from the Ga (2+) - activated photoprocein aequorin.

C. Absorbs light maximally at 395 nm and exhibits a smaller absorbance peak at 470 nm. The fluorescence emission spectrum peaks at 509 nm with a shoulder at 540 nm.

C. SUBUNIT: Monomer.

C. SUBUNIT: Monomer.

C. SUBUNIT: Monomer.

C. Modified amino acid residues. The chromophore is formed upon conditied amino acid residues. The chromophore is formed upon cyclisation of the residues Ser-dehydrofyr-Gly.

C. Ordinarios as a fluorescent protein and ubiquitous tool for making chimeric proteins of GPP linked to other proteins where it fuortions as a fluorescent protein tag GPP toderates N-and C-terminal fusion to a broad variety of proteins. It has been expressed in bacteria, yeast, slime mold, plants, Drosophila, cebrafish, and in mammalian cells. As a noninvasive fluorescent marker in living cells, it allows for a wide range of applications where it may function as a cell lineage tracer, reporter of gene expression, or as a measure of protein-protein interactions.

NOTE=ISBUE II of June 2001;

C. Ordinario and C. Ordinary of protein-protein interactions.
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                      CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF MUTANT WITH YELLOW EMMISSION
                    X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF MUTANT WITH YELLOW EMMISSION MEDLINE=98455509; PubMed=9782031; Wachter R.M., Elsliger M.A., Kallio K., Hanson G.T., Remington S.J.; "Structural basis of spectral shifts in the yellow-emission variants of green fluorescent protein."; Structure 6:1267-1277(1998).
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EMBL, MG2653, AAA27721.1; --
EMBL, L29345; AAA58246.1; --
EMBL, X96418; CAA65278.1; --
PIR, J30692; JQ1514; --
PDB, 139C; 17.NOV-00.
PDB, 13FP, 07-UUL-97.
PDB, 13FP, 07-UUL-97.
PDB, 12MA, 16-UNW-97.
PDB, 12MA, 20-AUG-97.
PDB, 12ME, 20-AUG-97.
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PDB, 13ME, 20-AUG-97.
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Gaps

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Length 238; Indels

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104 DGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADK-QKNGI 162 365 DEEIDLTKQAFVEHGKLVNSDEFDGKNF--DGAFNG-879 AA. diphosphate + L-leucyl-tRNA(Leu). Xanthomonadaceae; Xylella. 203 STQSALSKDPN 213 462 GVKSPINADPN 472 STANDARD; Xylella fastidiosa. SEQUENCE FROM N.A. NCBI_TaxID=2371; STRAIN=9a5C; SÝL XYLFA Q9PBG8; 163 SYL_XYLFA g g ò qq ð This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). 181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238 50 TTGKLPVPWPTLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKD-----59; 7.2%; Score 91.5; DB 1; Length 861; Indels 60; 26; Mismatches

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                                      461
                                                                                                                                                                                                                                                             409 GKROVNYRLRDWGVSRORYWGAPIPMLTLENGDVVPA-----PMEDLPIILPEDVVMD
----IADKLEKLGV
                    ---KVNFKIRH--------NIEDGSVQLADHYQQNTPIGDGPVLLPDNHYL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
18-PEB-2003 (Rel. 41, Last annotation update)
Leucyl-ERNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
LEUS OR XF2176.
                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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Nature 413:852-856(2001)
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MEDLINE=222531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.,
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CI18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 TTGKLPVPWPTLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNY--
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InterPro; IPR001300; tRNA-synt la.
InterPro; IPR001412; tRNA-synt la.
InterPro; IPR001412; tRNA-synt l.
InterPro; IPR001408; ValRS IleRS edit.
PRIMTS; PR0013; tRNA-synt l. 1.
PRINTS; PR00185; TRNASYNTHLEU.
TIGRPAMS; TIGR00186; leuS.
PROSTIE; PS00178; AA TRNA LIGASE I; 1.
Aminoacyl-tRNA synthètase; Proteïn biosynthesis; Ligase; ATP-binding;
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MEDLINE-21534947; PubMed=11677608;
MEDLINE-21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Fellwell T., Hanlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
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10-OCT-2003 (Rel. 42, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
LEUS CR STY0699 OR T2219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.0%; Score 89.5; DB 1; Length 879;
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"KMSKS" REGION.
ATP (BY SIMILARITY).
9FDCCB992092919E CRC64;
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29; Mismatches
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879 AA; 99796 MW;
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637 641
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                                                                                                                                                                                                                                                                                                                                                                                                     BINDING
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SYL, SALTI
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=LT2534948; PubMed=11677609;
MCClolland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., McClolland M., Sanderson K.E., Spieth J., Dante M., Du F., Hou S., Layman D., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium LT2.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002302; Leu-tRNAsyntla.
InterPro; IPR002302; Leu-tRNAsyntla.
InterPro; IPR002302; Leu-tRNA-synt la.
InterPro; IPR003008; ValRA-synt la.
InterPro; IPR009008; ValRS_IlaRS_edit.
Pfam; PF00133; tRNA-synflla.
ITGRPAMS; TIGR00395; TRNASYNFHLEU.
TIGRPAMS; TIGR00395; leub bact; 1.
PROSTIE; PS00118; AA TRNA_LIGASE I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
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                                                                                               -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
LEUS OR STM0648.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBL_TaxID=602;
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-!- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP
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622 622 ATP (BY SIMILARITY).
860 AA; 96940 MW; 2F95E480BBAB23C4 CRC64;
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23.3%; Pred. No. 15;
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                               diphosphate + L-leucyl-tRNA(Leu).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
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Best Local Similarity 23.35.
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Sugino A.;
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                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0985; TRNASYNTHLEU.
TIGRFAMB; TIGRO0396; leuS bact; 1.
PROSITE; PS00178; AA TRNA_LIGASE I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                           diphosphate + L-leucyl-tRNA(Leu).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
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MEDLINE=96310631; PubMed=8740425;
Sen-Gupta M., Lyck R., Fleig U., Niedenthal R.K., Hegemann J.H.;
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Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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01-AUG-1991 (Rel. 19, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
DNA polymerase epsilon, catalytic subunit A (EC 2.7.7.7) (DNA
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MEDLINE=90381771; PubMed=2169349;
Morrison A., Araki H., Clark A.B., Hamatake R.K., Sugino A.;
"A third essential DNA polymerase in S. cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 860;
CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP +
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ATP (BY SIMILARITY).
DS003584DFBCCAB6 CRC64;
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6.9%; Score 87.5; I
Best Local Similarity 23.3%; Pred. No. 15;
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InterPro; IPR002302; Leu-tRNAsyntla.
InterPro; IPR001302; ERNA-synt la.
InterPro; IPR001412; tRNA-synt I.
InterPro; IPR009008; ValRS ILERS edit.
Pfam; PF00133; tRNA-synt 1: 1.
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POL2 OR DUN2 OR YNL262W OR N0825.
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623 "KN
622 ATE
; 96985 MW; I
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622 63
860 AA;
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P21951;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 FFKDDGNYKTR--AEVKFEGDTLVNR------IELKGIDFKEDGNILGHKLEYNYN 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPLICATION.
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate + {DNA}(N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- SUBUNIT: CONSISTS OF FIVE SUBUNITS (200 kDa, 80 kDa, 34 kDa, 30 kDa, AND 29 kDa).
-:- SUBGELIGIAR LOCATION: Nuclear.
-:- SUBGELIGIAR LOCATION: Nuclear.
-:- DOMAIN: THE DNA POLYMERASE ACTIVITY DOMAIN RESIDES IN THE N-TERMINAL HALF OF THE PROTEIN, WHILE THE C-TERMINUS IS NECESSARY FOR COMPLEXING SUBUNITS B AND C.
-:- MISCELLANBOUS: In eukaryotes there are five DNA polymerases: alpha, beta, gamma, delta.
-:- SIMILARITY: Belongs to the DNA synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 LPVPWP-TLVTTLSYGVQCFSRYPDHM------KQHDFFKSAMPEGYV----QERTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                883 LPKSFPETYFPTLENGKKLYLSYPCSMLNYRVHQKFTNHQYQELKDPLNYIYETHSENTI
                                                                                                                                                                                                                                                                                                                                    "DNA polymerase II, the probable homolog of mammalian DNA polymerase epsilon, replicates chromosomal DNA in the yeast Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31; Gaps
"The sequence of a 24,152 bp segment from the left arm of chromosome XIV from Saccharomyces cerevisiae between the BNI1 and the POL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBO J. 11:733-740(1992).
-!- FUNCTION: DNA POLYMERASE II PARTICIPATES IN CHROMOSOMAL DNA
                                                                                                                                                                                                                                                          Araki H., Ropp P.A., Johnson A.L., Johnston L.H., Morrison A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R EMBL; M60416; AAA88711.1; -.

R EMBL; 271538; CAA46169.1; -.

R EMBL; 271538; CAA46169.1; -.

R EMBL; 271538; CAA46169.1; -.

R Germonline; 143268; -.

Germonline; 143268; -.

R GGD; SO005206; POL2.

R GG; GO:0000731; P:DNA repair synthesis; IMP.

R InterPro; IPR006134; DNA_Pol_B dom.

R InterPro; IPR006134; DNA_Pol_B dom.

R Pfam; PF00116; DNA_Pol_B = xco.

R Pfam; PF00116; DNA_Pol_B 1.

R PARAT; SW00486; POLEC; 1.

R PROSITE; PS00116; DNA_POLYMERASE B; FALSE_NEG.

R PROSITE; PS00116; DNA_POLYMERASE B; PALSE_NEG.

R Transferase; DNA-directed DNA_Polymerase; DNA replication;

T NA_PING 2108 2181

POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.9%; Score 87.5; DB 1; Length 2222;
28.2%; Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     644 644 M -> I (IN POL2-9 TS MUTANT).
710 710 P -> S (IN POL2-18 TS MUTANT).
2222 AA; 255669 MW; CBCDDE2AB147D65B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Mismatches 49; Indels
                                                                                                                                                                                                                           MEDLINE=92164663; PubMed=1537345;
                                                                                                                                                                                         TEMPERATURE SENSITIVE MUTANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 28.2%
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | |:: |
1000 SDIFKVFLEGD 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 S--HNVYIMAD 156
                                                                                                               Yeast 12:505-514(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                        cerevisiae.";
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689
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689 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45
446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acetyl-CoA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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TISSUB-Brain, and Testis;

MEDLINE-2238257; PubMed-1247932;

MEDLINE-2238257; PubMed-1247932;

MEDLINE-2238257; PubMed-1247932;

MEDLINE-2238257; PubMed-1247932;

MEDLINE-2238257; PubMed-1247932;

MA Clausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Hale S., Garcinici P., Prange C.,

Richards S., Worley K.C., Hale S., Garcinici P., Prange C.,

N. Milalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Makealey J., Helton B. Ketterman M., Myers R.M.,

Blakealey R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

M. Schmerzh A., Schein J.B., Jones S.J.M., Marra M.A.,

M. Schein J.B., Jones S.J.M., Marra M.A.,

M. Schein J.B., Jones S.J.M., Marra M.A.,

Rodriguez A.C., Grimwood S.J.M., Marra M.A.,

Rodriguez A.C., Grimwood S.J.M., Marra M.A.,

Rodriguez A.C., Grimwood S.J.M., Marra M.A.,

Rodriguez A.C., Grimwood S.J.M., Marra M.A.,

Rodriguez A.C., Grimvood S.J.M.,

Rodrigu
                                                                                                                                                                                                                                                                                                                                                                                 Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., ABDLINE=21638749; PubMed=11780052; Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Andelda J.P., Babbage A.K., Baggalley C.L., Bailey J., Barlow K.F., Baggalley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Brown A.J., Bailey J., Burlil W.D., Buller A.P., Carder C., Carter N.B., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., Clegg S., Cobley V.E., Collier R.E., Carder C., Carter N.B., Coulson A., Covile G.J., Deadman R., Dhami P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Blington A.G., Frankland J.A., Fraser A., French L., Garner P., Ammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Howken D., W., Wimber C., Orliftiths M.N.D., Gwilliam R., Hall R.E., Ammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Awarsh V.L., McConnachhe L.J., McLay K., McMurray A.A., McConnachhe L.J., McLay K., McMurray A.A., Milliws W.J., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Awarsh V.L., Scott C.E., Sehward C.A., Shownkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Shownkeen R., Shan R.M., Sycamore N., Taylor R., Tracey A., Tromans A.C., Vaudin M., Wallis J.M., Whittewer P., Whiltey D.L., Williams L., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 169-689 FROM N.A. (ISOFORM 1).
TISSUE=Placenta, and Tongue;
Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                         AC2L HUMAN STANDARD, PRT, 689 AA.
Q9NUB1, Q81V99; Q8N234; Q96J11; Q96JX6; Q9NU28;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Acctyl.coensyme A synthetase 2-11ke, mitochondrial precursor (EC 6.2.1.1) (Acetyl-CoA ligase 2) (Acetyl-COA synthetase 2-ACAS2L OR KIAA1846.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rogers
                RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ů
Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Irie R., Sato H., Yamanoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawai H., Murakawa K., Tanatahashi-Fujii A., Oshima A., Sugiyama A., Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishibashi T. Kawai Y., Washatsu A., Kanehori K., Suzuki Y., Sugano S., Ishii S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Sugano S., Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
MEDLINE=21245130; PubMed=11347906;
MEDLINE=21245130; PubMed=11347906;
Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
Nagase T., Nakayama M., Saguences of unidentified human genes. XX.
The complete sequences of 100 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for oxidation through the tricarboxylic cycle to produce ATP and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for large proteins in vitro.";
DNA Res. 8:85-95(2001).
-!- FUNCTION: Converts acetate to acetyl-CoA so that it can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- CAUTION: Ref.1 (CABB1884) sequence differs from that shown due erroneous gene model prediction.
-!- CAUTION: Ref.3 sequence differs from that shown due to a frameshift in position 250 and numerous sequencing errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACETYL-COENZYME A SYNTHETASE 2-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CO(2) (By similarity).
-!- CATALYTIC ACTIVITY: ATP + acetate + CoA = AMP + diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q9NUB1-2; Sequence=VSP 007249;
Note=No experimental confirmation available;
-!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.8%; Score 87; DB 1; Length 689;
4.1%; Pred. No. 13;
ve 16; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTIG=VSP 007249.
V -> M (IN REF. 2; AAH39261).
V -> M (IN REF. 2; AAH44589).
66E84E39302AD08B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; ABUDS 49; DECASSINGENCE: 16091; ACASSINGENCE: 16091; ACASSINGENCE: 16091; AMP-binds: 10 PROSITE; PRO0455; AMP_BINDING; 1. PROSITE; PS00455; AMP_BINDING; 1. PROSITE; PS00455; AMP_BINDING; 1. ALLERNATIAL); 36 MITOCHONDRION (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 336-689 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q9NUB1-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AK027817; BAB55390.1; ALT INIT.
EMBL; AK092295; BAC03853.1; ALT_SEQ.
EMBL; AB058749; BAB47475.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL035661; CAB75500.1; -.
EMBL; AL080312; CAB81884.1; ALT_SEQ.
EMBL; BC039261; AAH39261.1; -.
EMBL; BC044588; AAH44588.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             488 V
74856 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 llarity 24.1%;
Conservative 1
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Matches 33; Conserv
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087065;
S F F F S
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                             FFGIVPVLMDEKGSV-----VEGSNVSGALCIS-----QAWPGMARTI--- 510
                                                             69 VQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRA---EVKFEGDTLVNRIE 125
                                                                               -----YGDHQRFVDAYFKAYP-GY-----YFTGDGAYRTEGGYYQITGRMDDVI---- 553
FIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLSYG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Geber A., Hitchcock C.A., Swartz J.E., Pullen F.S., Marsden K.E., Kwon-Chung K.J., Bennett J.E.;
"Deletion of the Candida glabrata ERG3 and ERG11 genes: effect on cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).

CATALYTIC ACTIVITY: Obtusifoliol + 3 O(2) + 3 NADPH = 4-alphamethy. - 5-alpha-ergosta-8,14,24(28)-trien-3-beta-ol + formate + NADP(+) + 3 H(2)O.

PATHWAY: Ergosterol biosynthesis.
SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rossier M.;

Rapid detection and identification of Candida albicans and
Torulogais (Candida) glabrata in clinical specimens by
Torulogaic candida) glabrata in clinical specimens by
species-specific nested PCR amplification of a cytochrome P-450
lanosterol-alpha-demethylase (LIA1) gene fragment.";
J. Clin. Microbiol. 32:1902-1907(1994).

-!- FALTION: Catalyzes Cl4-demethylation of lanosterol which is
critical for ergosterol biosynthesis. It transforms lanosterol
into 4,4'-dimethyl cholesta-8,14,24-triene-3-beta-ol (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; 1.
Electron transport; Oxidoreductase; Monooxygenase; Membrane; Heme;
                                                                                                                                                                                                                                     CP51 CANGA STANDARD; FKI; 53.4...

CP5859, Q02312;

01-0CT-1996 (Rel. 34, Last sequence update)

10-0CT-2003 (Rel. 42, Last annotation update)

10-0CT-2003 (Rel. 42, Last annotation update)

20-0CT-2003 (Rel. 42, Last annotation update)

10-0CT-2003 (Rel. 42, Last annotation update)

11-0-0CT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ATCC 2001;
MEDLINE=95081364; PubMed=7989540;
Burgener-Kairuz P., Zuber J.P., Jaunin P., Buchman T.G., Bille J.,
                                                                                                                                                                                                                                                                                                                                                                Candida glabrata (Yeast) (Torulopsis glabrata).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            viability, cell growth, sterol composition, and antifungal
susceptibility.";
Antimicrob. Agents Chemother. 39:2708-2717(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; S75389; AAB32679.1; -.
InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; p450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96161286; PubMed=8593007;
                                                                                                                                                           -----NISGHRL 560
                                                                                                                            126 LKGIDFKEDGNILGHKL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L40389; AAB02329.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 60-473 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=5478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=2001-L5;
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WEDLINE-22421331; PubMed=12533478;

WEDLINE-22421331; PubMed=12533478;

WA SLUYB M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,

A Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,

A Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,

A Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,

A Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,

A Marino C.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E.,

A Marino C.L., Giglioti B., Abreu I.L., Alves L.M.C., do Amaral A.N.,

Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,

A Gruha A.F., Ferrile R.C., Ferro J.A., Formigheri E.F., Kishi L.T.,

A Geouza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G.,

A Circello E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 KOHDFFKSAM-PEGYV-----OERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDF 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191
                                                                                                                                                                                                                                                                                                                                                       79
                      472 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
64 I -> M (IN REF. 2).
473 I -> T (IN REF. 2).
61305 MW, A0506C17507E6EF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                   25 GHKFSVS---GEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLSYGVQCFSRYPDH--M
                                                                                                                                                                                                                                                                                                                                                                                                                      109 GHEFIFNAKLADVSAEAAYSHL-------TIPVFGKGVIYDCPNHRLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 EQKKFVKGALTKEAFVRYVPLIAEBIYKYFRNSKNFKINENNSGIVDVMVSQPEM--TIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 KEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 185:1018-1026(2003).
-!- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP +
diphosphate + L-leucyl-tRNA(Leu).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Comparative analyses of the complete genome sequences of Pierce's disease and citrus variegated chlorosis strains of Xylella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leucyl-RNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
LEUS OR PD1230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                     6.8%; Score 86.5; DB 1; Length 533; 11.4%; Pred. No. 10;
                                                                                                                                                                                                     Query Match
Best Local Similarity 21.4%; Pred. No. 10;
Matches 44; Conservative 32; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xylella fastidiosa (strain Temeculal / ATCC 700964)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               879 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 GPVLLPDNHYLSTQSALSKDPNEKRD 217
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Sterol biosynthesis; NADP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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473
533 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=183190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fastidiosa.";
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                                                           CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 TAYGLRFGSEC-------KECEKGGFVQPQTVYTYTKNEKLQESEVNSIYT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 -----NYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMAD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258 INVNGQEVVKSETRAKVTFVEESKINR-EIK------KVSGPKEEIVYSMENEKLIEQ 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 MESDKDSLFFNVHEKTMEGDCEV---AYTIVQEG-GKTIYTKSVNFDKCITR-----PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPMPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEG-YVQERTIF---FKDDG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campylobacter jejuni.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WEDLINE=20150912; PubMed=10688204; Ketley J.M., Churcher C., Parkhill J., Wren B.W., Mungall K., Ketley J.M., Chullingworth T., Davies R.M., Feltwell T., Holroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Pen C.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
FRMA (Uracil-5-)-methylrransferase (EC 2.1.1.35) (FRNA (M-5-U54)-methyltransferase) (RUMT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 1603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        30 Y -> V (IN REF. 3).

69 L -> V (IN REF. 2).

87 EVAYT -> RSELH (IN REF. 2).

75 T -> S (IN REF. 2).

186307 MW; E303170325BC99BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 KQKNG-----IKVNFKIRHNIEDGSVQLADHYQQNTP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309 FYKQGDKAEVNPFKAIEIEQKV-EQLEEIFRQIQEH-EQNTP 348
                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
VITELLOGENIN 4.
VWFD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.8%; Score 86.5; I
                                                                                                                                                                                                                                                                                                                                                                          family; Signal.
   subsequently taken up by the gonad.
                                                                                                                                                                                                                                                                                      transprt_N.
                                                                                                                                                                                                                                             PIR, A43084; A43384.

WormPep, F59D8.2; CE26817.
InterPro; IPR001747; Lipid_transprt.
InterPro; IPR001747; UWF_D.
Pfam; PF0147; Vitellogenin_N; I.
SMART; SM0638; LED N; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Campylobacteraceae; Campylobacter,
                                                                                                                                                                                                EMBL; AC024137; AAK09074.1; -.
                                                                                                                                                                                                                  EMBL; M11498; AAA28163.1; -. EMBL; X02754; CAA26531.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 23.4%;
les 52; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                        Storage protein; Multigene SIGNAL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                            1603
1455
30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=NCTC 11168;
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169
183
275
1603
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TRMA_CAMJE
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                                                                                                                                                                                                                                                                                                                                                                          TTGKLPVPWPTLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNY-- 107
                                                                                                                                                                                                                                                                                                                                                                                                           321 TNEQLPV-WVANFVLMAYGTGAVMAVPGHDQRDQEF--ANKYGLPIRQVIALKEPKNQDE 377
                                                                                                                                                                                                                                                                                                                                                                                                                                               -----KTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 MADKQKNG-IKVNFKIRHNIEDGSVQLADHYQQNTPI------GDGPVLLPDN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---RÖGRGORRVNYRLR----DWGVSRORYWGCPIPVIYCPTCGAVPVPENOLPVILPEN 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE=85269641; PubMed=4022780;
MEDIINE=85269641; PubMed=4022780;
MEDIINE=85269641; PubMed=4022780;
Spieth J., Denison K., Kirtland S., Cane J., Blumenthal T.;
The C. elegans vitellogenin genes: short sequence repeats in the promoter regions and homology to the vertebrate genes.";
Nuclei. Acids Res. 13:5283-5295(1985).
-!- FUNCTION: Precursor of the egg-yolk proteins that are sources of nutrients during embryonic development (Potential).
-!- SUBCELULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Synthesized in Caenorhabditis only by 32 cells building the intestine of adult hermaphroditic individuals; they are cotranslationally secreted into the body cavity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  378 STWEPDVWRDWYADKTR---EFE---LINSAEFDGLDYQGAFEVLAERFE-----
EMBL; AE012557; AA029080.1; ALT_INIT.

HAWAP; MF 00049; -; I
Interbro; IPR002302; Leu-tRNAsyntla.
Interbro; IPR002300; ERNA-syntla.
Interbro; IPR001412; ERNA-syntla.
Interbro; IPR001908; VaIRS_IIERS_edit.
Pfam; PF00133; ERNA-syntli.
PRINTS; PR00985; TRNASYNTHLEU.
TIGRFAMS; TIGR00396; TENDASYNTHLEU.
PROSITE; PS00178; AA_TRNA_LIGASE; 1.
PROSITE; PS00178; AA_TRNA_LIGASE; 1.
Aminoacyl-ERNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
Eukaryɔta; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                       57;
                                                                                                                                                                                                                                                                                                        DB 1; Length 879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRANIN-Bristol N2;
Waterston R1;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blumenthal T., Spieth J., Zucker E.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                 ATP (BY SIMILARITY).
4C2EE01B8FDC497E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIT4_CAEEL STANDARD; PRT; 1603 AA. P18947; Q9BPP3; 01-NOV-1990 (Rel. 16, Created) 10-CCT-2003 (Rel. 42, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                  "KMSKS" REGION
                                                                                                                                                                                                                                                                                                    6.8%; Score 86.5; D
22.2%; Pred. No. 19;
tive 28; Mismatches
                                                                                                                                                                                                                  "HIGH" REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 -HYLSTQSALSKDPNEKR 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        475 VAFSGTGSPIKTDPEWRK 492
                                                                                                                                                                                                                                                                   99823 MW;
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                                                                                                                                                                                                                                                                                                                     Local Similarity 22.2 tes 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vitellogenin 4 precursor.
VIT-4 OR F59D8.2.
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641
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879 AA;
                                                                                                                                                                                                 Complete proteome.
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thylakoid membrane.
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YCO3_KLEPN
ID YCO3_KLEPN
AC Q48449;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 KQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKF--EGDTLV------NRIELKG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 IDFKED-------GNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIE 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 LDFADEKICAFMPRLLEYLRQDNKLKEKL-----FGVEFLTTKQE--LSITLLYHKNIE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73
                                                            reveals hypervariable sequences.";
Nature 403:665-668(2000).
-!- FUNCTION: Catalyzes the formation of 5-methyl-uridine at position 54 (M-5-U54) in all tRNA (By similarity).
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-homocysteine + tRNA containing thymine.
-!- Similarity: Belongs to the RNA M5U methyltransferase family. TrmA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M., Whitehead S., Barrell B.G.; "The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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"Nucleotide sequence of the cyanelle DNA from Cyanophora paradoxa.";
Plant Mol. Biol. Rep. 13:327-332(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPKUU1300, P. 1. 1.
PROSITE, PS01230; TRMA 1; 1.
PROSITE, PS01231; TRMA 2; FALSE_NEG.
Transferase; Methyltransferase; tRNA processing; Complete proteome.
Transferase; Methyltransferase; tRNA processing; Complete proteome.
S-ADENOSYLMETHIONINE BINDING (BY
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16-OCT-2001 (Rel. 40, Last annotation update)
Photosystem II 44 kDa reaction center protein (P6 protein) (CP43)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=UTEX LB 555 / Pringsheim;
Stirewalt V.L., Michalowski C.B., Loeffelhardt W., Bohnert H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.8%; Score 86; DB 1; Length 357;
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18; Mismatches
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STRAIN=UTEX LB 555 / Pringsheim;
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL139076; CAB73096.1; -.
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HAMAP; MF 01011, -; IIICEPPCO; IPR0000651; SAM bind.
INCEPPCO; IPR001566; TAMĀ.
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(Rel. 33, Last seq
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nes 30; Conservative
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357 AA;
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                                                                                                                                                                                                                           subfamily.
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SEQUENCE
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365 LT-KIKYDIQPWQERRAABYMTHAPLGSLNSVGGVATEINSVNYVSPRSWLS-----TS 417
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Loeffelhardt W., Stirewalt V.L., Michalowski C.B., Annarella M., Farley J.Y., Schluchter W.M., Chung S., Newmann-Spallart C., Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.; "The complete sequence of the cyanelle genome of Cyanophora paradoxa: the genetic complexity of a primitive plastid."; (In) Schenk H.E.A., Herrmann R., Jeon K.W., Mueller N.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 GHKFSVSGEGEGDATYGKLTLKFICTTGKL-----PVPWP--TLVTT----LSYGV---
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Enterobacteriaceae, Klebsiella.
                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: The 43 kDa protein (p6) is a component of the core photosystem II. It is a chlorophyll binding protein.
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Photosynthesis; Photosystem II; Thylakoid; Chlorophyll; Cyanelle;
                                                                                                                                                                                                                              Schwemmler W. (eds.);
Eukaryotism and Symbiosis, pp.40-48, Springer-Verlag, Heidelberg
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1-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last amnotation update)
Hypothetical 55.8 kba protein in cps region (ORP3).

    -!- SIMILARITY: Belongs to the psbB / psbC family

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21.0%; Pred. No. 9.4;
tive 35; Mismatches
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InterPro; IPR000932; PSIIprot
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Matches 57; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 YIMADKQKNGIKVNFKIRHNIEDGSVQLADH------YQQNTPIGDGPVLL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 YILKDKYSEKISVEIMDHKKİKNIGMNAYLHVSKGSSKNPYLSIIKYNENKFNGKSPIIL 267
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01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
P protein [Includes: DNA-directed DNA polymerase (EC 2.7.7.7); RNA-directed DNA polymerase (EC 2.7.7.7);
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MEDLINE=8833160; PubMed=3418788;
Sprengel R., Kales B.F., Will H.;
"Isolation and characterization of a hepatitis B virus endemic in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
MANGAREES 2 (BY SIMILARITY).
MANGAREES 1 AND 2 (BY SIMILARITY).
MANGAREES 1 (BY SIMILARITY).
MANGAREES 1 (BY SIMILARITY).
MANGAREES 1 (BY SIMILARITY).
MANGAREE 1 AND 2 (BY SIMILARITY).
W, 4E181EEBEB481FE3 CRC64;
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-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
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ACT SITE 282 282 OCTENTIAL.
ACT SITE 356 POTENTIAL.
METAL 270 270 MANGANESE
                                                                                                                                                                                                                                                                                                                                         HAMAP; MF_00181; -; 1.
InterPro; IPR00819; Peptidase_M17_C.
InterPro; IPR00823; Peptidase_M17_N.
Pfam; PF00883; Peptidase_M17; I.
Pfam; PF00789; Peptidase_M17; I.
PRINTS; PR00481; LANNOPPTASE.
PROSITE; PS00631; CXTOSOL_AP; 1.
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270 MA
275 MA
293 MA
354 MA
354 MA
56643 MW;
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SEQUENCE
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                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 QCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGD-TLVNRIELKG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 QMVGEDESGYLPSANMFLGGIEGHH-GWGKDAVNWYVEAHDTRTNMSRTNYSYTHHIYKD 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       399 G-----YYQQGYPLGDAMGGDGQLFAGKVELITENNQRWSTRLAYAKVNPKDQSINKAF 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 QSFSSFWDGFTGHD------NTGTDNEPGNQLAGFDFKFKLEPTLGWPVSFYG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 IDFKED------GNILGHKLEYNYNSHNVYIMA-DKQKNGIKVNFKIRHNI-ED 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 GSVQLADHYQQNTPIGDG------PVLLPDNHYLSTQSALSK-DPNEKRDHMVL 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALTICA ATTIVITY: Release of an N-terminal amino acid, Xaa-|-Xbo-, in which Xaa is preferably Leu, but may be other amino acids including Pro although not Arg or Lys, and Xbb may be Pro. COFACTOR: Binds 2 manganese ions per subunit (By similarity). SUBJCELULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: Belongs to peptidase family M17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation update)
Probable cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLIN3=22297718; PubMed=12219091;
Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                           in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . Genet. 32:402-407/2002/.
FUNCTION: Presumably involved in the processing and regular turnover of intracellular proteins. Catalyzes the removal of unsubstituted N-terminal amino acids from various peptides (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterciacteriaceae, Wigglesworthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome sequence of the endocellular obligate symbiont of tsetse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48;
                                                                                                                      responsible for sective K2 capsular polysaccharide synthesis virulent strain Chedid.";
J. Bacteriol, 177:1788-1796(1995),
MEDLINE=95204345; PubMed=7896702;
Arakawa Y., Wacharotayankun R., Nagatsuka T., Ito H., Kato N.,
                                                                                                           cps region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
6.8%; Score 86; DB 1; Length 504;
Best Local Similarity 24.0%; Pred. No. 10;
Matches 46; Conservative 27; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .l protein.
504 AA; 55782 MW; AD887595CFDFDFAB CRC64;
                                                                                                    "Genomic organization of the Klebsiella pneumoniae
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Nat. Genet. 32:402-407(2002).
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SEQUENCE 50
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Q8D295;
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(See http://www.isb-sib.ch/announce/
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197 TWEQKHLVPQQHGAYSSKINDRQESRRRRIITATSSRKNDSSRI------FGAHN---- 245
                                                                                                                                                                                                                                                                                                                                                                                                                                246 -----NGRKISY---HSTRDGSHRLSGRTSDPTSRGALAGGDSTPIGPGSTAAHPSTHHV 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 T-------RAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIM 154
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                                                     BMBL; M22056; AAA45738.1; -
PIR; A30082; JDVLHH.
InterPro; IPR001462; DNApol_viral_C.
InterPro; IPR001462; DNApol_viral_N.
InterPro; IPR00477; RVT8e.
Pfam; PF00242; DNA_pol_viral_N; 1.
Pfam; PF00242; DNA_pol_viral_N; 1.
Pfam; PF00078; rvt; 1.
ProDom; PD000814; DNApol_viral_C; 1.
ProDom; PD000814; DNApol_viral_C; 1.
Transferase; RNA-directed DNA polymerase; Hydrolase; NNClease; Endonuclease; DNA replication; DNA-binding.
SEQUENCE 788 AA; 90070 MW; FB44F38F75EADF44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    65; Gaps
                                                                                                                                                                                                                                                                                                                          Query Match 6.7%; Score 85.5; DB 1; Length 788; Best Local Similarity 19.7%; Pred. No. 20; Matches 40; Conservative 32; Mismatches 66; Indels 63
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Search completed: June 21, 2004, 15:55:24 Job time: 7.55556 secs

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2 VSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cocurrence of green fluorescence protein in diazotrophic bacteria Azomonas and Azotbacter."

"Occurrence of green fluorescence protein in diazotrophic bacteria Azomonas and Azotbacter.";

Submitted (NOV-2000) to HE EMBL/GenBank/DDBJ databases.

EMBL; AF324408; AAN86140.1; -.

GO; GO:0006091; P:energy pathways; IEA.

InterPro; IPR009017; GFP_like.

InterPro; IPR009017; GFP_like.

PRINTS; PR0153; GFP; 1.

PRINTS; PR01229; GFPUORESCENT.

PRODM; PR013756; Green fl protein; 1.

SEQUENCE 238 AA; 26914 WW; F84840FIF9064018 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azotobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vi-mak-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
2289GFP
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086LV7
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Q8MU48
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Q962P9
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Q9U6Y3
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OBGHE2;
01-MAR-2003 (TrEMBLrel.
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STRAIN=DSM2289;
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                                                                                             June 21, 2004, 15:45:30 ; Search time 30.6667 Seconds
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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sp. bacteria: *
sp. fungl: *
sp. human: *
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sp. mammal: *
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sp. organelle: *
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62 VTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERIFFKDDGNYKTRAEVKFEGDTLV 121

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61 VITFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTLV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLAGFVTAAGITLGMDELYK 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPMPTL
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"Occurrence of green fluorescence protein in diazotrophic bacteria Azomonas and Azotobacter.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF324406; AAN86138.1; -..
GO; GO: 0006091; P: energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IPR009017; GFP_like.
Pfam; PF01353; GFP; 1.
                                                                                                                                                                                                            Koranyi P., Berenyi M., Burg K.; Cocurrence of green fluorescence protein in diazotrophic bacteria Azomonas and Azotobacter."; Azomonas and Azotobacter."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Azotobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.8%; Score 1233; DB 2; Length 238; 97.1%; Pred. No. 2.9e-95;
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ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 26902 MW; 15FE9B9C5B4F6B89 CRC64;
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PRODOM; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 26887 MW; E0E1616BD2AF6188 CRC64;
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GO; GO:0006091; P:energy pathways; IBA.
InterPro; IRR009017; GFP_like.
InterPro; IPR000786; Green_fl_protein.
Pfam; PF01353; GFP; 1.
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01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
Green fluorescence protein.
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Matches 231; Conservative
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                                                                                                                                                   NCBI_TaxID=116849;
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                   Azomonas agilis.
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01-OCT-2003
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                                                                      61 VITFGYGVQCFARYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
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  VITFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                           NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
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                                                                                                                             HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLAGFVTAAGITLGMDELYK 239
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MEDLINE=96305137; PubMed=8707053;
Ornack B.P., Valdivia R.H., Falkow S.;
"FACS-optimized mutants of the green fluorescent protein (GFP).";
Gene 173:33-38(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Yeast Enhanced Green Fluorescent Protein (YEGFP): a reporter of expression in Candida albicans.";
Microbiology 0.0-0(1996).
EMBL; U73901; ABB18957.1; -
HSSP; P42212; 1BFP.
                                                                                                                                                                                                                                                                                                                                                                                                           Aeguorea victoria (Jellyfish).
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aeguoreidae; Aeguorea.
NCBI_TaxID=6100;
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26840 MW; A28622809A9DEA60 CRC64;
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01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Green fluorescent protein mutant 3.
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97.1%; Pred. No. 1.9e-95;
iive 2; Mismatches 5;
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InterPro; IPR009017; GFP_like.
InterPro; IPR000786; Green_fl_protein.
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PRINTS; PR01229, GFLUORESCENT.
ProDom, PD013756; Green fl pro
SEQUENCE 238 AA, 26840 MP,
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RESULT 3 Q8GHE4 ID Q8GH AC Q8GH DT 01-M

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121 NRIELKGIDFKEDGNILGHKMEYNYNSHNYYIMGDKPKNGIKVNFKIRHNIKDGSVQLAD 180
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                                                                                                                                                                                                                                                                          Aequorea victoria (Jellyfish).
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=6100;
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q.,
Li S.J., Xia N.S.,
"Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5; Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Markins J.N.; dempbell A.K.; Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases. Bubmitted (JAN-1995) to the EMBL/GenBank/DDBJ databases. R Submit; X83960; CAA58790.1; -. FPR 15.050629; JQ1514. R HSSP; P42212; JBFP. GO; GO:0006091; P:energy pathways; JEA. R InterPro; JPR009017; GFP_11ke. R InterPro; JPR009017; GFP_11ke. R InterPro; JPR009017; GFP_11ke. R Pfam; PF01353; GFP; 1. PRINTS; PR01229; GFLUORESCENT. R ProDom; PD013756; Green_fl_protein; 1. ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_protein; 1. R ProDom; PD013756; Green_fl_prot
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF43431; AAL33916.1; -.
GO; GO:0006091; P:enercyp pathways; IEA.
InterPro; IPR009017; GPP_like.
InterPro; IPR0090786; Green_fl_protein.
                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Green fluorescent protein (Fragment).
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Last annotation update)
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Best Local Similarity 92.99
Matches 221, Conservative
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
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Watkins J.N., Campbell A.K.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.

EMBL; X83959; CA558789-1; -.

R HSS; P42212; JGPL.

R GO; GO:0006091; P:energy pathways; JEA.

InterPro; IPR009017; GFP_like.

InterPro; IPR009017; GFP_like.

R Pfam; PF01353; GFP; J.

R Pfam; PF01353; GFP; J.

R PRINTS; PR01229; GFLUORESCENT.

R PRINTS; PR01229; GFLUORESCENT.

R PODOM; P0013756; Green_fl_protein; J.
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    Pred. No. 3.5e-95;
2; Mismatches 5; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Green fluorescent protein (Fragment).
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97.1%;
    Best Local Similarity 97.1
Matches 231; Conservative
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Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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                                                                                                                Length 238;
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PRINTE, PR01229, GFLUORESCENT.
PRODON, PD013756; Green fl protein; 1.
PRODENCE 238 AA, 27049 WW, 8185D0E5E529012B CRC64;
PRINTS, PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl_protein; 1.
SEQUENCE 238 AA; 27015 MW; 6B8FD75E88926903 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                          84.8%; Score 1080; DB 5;
81.9%; Pred. No. 1.8e-82;
ive 20; Mismatches 23;
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Pred. No. 4e-82;
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81.5%; Pred. No. -c...
144. 20; Mismatches
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Matches 194; Conservative
                                                                                                                                                                          Matches 195; Conservative
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                                                                                                                                            Best Local Similarity
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Q8WP95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VSKGEELFTGVVPILVELDGDVNGHKFSVSGEGGEGDATYGKLTLKFICTTGKLPVPWPTL
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Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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                                                                                                                                                               Aequorea macrodactyla.
Eukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroìda, Leptomedusae,
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Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q.,
Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                             macrodactyla.";
Submitted (OCT-2011) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-2011) to the EMBL/GenBank/DDBJ databases.
EMBL; AR4534913 AAL3318.1;
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR000917; GFP_like.
InterPro; IPR000786; Green_fl_protein.
PRINTS; PR01259; GFL00RESCBNT.
PRODOM; PD013756; Green_fl_protein; 1.
SEQUENCE 238 AA; 26956 WW; 75521EAF0CEBA73A CRC64;
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Last annotation update)
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Last annotation update)
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82.4%; Pred. No. 8.6e-82;
iive 17; Mismatches 25;
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01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2003 (TrEMBLrel. 25,
                                                             01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25, green fluorescent protein.
                                              01-MAR-2002 (TrEMBLrel. 20,
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Best Local Similarity 82.4%
Matches 196; Conservative
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PRELIMINARY;
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122 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
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Q8WTC9
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Q8WTC7
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
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                                                                                                                                                                                                                                        ; Score 1070; DB 5; Length 2; Pred. No. 1.3e-81; 20; Mismatches 25; Indels
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
Submit Red (OCT-2011) to the EMBL/GenBank/DDBJ databases.
EMBL, AF435429; AAL33914.1; -.
GO, GO:0006091; P:energy pathways; IEA.
InterPro: IPR000917; GFP_1ike.
InterPro: IRR000786; Green_fl_protein.
PF01353; GFP; I.
  (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                      EMBL; AF435427; AAL33912.1; -. GO; GO: 0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IPR000786; Green_fl_protein.
Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
PRODOM; P0013756; Green_fl_protein; 1.
SEQUENCE 238 AA; 26997 MW; 5F80A192173CB84D CRC64;
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PRODOM; PRO13756; Green fl protein; 1.
SEQUENCE 238 AA; 27047 MW; 5F80Al8FALE7C84D CRC64;
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Last sequence update)
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81.1%; Pred. No. 1.5e-81;
iive 20; Mismatches 25;
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Best Local Similarity 81.1%;
Matches 193; Conservative 2
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NCBI_TaxID=147615;
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Best Local Similarity
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    Submitted
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08WTCB
AC Q8WTCB
DT 01-MADT
DT 01-MADT
DT 01-OC
DE Green
GR Aeque
OC BUKAI
OC REUKAI
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62 VITLSYGVOCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
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                                                                           182 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLAGFVTAAGITLGMDELYK 239
                                                                                                          181 HYOTNVPLGDGPVLIPINHYLSYQTAISKDRNETRDHMVFLEFFSACGHTHGMDELYK 238
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Li S.J., Xia N.S.;
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI TaxID-147615;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 macrodactyla.";
Submitted (OCT-2011) to the EMBL/GenBank/DDBJ databases.
EMBL; AR435428; AAL33913.1;
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR000917; GFP_like.
InterPro; IPR000786; Green_fl_protein.
PRINTS; PR01259; GFLUORESCENT.
PRODM; PD013756; Green fl_protein; 1.
SEQUENCE 238 AA; 27031 MW; 5F80A19C19DC584D CRC64;
                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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121

61 VTTLGÝGILCFARYPEHMKANDFPKSAMPEGÝIQERTIFFQDDGKYKTRGEVKFEGDTLV 120

62 VTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV

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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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                                                                                               Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Li S.J., Xia N.S.; "Colorful mutants of green fluorescent protein from Aequorea
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"Colorful mutants of green fluorescent protein from Aequorea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26; Indels
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                         macrodactyla.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 27002 MW; BD5BA2982264C018 CRC64;
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ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 27018 MW; 75521EA5534E573A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.8%; Score 1067; DB 5;
81.1%; Pred. No. 2.3e-81;
iive 20; Mismatches 25;
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                                                                                                                                                                                                                                                            EMBL; AF455430; AA133915.1; -.
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR000917; GFP like.
InterPro; IPR00078; Green_fl_protein.
Pfam; PF01353; GFP; 1.
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GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR000917; GFP_like.
InterPro; IPR000786; Green_fl_protein.
Pfam; PF01353; GFP; 1.
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Best Local Similarity 81.1
Matches 193; Conservative
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[1]
SEQUENCE FROM N.A.
                                                                     STRAIN=GFPxm191uv;
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122 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
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Montastraea cavernosa (great star coral).
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia; Favilna; Favilae; Montastraea.
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Falkowski P.G., Sun Y.;
Falkowski P.G., Sun Y.;
Wontastraea cavernosa fluorescent protein.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AV056460; AAL17905.1;
EMBL, AV056460; Penergy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IPR009017; GFP_like.
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Last annotation update)
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PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl protein; 1.
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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Matches 64; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

June 21, 2004, 15:41:49; Search time 47.1111 Seconds (without alignments) 1433.395 Million cell updates/sec

1276 1 MVSKGEELFTGVVPILVELD......VLgGFVTAAGITLGMDELYK 239 score: Title: Perfect sc Sequence:

US-09-887-784-222G

1586107 segs, 282547505 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

1586107 Fotal number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2001s:*
geneseqp2003ss:*
geneseqp2003bs:* A_Geneseq_29Jan04:* 1: genesecm1020. Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

•	Description	Aae17518 Enhanced	Abr40352 Human ami	Aag65781 Amino aci	Aag65782 Amino aci	Aael7517 Enhanced	Aab22882 Enhanced				Aab85900 A. victor	Aab31171 Amino aci	Aag66198 A. victor	Abg94444 Protease			Aag79829 Green flu	Abr83616 Green flu	Ada38074 Aequorea	Abu63204 Aequorea	Adc18358 EGFP (enh	Abw00914 Aeguorea	Ade28570 Enhanced	Abm79011 Enhanced	Aag68319 Jellyfish	Aau99804 Biomembra
SOLUTION	ID.	AAE17518	ABR40352	AAG65781	AAG65782	AAE17517	AAB22882	AAY54349	AAY79584	AAB50804	AAB85900	AAB31171	AAG66198	ABG94444	AAE14599	AAE34958	AAG79829	ABR83616	ADA38074	ABU63204	ADC18358	ABW00914	ADE28570	ABM79011	AAG68319	AAU99804
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AAW97451 AAU99803 AAU99802 AAU99800 AAU99801	AAY50142 AAB24252 AAU10888 ADE28562 ADE28564	ADE28568 ADE28566 AAB22860 AAY79638 ABG94422	AAY42181 ABR83620 AAY54359 ABR83621
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# ALIGNMENTS

/note= "Wild type Glu substituted with Gly; This corresponds to position 222 in the wild type protein" /note= "Wild type Phe substituted with Leu; This corresponds to position 64 in the wild type protein" Misc-difference 223 Jellyfish; green fluorescent protein, GFP; protein redistribution; cellular function; genetic reporter; mutant; Stoke's shift; mutein. Enhanced F64L-E222G jellyfish green fluorescent protein mutant. Key Location/Qualifiers Misc-difference 65 AAE17518 standard; protein; 239 AA. (first entry) Aequorea victoria. Synthetic. 22-APR-2002 AAE17518; RESULT 1 AAE17518 A CONTRACTOR OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT O

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27-DEC-2001.

19-JUN-2000; 2000DK-00000953. 20-JUN-2000; 2000US-02126B1P. 10-MAY-2001; 2001DK-00000739. 10-MAY-2001; 2001US-0290170P. 18-JUN-2001; 2001WO-EP006848

(BIOI-) BIOIMAGE AS

Thastrup 0; Bjorn SP, Pagliaro L,

WPI; 2002-098224/13. N-PSDB; AAD28163.

Novel fluorescent protein in in vitro assay for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution, has a green fluorescent protein with F64L and E222G mutation.

Claim 9; Page 37; 41pp; English.

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The invention relates to a fluorescent protein derived from green fluorescent protein (GFP) or its analogue. The GFP containing mutations at FactL and B2226 has a bigger compared to other GFPs making it very suitable for high throughput screening due to better resolution. The fluorescent protein is useful in invitro assays for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution. The fluorescent protein is useful in studying celling in the fluorescent protein is a protein tags in transgenic animals, living and fixed cells; organelle tags, secretion marker and genetic reporter. The fluorescent protein is also useful as a call or organelle integrity marker, a marker for changes in combination with fluorescence activated cell sorting (FACS). The novel proteins can also be used as reporters on monitor live or dead biomass of corganisms, such as fungi. The fluorescent protein is also useful as markers in transcriptional and translational protein are for bacterial detection. Transposons encoding the fluorescent protein are useful for screening promoters and for tagging plasmids and chromosomes. The fluorescent protein encoding the fluorescent protein for designing diagnostic tool. The present sequence is a DNA encoding cenhanced F641-E222G jellyfish green fluorescent protein (GFP) mutant
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Pred. No. 1.4e-122;
0; Mismatches 1;
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11-OCT-2001; 2001US-0328896P.
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Best Local Similarity
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The invention relates to a novel cell, comprising three heterologous conjugates (HC), a first HC (HCI) comprising an anchor protein that specifically binds to an internal structure within the cell conjugated to an interactor protein (IP) of type A, a second HC (HC2) comprising IP of type B conjugated to a first protein of interest, and a third HC (HC3) comprising a second protein of interest conjugated to detectable group. The cell is useful for detecting if a compound disrupts or induces the interaction between two intracellular proteins. The cell is also useful for accompandate the interaction between two exemplification of the invention
                                                                        Novel cell for identifying modulators of protein interaction, contains a first conjugate comprising anchor protein, second conjugate having type B interactor protein and third conjugate with detectable group.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
99.2%; Score 1266; DB 6;
Best Local Similarity 99.6%; Pred. No. 2.6e-122;
Matches 238; Conservative 0; Mismatches 1;
                                                                                                                                                    Disclosure; Page 112-113; 118pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG65781 standard; protein; 893 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-APR-2001; 2001WO-DK000264.
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29-MAY-2000; 2000DK-0000849.
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                  2003-430211/40.
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                                    N-PSDB; ACC72604
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 363 AA;
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The invention relates to determining, if a compound, is a dislocator of PDB4. The method comprises testing if the compound removes PDB4 spots, which may optionally be induced by a Rolipram-like reference compound, and testing if it inhibits the catalytic activity of the PDB4, where the compound is a dislocator of PDB4, if it removes PDB spots and if it does not inhibit the catalytic activity of PDB4. The method is useful for dientifying compounds useful for the treatment of diseases of the central nervous system such as joint inflammation, Crohn's diseases of the central nervous system such as joint inflammation, Crohn's disease, inflammatory bowel disease, respiratory diseases, chronic obstructive pulmonary disease (CDP), including asthma, chronic bronchicis, pulmonary emphysema, psoriasis, bone resorption diseases, reperiusion injury, cancer and HIV infection. The use of a reagent that can mimic or reverse the effect of the compound with affinity for the catalytic site on intracellular distribution of the PDB for the preparation of a medicament. The present sequence represents the amino acid sequence of a HSPDB4A1-E222G fusion
                                                                                                                                        Determining if a compound is a dislocator of PDB4 for identifying compounds for treating CNS and inflammatory disease comprises identifying compounds which remove PDE4 spots.
  Bjorn SP, Thastrup O, Almholt DC;
                                                                                                                                                                                                                                          Example 1; Page 156-160; 160pp; English.
Scudder KM,
                                                                      WPI; 2001-611727/70
                                                                                               N-PSDB; AA166852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 893 AA;
                         Praestegaard M;
BR.
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  Terry
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714 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120 715 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 774 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVQLA 180 09 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLGGFVTAAGITLGMDELYK 239 835 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWVLLGFVTAAGITLGMDELYK 893 655 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPMPT 1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT Gaps ö Score 1266; DB 4; Length 893; Pred. No. 9.6e-122; 0; Mismatches 1; Indels ( Query Match 99.2%; Best Local Similarity 99.6%; Matches 238; Conservative ( 61 121 181 ò 8 ò 셤 ઠે g 8 셤

AAG65782 standard; protein; 1132 AA AAG65782; RESULT

07-JAN-2002 (first entry)

Amino acid sequence of HSPDE4A4-E222G fusion protein.

PDE4; central nervous system; antiinflammatory; cytostatic; nootropic; autoimmune; ischemic; osteopathic; GFP; green fluorescent protein; fusion protein.

Aequorea victoria. Homo sapiens

WO200179526-A2

Enhanced F64L jellyfish green fluorescent protein mutant.

22-APR-2002 (first entry)

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1014 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 1073
                                                                                                                                                                                                                                                                                                          Determining if a compound is a dislocator of PDE4 for identifying compounds for treating CNS and inflammatory disease comprises identifying compounds which remove PDE4 spots.
                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to determining, if a compound, is a dislocator of PDE4. The method comprises testing if the compound removes PDE4 spots, which may optionally be induced by a Rolipram-like reference compound, and testing if it inhibits the catalytic activity of the PDE4, where the compound is a dislocator of PDE4, if it removes PDE spots and if it does not inhibit the catalytic activity of PDE4. The method is useful for identifying compounds useful for the treatment of diseases of the central nervous system such as. depression and for the treatment of inflammatory disease such as joint inflammation, Crohn's disease, inflammatory disease, respiratory disease, chronic obstructive pulmonary disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 DHYQQNTPIGDGFVLLPDNHYLSTQSALSKDPNEKRDHMVLGGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (COPD), including asthma, chronic bronchitis, pulmonary emphysema, endotoxic shock, toxic shock syndrome, systemic lupus erthematosis, psoriasis, bone resorption diseases, reperfusion injury, cancer and HIV infection. The use of a reagent that can mimic or reverse the effect of the compound with affinity for the catalytic site on intracellular distribution of the PDE for the preparation of a medicament. The present sequence represents the amino acid sequence of a HSPDE4A4-E223G fusion
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                                                                                                                                                                                   Thastrup O, Almholt DC;
                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 162-167; 160pp; English.
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                                                                                                                                                                                   Scudder KM, Bjorn SP,
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                                      11-APR-2001; 2001WO-DK000264.
                                                                             17-APR-2000; 2000DK-0000651.
29-MAY-2000; 2000DK-00000849.
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                                                                                                                                            BIOI-) BIOIMAGE AS
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                                                                                                                                                                                                         Praestegaard M;
25-OCT-2001,
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Aequorea victoria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-FEB-1999;
08-MAR-1999;
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                                                                                                                                                                                                                                          10-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                121
                                                                                                                                                                                                        AAB22882;
                                                                                                                                                        AAB22882
                                                                                                                                    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a fluorescent protein derived from green fluorescent protein (GPP) or its analogue. The GPP containing mutations are Fefia and E252G has a bigger compared to other GPP's making it very suitable for high throughput screening due to better resolution. The fluorescent protein is useful in invitro assays for measuring protein redistribution. The fluorescent protein is useful in studying cellular cfunctions in living cells, as protein tags in transgenic animals, living and fixed cells, organelle tags, secretion marker and genetic reporter. The fluorescent protein is also useful as a cell or organelle integrity marker, a marker for changes in cell morphology, as transfection marker, and as a marker to be used in combination with fluorescence activated cell incorting (RACS). The novel proteins can also be used as reporters to monitor live or dead biomass of organisms, such as fungi. The fluorescent corpuction is also useful as markers in transcriptional and translational corpusing for performing transposon vector mutagenesis and as a reporter corpused. For bacterial detection. Transposons encoding the fluorescent protein are useful for screening promoters and for tagging plasmids and chromosomes. The fluorescent protein engine performing an engine promoter of the proposition of a phage is useful for screening promoters and for tagging plasmids and chromosomes. The fluorescent protein engineered into the genome of a phage is useful for the parameters of the fluorescent protein engineered into the genome of a phage is useful for the parameters of the fluorescent protein engineered into the genome of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage of a phage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel fluorescent protein in in vitro assay for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution, has a green fluorescent protein with F64L and E222G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agnostic tool. The present sequence is enhanced F64L
                                                                                                                                        /note= "Wild type Phe substituted with Leu; This corresponds to position 64 in the wild type protein"
Jellyfish; green fluorescent protein; GFP; protein redistribution; cellular function; genetic reporter; mutant; Stoke's shift; mutein.
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                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                       Thastrup 0;
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                                                                                                                                                                                                                                                                                               19-JUN-2000; 2000DK-0000953.
20-JUN-2000; 2000US-02126BIP.
10-MAY-2001; 2001DK-0000739.
10-MAY-2001; 2001US-0290170P.
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Best Local Similarity 99.2
Matches 237; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       Bjorn SP, Pagliaro L,
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                                                      Aequorea victoria.
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                                                                                                                                                                                                                                 27-DEC-2001
                                                                      Synthetic
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The invention relates to systems, methods and reagents for cell-based screening or detection of compounds which affect particular biological functions. The methods of the invention utilise fluorescent biological functions. The methods of the invention utilise fluorescent biological calcular distribution of at least the fluorescent alteration in the cellular distribution of at least the fluorescent cancer. C. dispay fused to a fluorescent protein (e.g., jellyfish green fluorescent protein (e.g., jellyfish green fluorescent correction (GFP), or derivatives thereof). Such biosensors are located in the cytoplasm, but on stress activation translocate to the mucleus. In the cytoplasm, but on stress activation proteins can be used to detect protease another embodiment biodetector proteins can be used to detect protease cativity. Such protease biodetector fusion proteins comprise one or more fluorescent proteins; a recognition signal which is cleaved by the protease, and at least one cellular localisation signal. The latter two components may be from heterologous sources. Due to the components may be from heterologous sources. Due to the components may be from heterologues sources. Due to the components of a single protein which is acted upon by the protease of interest, the region of the cell. Once acted on by the protease of interest, the constant protein signal attached to the fluorescent protein enables the fluorescent protein to be directed to a different cellular compartment after cleavage of the protease recognition sequence. The change in distribution of the fluorescent protein can be detected using imaging methods with a high degree of spatial resolution. The methods and imaging methods with a high degree of spatial resolution.
Biodetector protein; fusion protein; recognition site; cellular targetting sequence; cellular localisation; fluorescent protein; protease activity detection; toxin detection; cellular stress detection; drug discovery; cell based screening.
                                                                                                                                                                                                                181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWVLLBFVTAAGITLGMDELYK 239
                                                                                                                                                            181 DHYQQNTPIGDGPVILPDNHYLSTQSALSKDPNEKRDHMVLGGFVTAAGITLGMDELYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enhanced green fluorescent protein (EGFP), SEQ ID NO:46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB22882 standard; protein; 239
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99US-00352171.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         analyzing optically.
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biosensors of the invention can be used to investigate a wide range of cellular activities and to screen compounds which modulate these extrivities. Biosensors containing a recognition site for caspase, for example, may be used for the screening of compounds which modulate apoptosis, while biosensors containing other protease recognition sites may be used for the detection of proteolytic toxins (such as anthrax lethal factor). The method provides improved target validation and candidate compound optimisation by combining many cell screening formats with fluorescence-based molecular reagents and computer-based feature and speed of data collection and faster evaluation of drug candidates. Sequences AAB22881-B222885 represent fluorescent proteins which may used as components of biosensor fusion proteins of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; emission intensity; EGFP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of the mutant green fluorescent protein EGFP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1255; DB 3;
Pred. No. 1.9e-121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fluorescent protein; green fluorescent fluorescence; pH detection; pH sensor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ncy
Misc-difference 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.4%;
98.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 239 AA;
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protein based on the Aequorea green fluorescent protein (GFP). The emission intensity changes as pH varies between 5 and 10 of the present protein are novel. The functional engineered fluorescent proteins show reversible changes in fluorescence over physiological pH ranges. They can be used for determining the pH of samples and cells. The polynucleotides can also be used to produce transgenic animals. The fluorescent protein pH sensors can be delivered to cells in the form of polynucleotides encoding the protein sensor fused to a targeting signal. The targeting signal incots the expression of the protein sensors to restricted cell locations. This makes it possible to measure the pH of a precisely defined cellular region or organelle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 LVTTLTYGVQCFSRYPDHMKQHDFFKSAMPGYVQERTIFFKDDGNYKTRAEVKFGDTL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09
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                                                                               New functional engineered green fluorescent proteins, used for measuring the pH in biological samples and cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLGGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                 sequence represents a functional engineered fluorescent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protease; biosensor; EGFP; signal peptide; cell screening; assay; analysis; drug discovery.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                98.4%; Score 1255; DB 3; 98.7%; Pred. No. 1.9e-121; iive 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY79584 standard; peptide; 239 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Olson K,
                                                                                                                                Disclosure; Page 9; 89pp; English
Wachter RM;
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99US-0136078P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 236; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CELL-) CELLOMICS INC
Tsien RY, Llopis J,
                              WPI; 2000-116540/10.
N-PSDB; AAZ45642.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGFP signal domain
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200026408-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-AUG-2000
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99US-00316919.

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Aequorea victoria; jellyfish; fluorescent protein indicator; green fluorescent protein; GFP; linker moiety; sensor; calmodulin-binding domain; mutant; mutein.
                                                                                                                                                                                                                                                                                                AAB50804 standard; protein; 239 AA
                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                               Jellyfish GFP mutant EGFP
                                                                                                                                                                                 236; Conservative
    WPI; 2300-365644/31
N-PSDB; AAA27573.
                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                             Sequence 239 AA;
                                                                                                                                                                                                                                                                                                                                                                         WO200071565-A2
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The present sequence is a fluorescnet protein used in the construction of a fluorescent protein indicator. The indicator comprises a sensor polypeptide that is responsive to a chemical, biological, electrical or physiological parameter, and a fluorescence protein functional group. The sensor polypeptide is operatively inserted into the fluorescent moiety. The fluorescent indicator is useful for detecting the presence of a response inducing member in a sample. The method involves contacting the sample which a change is indicator and detecting a change in fluorescence, in which a change is indicative of the effect of the parameter on the sensor polypeptide. The novel fluorescent proteins are advantageous due to their transfer)-based sensors
                                                                                                                                                                                                                                                                                                                    Novel fluorescent proteins comprising a sensor protein inserted into them, useful for measuring the response of a sensor biological, chemical, electrical or physiological parameter in vivo or in vitro.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 24; 94pp; English.
17-MAY-2000; 2000WO-US013684.
                                                                                                                                (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                           Baird GA;
                                                                                                                                                                                                                                              2001-032017/04.
                                                                                                                                                                                                                                                                       N-PSDB; AAC90488
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                                                        21-MAY-1999;
21-MAY-1999;
                                                                                                                                                                                           Tsien RY,
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                                                                                                                                                                                                                                                                 The present sequence is that of the EGFP signal domain, which can be included in novel recombinant protease biosensors (FBS) of the invention. The PBS (see AAY79628-4) comprise: a first domain (see AAY79529-7).

Comprising at least 1 detectable polypeptide signal such as the present sequence; a second domain (see AAY79588-622) comprising at least 1 cactant target sequence. A recombinant nucleic comprising at least 1 reactant target sequence. A recombinant nucleic acid (see AAA7677-43) encoding the PB, an expression vector, and a compound see AAA7677-43) encoding the PB, an expression vector, and a contacting a host cell are also claimed. A claimed method for identifying compounds that modify protease activity in a cell involves contacting a host cell that possesses the recombinant PB with a test compound, and determining the PB distribution in the host cell, where changes in the distribution of the PB are correlated with modification of protease activity by the test compound. Claimed kits for identifying compounds that modify protease activity in a host cell include the recombinant nucleic activity, and to identify specific activity based activation of enzymatic activity, and to identify specific activity based
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                                                                                                          Recombinant nucleic acid encoding a protease biosensor useful for fluorescence based cell and molecular biochemical assays for drug discovery comprising three operably linked nucleic acid sequences
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Pred. No. 1.9e-121;
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                                                                                     1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTKFICTTGKLPVPWPT
                                                                                                                                   LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Melanin concentrating hormone receptor; MCHR; MCH; chimeric; fusion; fluorescent polypeptide; orexigenic; anabolic; food intake; GFP; green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A. victoria green fluorescent protein (GFP) and linker sequence.
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Score 1255, DB 4; Length 239;
Pred. No. 1.9e-121;
1; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                    AAB85900 standard; protein; 239 AA
     Query Match 98.4%;
Best Local Similarity 98.7%;
Matches 236; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
Aeguorea victoria.
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99FI-00001296.

07-JUN-1999;

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                                                                                                                                                                                                             The invention provides melanin concentrating hormone (MCH) receptor (MCHR) chimeric and fusion proteins. The MCHR chimeric proteins comprise MCHR polypeptide regions from different species. The MCHR fusion protein comprise MCHR polypeptide region and a fluorescent polypeptide region protein joined directly, or via a linker, to the carboxy side of the MCHR pelypeptide region. The MCHR fusion proteins can be expressed by standard recombinant methodology. MCH action promotes feeding (orexigenic) and up regulation of MCH activity stimulates food intake. The present sequence represents a A. victoria green fluorescent protein (GFP) and a linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                              Fusion proteins comprising melanin concentrating hormone receptor peptides and fluorescent proteins, useful for identifying appetite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Growth rate, death rate, reporter gene, luminescent protein, fluorescent product, luciferase, green fluorescent protein, GFP
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                                                                                                                                                                                                                                                                                                                                                             98.4%; Score 1255; DB 4; Length 239; 98.7%; Pred. No. 1.9e-121; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of a green fluorescent protein (GFP).
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                                                                                                                                                                                       Claim 2; Page 14; 71pp; English.
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                      14-MAR-2001; 2001WO-US008071
                                            15-MAR-2000; 2000US-0189698P
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                                                                (MERI ) MERCK & CO INC
                                                                                                             WPI; 2001-565791/63.
                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                         N-PSDB; AAH47304
                                                                                                                                                                                                                                                                                                                                        Sequence 239 AA;
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 20-SEP-2001
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                                                                                                                                                                     stimulants
                                                                                       Marsh DJ;
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The specification describes a method for assessing the growth rate and death rate of a micro-organism within a predetermined time period in a desired environment. The method comprises introducing at least two reporter genes encoding luminescent and/or fluorescent products into the micro-organisms, incubating the micro-organism within the desired environment, and detecting luminescence and/or fluorescence after a predetermined time period. Use of two different markers within a micro-organism enables the differentiation between growth and death rates. The method is used to assess the growth rate and death rate of a micro-organism within a predetermined time period in a desired environment. The present sequence represents a green fluorescent protein (GFP), and is encoded by a plasmid which encodes luminescent and fluorescent proteins, and is used in the method of the invention
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                                                                                                                                                                                                                                                                                 Assessing growth and death rates of a micro-organism in a desired environment, by introducing 2 reporter genes encoding luminescent and fluorescent products and detecting luminescent fluorescence.
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Matches 236; Conservative
                                                                                                                                                                             WPI; 2001-061737/07
                                                                                                       Lilius E, Virta M;
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                                                                                                                                                                                                               N-PSDB; AAC86954
                                 VIRTA M.
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(LILI/) LILIUS
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99US-00398965.
99US-00430656.
99US-0168408P.
                                         (GIUL/) GIULIANO K.
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                  screening system
                                                                                                                                                                                                                                                                                                                                                                    Sequence 239 AA;
                                                                                                     N-PSDB; ABS71491
                                                   KAPUR R
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   17-SEP-1999;
           29-OCT-1999;
                      01-DEC-1999;
                                                                       Giuliano K,
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                                                                                                                         fluorescence characteristic and having a function of showing stable fluorescence characteristic and having a function of showing stable fluorescence characteristic in acid region. A method for the preparation of a cyan-green fluorescent protein is provided which involves a transformant transformed by a recombinant vector comprising the gene, where the transformant is cultured and the protein is collected from the culture. The present sequence represents the A. victoria green fluorescent protein (EGFP)
                                                                                                                                                                                                                                                                                                                                                                     VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                                                                                                                                                                                                                                    VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detection, classification; identification; toxin detection; protease;
ADP-ribosylating toxin; cytotoxic phospholipase; exfoliative toxin;
                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                  Length 239;
                                                                                                                                                                                                                                                 Score 1255; DB 5;
Pred. No. 1.9e-121;
                                                                                             gene encoding cyan-green fluorescent protein
                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protease biosensor signal sequence #6.
                                                                                                                  Example; Page 14; 20pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG94444 standard; protein; 239
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98US-00031271.
99US-0123152P.
99US-0123399P.
99US-00352171.
                                                                                                                                                                                                                                                  98.4%;
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      04-AUG-2000; 2000JP-00237165
                         04-AUG-2000; 2000JP-00237165
                                           (RIKA ) RIKAGAKU KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                           Best Local Similarity 98.7
Matches 236; Conservative
                                                                2002-299190/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       toxic threat agent.
                                                                           N-PSDB; ABL40628
                                                                                                                                                                                                                               Sequence 239 AA;
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26-FEB-1999;
08-MAR-1999;
12-JUL-1999;
31-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                          121
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                                                                                                                                                                                                                                                   Query Match
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The invention describes methods of automated detection, classification
and identification comprising treating cells containing luminescent
creporter molecules (I) in array of locations with a test substance, where
cc reporter molecules (I) in array of locations with a test substance,
clocation to obtain luminescent signals and converting optical information
cc into digital data to interpret presence of toxins in the test substance.
The method are useful for detection of toxins chosen from proteases, ADP-
cribosylating toxins, cytotoxic phospholipases, and exfoliative toxins.
Cr Three classes of cell-based luminescent reporter molecules such as
detectors, classifiers and identifiers are described and serve as
creporters of toxic threat agents. The first two levels of
characterisation ensure a rapid readout of toxin class without
cs characterisation ensure a rapid readout of toxin class without
cs several complex mixtures of known toxins. This is the amino acid sequence
cs arcrificing the ability to detect many new mutant toxins or dissect
cs arcrificing the ability to detect many new mutant toxins or dissect
cs arcrificing the ability to detect many new mutant toxins or dissect
cs arcrificing the ability and a known toxins. This is the amino acid sequence
cs of a protease biosensor related signal sequence used in the cell-based
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                                                                                                                                                                                                          of
or
                                                                                                                                                                          Automated cell-based toxin detection, classification, and/or identification by treating cells involves use of three classes luminescent reporter molecules such as detectors, classifiers cidentifiers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1255; DB 5; Length 239;
Pred. No. 1.9e-121;
1; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aequorea victoria enhanced green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                     Example 10; Fig 29A; 214pp; English
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Kapur R;
                                                                             2002-634730/68.
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Best Local Similarity
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The invention relates to a method for mutagenesis that comprises synthesising a mutated strand and a complementary strand by use of synthesising a mutated basically comprises a DNA synthesis in which one cor more primers that have a nucleotide sequence containing at least one or more primers that have a nucleotide sequence containing at least one mutation and a phosphorylated 5-terminus are annealed to a template DNA and then subjected to an elongation reaction using a thermostable high-fidelity DNA polymerase, after which the phosphorylated 5-terminus and then subjected terminus are ligated by means of a thermostable bNA ligase to synthesise a circular DNA containing the primers, a digestion in which the step of DNA synthesis is repeated several fines to amplify the DNA containing the primers and then, at least DNAs other than the amplified circular DNA are digested into several fragments; and a double-stranded CC of digestion as megaprimers, the megaprimers are annealed to the circular DNA synthesis of which, with the several fragments obtained in the step of DNA synthesis and which, with the several fragments obtained by the circular DNA synthesis and adoptined by an elongation reaction performed using the thermostable high-fidality DNA polymerase. The method is useful for mutagenesis, particularly for introducing cantenin mutations at certain sites of the nucleotide sequence. The present method is simple, speedy, economical and widely applicable. The present sequence is Agueured victoria enhanced green fluorescent protein (GFP) used for mutagenesis in an exemplification of the invention. The EGFP is derived the strain gives in the green fluorescent protein (GFP) sequence of Agueurea
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'note= "Wild-type GFP Met-Ser are replaced with Met-Val-
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                                                                                                                                                                "GFP Ser65 is replaced by Thr"
                                                                                                                         "GFP Phe64 is replaced by Leu"
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llarity 98.7%; Pred. No. 1.9e-121;
Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 13-14; 31pp; English.
                     Location/Qualifiers
                                                                                                                                                                                                                                                                                           03-AUG-2001; 2001EP-00306650
                                                                                                                                                                                                                                                                                                                                  04-AUG-2000; 2000JP-00237166
                                                                                                                                                                  /note=
                                                                                                                           /note=
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                                                                                                                                            Misc-difference 66
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N-PSDB; AAD27910.
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                                      Misc-difference
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                                                                                                   Misc-difference
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The present invention relates to chimeric phosphorylation indicators comprising a phosphorylation polypeptide and a fluorescent protein or in operative linkage, a donor molecule, a phosphorylatable domain. a phosphoaminoacid binding domain. (PAABD) and an acceptor molecule. The phosphoaminoacid binding domain. (PAABD) and an acceptor molecule. Kinases or phosphatases in a biological sample. They are also useful in high throughput analysis e.g. for detecting a kinase inhibitor or phosphatase inhibitor. The present sequence is Aequorea victoria enhanced green fluorescent protein (EGFP) used in the invention
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DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLGGFVTAAGITLGMDELYK 239
              181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 239
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                                                                                                                                                                                                                                        detection; phosphatase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                         Aequorea victoria enhanced green fluorescent protein (EGFP).
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                                                                                                                                                                                                                                        Phosphorylation indicator; fluorescent protein; ckinase; enhanced green fluorescent protein; EGFP.
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Pred. No. 1.9e-121;
1; Mismatches 2;
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                                                                                                             AAE34958 standard; protein; 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 98.4%;
Local Similarity 98.7%;
les 236; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang
                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                       Aequorea victoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              operative linkage
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                                                                                                                                                                           28-MAY-2003
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181
                                                                                                                                           AAE34958;
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131 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 239

Search completed: June 21, 2004, 15:54:13 Job time : 47.1111 secs

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Sequence 46, Appli
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                                                                                                                                     June 21, 2004, 15:46:55 ; Search time 12.7778 Seconds (without alignments) 965.630 Million cell updates/sec
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                                                                                                                                                                                                                                                               1276
1 MVSKGEELFTGVVPILVELD......VLgGFVTAAGITLGMDELYK 239
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/cgm2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgm2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-513-93A-46

US-09-502-641-3

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US-09-962-102-1

US-09-164-946-1

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US-09-172-06-1

US-09-172-06-1

US-09-171-197-129

US-09-171-197-113

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Maximum Match 100%
Listing first 45 summaries
                                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Sequence 2, Appli Sequence 6, Appli Sequence 4, Appli Sequence 75, Appl Sequence 51, Appl Sequence 11, Appl Sequence 139, Appl Sequence 139, Appl Sequence 141, Appl Sequence 141, Appl Sequence 176, Appl Sequence 178, Appl Sequence 61, Appl Sequence 61, Appl Sequence 61, Appl Sequence 61, Appl Sequence 61, Appl Sequence 61, Appl Sequence 61, Appl Sequence 61, Appl Sequence 61, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 117, Appl Sequence 117, Appl		SAMPLE	ength 239; Indels 0; Gaps 0;	KLTLKFICTTGKLPVPWPT 60 	KDDGNYKTRAEVKFEGDTL 120                     KDDGNYKTRAEVKFEGDTL 120	IKVNFKIRHNIEDGSVQLA 180                     KVNFKIRHNIEDGSVQLA 180	GGFVTAAGITLGMDELYK 239                 LEFVTAAGITLGMDELYK 239
US-08-818-252-2 US-08-818-252-6 US-08-818-253-4 US-08-818-253-4 US-09-417-197-75 US-09-417-197-71 US-09-417-197-19 US-09-417-197-139 US-09-417-197-143 US-09-417-197-143 US-09-417-197-143 US-09-417-197-143 US-09-417-197-17 US-09-417-197-17 US-09-417-197-19 US-09-417-197-19 US-09-417-197-19 US-09-417-197-19	ALIGNMENTS	i M. M. CENT PROTEIN SENSORS FOR NG THE PH OF A BIOLOGICAL. 105/09/172,063 0-13 09/094,359 6-09 ws Version 4.0	<pre>Score 1255; DB 3; L ; Pred. No. 2.5e-127; 1; Mismatches 2;</pre>	MVSKGEELFTGVVPILVELDGDVNGHKRSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT 	LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 	VNRIELKGIDFKEDGNILGHKLEYNYNSHNYYIMADKQKNGIKVNFKIRHNIEDGSVQLA 	DHYQQNTPIGDGBVLLPDNHYLSTQSALSKDPNEKRDHMVLGGFVTAAGITLGMDELYK 
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6		on US/09;  ger Y. Atsushi uan Rebekka N FLUORESCIE MEASURIN T/071001 NUMBER: 1998-10. NUMBER: 1998-10. victoria	98.4% 98.7% ive	TGVVPILVI          TGVVPILVI	QCFSRYPDE           QCFSRYPDE	DFKEDGNII          DFKEDGNII	GDGPVLLPI          GDGPVLLPI
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		LT 1 9-172-063-3 quence 3, Application US/0 quence 3, Application US/0 NERAL INFORMATION: PPLICANT: 6150176 PPLICANT: Tsien, Roger Y. PPLICANT: Miyawaki, Atsush PPLICANT: Miyawaki, Atsush PPLICANT: Remington, S. Ja PPLICANT: Remington, S. Ja PPLICANT: Remington, S. Ja PPLICANT: Remington, S. Ja PPLICANT: Remington, S. Ja PPLICANT: PREMING POLYS/07100 URENT PREMING DATE: 1998-1 ARLIER APPLICATION NUMBER: URRENT FILING DATE: 1998-1 OWHER OF SEQ ID NOS: 38 OT DN 03 LENGTHARE: FastSEQ for Windo OTHORS: YARIANT REATURE: PRATURE: PRAT	Similarity 6; Conservat	NSKGEELF           NSKGEELF	CVTTLSYGV	NRIELKGI           NRIELKGI	DHYQQNTPI          DHYQQNTPI
1255 1255 1255 1255 1255 1255 1255 1255		ULT 1 09-172-063-3 equence 3, Ap atent No. 615 BENERL INFORM APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT: M APPLICANT	atch sal 23	н н	61 1	121 7	181 I
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TYPE: PRT
ORGANISM: Aequorea victoria
FEATURE:
NAME/KEY: VARIANT
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US-09-602-641-3
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US-09-920-922-2
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                          Sequence 46, Application US/09513783A
Fatent Nc. 641659
GENERAL INFORMATION:
APPLICANT: Gulliano, Kenneth A.
TITLE OF INVENTION: A System for Cell Based Screening
TITLE FFERENCE: 97-022-11
CURRENT APPLICATION NUMBER: US/09/513,783A
CURRENT FILING DATE: 2000-02-25
SOFTWARRE: Patentin Ver. 2.0
SOFTWARRE: Patentin Ver. 2.0
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; Sequence 4, Application US/09316919
; Sequence 4, Application US/09316919
; Patent No. 6469154
; GENERAL INFORMATION:
; APPLICANT: Taien, Roger Y.
; TITLE O! INVENTION: FLUORESCENT PROTEIN INDICATORS
; FILE REPERFORCE: 0.257/073001
; CURRENT PAPLICATION NUMBER: US/09/316,919
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 63
; SEQ ID NO 9.
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Pred. No. 2.5e-127;
1; Mismatches 2;
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Best Local Similarity 98.7%;
Matches 236; Conservative
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; ORGANISM: Aequorea victoria
US-09-316-919-4
  RESULT 2
US-09-513-783A-46
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61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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APPLICANT: Miyawaki, Atsushi
APPLICANT: Miyawaki, Atsushi
APPLICANT: Miyawaki, Atsushi
APPLICANT: Machter, Rebeka M.
APPLICANT: Machter, Ramington, S. James
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
TITLE OF INVENTION: MASSIRING THE PH OF A BIOLOGICAL SAMPLE
FILE REPERBENC: 07257/071001
CURRENT APPLICATION NUMBER: US/09/602,641
CURRENT FILING DATE: 1998-10-13
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 239
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Pred. No. 2.5e-127;
1; Mismatches 2; Indels 0
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APPLICANT: Sawano, Asako
TITLE OF INVENTION: METHOD FOR MUTAGENESIS
FILE REFERENCE: 11283-012001
CURRENT APPLICATION NUMBER: US/09/920,922
CURRENT FILING DATE: 2001-08-02
PRIOR PILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 9
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; Sequence 3, Application US/09602641
; Patent No. 6608189
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Best Local Similarity 98.7%;
Matches 236; Conservative
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; Patent No. 6306600
US-09-364-946-1
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APPLICANT: Kain, Steve
APPLICANT: Li, Xianqiang
TITLE OF INVENTION: Rapidly Degrading GFP-Fusion Proteins and Methods
TITLE OF INVENTION: of Use
FILE REFERENCE: D6100
CURRENT APPLICATION NUMBER: US/09/062,102
CURRENT FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: US 60/060,855
EARLIER FILING DATE: 1997-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: Sequence of the EGFP-MODC422-461 fusion protein.
; Patent No. 6130313
US-09-062-102-1
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Pred. No. 3.1e-127;
1; Mismatches 2;
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 98.7%;
Matches 236; Conservative
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                                                          TYPE: PRT
ORGANISM: Aequorea victoria
                                                                                                                                           Query Match 98.4
Best Local Similarity 98.7
Matches 236; Conservative
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US-09-062-102-1
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Sequence 1, Application US/09364946

Patent No. 630600

GENERAL INFORMATION:
APPLICANT: Kain, Steve

APPLICANT: Li, Xianqiang

TITLE OF INVENTION: GUG

TITLE OF INVENTION: Bapidly Degrading GFP-Fusion Proteins and Methods

TITLE OF INVENTION: US/09/364,946

CURRENT APPLICATION NUMBER: US/09/364,946

CURRENT PILING DATE: 1999-07-30

CURRENT PILING DATE: 1999-11-13

NUMBER OF SEQ ID NOS: 14

LENGTH: 281
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OTHER INFORMATION: Sequence of the BGFP-MODC422-461 fusion protein.
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Sequence 2, Application US/09513783A

Patent No. 6416959

GENERAL INFORMATION:
APPLICANT: Giuliano, Kenneth A.
TITLE OF INVENTION: A System for Cell Based Screening
FILE REFERENCE: 97-022-L1

CURRENT APPLICATION NUMBER: US/09/513,783A

CURRENT FILING DATE: 2000-02-25

NUMBER OF SEQ ID NOS: 180

SOFTWARE: PatentIn Ver. 2.0

LENGTH: 294
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Pred. No. 3.1e-127;
1; Mismatches 2;
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ORGANISM: artificial sequence
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Best Local Similarity 98.7%;
Matches 236; Conservative
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                                      61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                             121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                            205 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 264
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; Sequence 21, Application US/09172063
; Patent No. 6150176
; GENERAL INFORMATION:
; APPLICANT: Hispanaki, Atsushi
; APPLICANT: Miyawaki, Atsushi
; APPLICANT: Mother, Rebekka M.
; APPLICANT: Remington, S. James
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: MASURING THE PH OF A BIOLOGICAL SAMPLE
; FILE REFERENCE: 07257/071001
; CURRENT APPLICATION NUMBER: US/09/172,063
; CURRENT FILING DATE: 1998-10-13
; EARLIER RAPPLICATION NUMBER: 09/094,359
; BARLIER FILING DATE: 1998-06-09
; NUMBER CF SEQ ID NOS: 38
; SOFTWARE: FRSTSEQ for Windows Version 4.0
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; Sequence 21, Application US/09602641
Patent No. 6608189
; GENERAL INFORMATION:
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LOCATION: (0)...(0)
OTHER INFORMATION: GT-EGFP
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Matches 236; Conservative
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LENGTH: 323
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APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
APPLICANT: Llopis, Juan

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us-09-085-305-6
; Sequence 6, Application US/09085305
; Patent No. 6191269
; General No. 6191269
; General Information:
    APPLICANT: Lovett, David H.
    APPLICANT: Lovett, David H.
    APPLICANT: Turck, Johanna
; TITLE OF INVENTION: Malignant Cancer Cells by Delivery of N-Terminal
; TITLE OF INVENTION: Interleukin-1-Alpha Pro-Piece Polypeptide
; TITLE OF INVENTION: Interleukin-1-Alpha Pro-Piece Polypeptide
; CORRESPONDENCE ADDRESS:
    ADDRESSE: Bozicevic & Reed, LLP
    STREET: 285 Hamilton Ave, Suite 200
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LVTTLSYCVOCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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0
APPLICANT: Wachter, Rebekka M.
APPLICANT: Remington, S. James
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
CURRENT FILING DATE: 2000-06-22
CURRENT FILING DATE: 2000-06-22
PRIOR PILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1255; DB 4;
Pred. No. 3.8e-127;
1; Mismatches 2;
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
ODERATING SYSTEM:
ODERATING SYSTEM:
ODERATING SYSTEM:
ODERATING SYSTEM:
OFFWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 98.7%;
Matches 236; Conservative
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                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Aequorea victoria
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: VARIANT
LOCATION: (0)...(0)
CTHER INFORMATION: GT-EGFP
US-09-602-641-21
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2 CLASSIFICATION:
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Sequence 127, Application US/09417197

Sequence 127, Application US/09417197

Patent No. 6518071

GENERAL INFORMATION:

APPLICANT: Ole THASTRUP, et al.

TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An Intring OF INVENTION: A Method For Extracting Quantitative Information Relating To An Intring OF INVENTION: On A Cellular Response

CURRENT FILING DATE: 1999-10-07

CURRENT APPLICATION NUMBER: US/09/417,197

CURRENT PALLORS: 143

SOFTWARE: PatentIn version 3.0

SOFTWARE: PatentIn version 3.0
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                        181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLGGFVTAAGITLGMDELYK 239
                                                           321 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 379
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Pred. No. 6e-127;
1; Mismatches 2; Indels
                                                                                                                                                                                           Sequence 48, Application US/09800170

Patent No. 648167

GENERAL INFORMATION:
APPLICANT: Kinsella, Todd
TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES
FILE REFERENCE: A-68614-1/DJB/MB/RM/
CURRENT APPLICATION NUMBER: US/09/800,170
CURRENT FILING DATE: 2001-08-28
PRIOR PILING DATE: 2000-03-06
NUMBER OF SEQ ID NOS: 90
SOFTHARE: Patentin version 3.1
SEQ ID NO 48
LENGTH: 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Synechocystis PCC6803
US-09-800-170-48
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 98.7%;
Matches 236; Conservative
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US-09-800-170-48
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APPLICANT: O1e THASTRUP, et al.
TITLE OF INVENTION:
APPLICANT: O1e THASTRUP, et al.
TITLE OF INVENTION:
On A Cellular Response
FILE REFERENCE: 3759-0110P
CURRENT APPLICATION NUMBER: U5/09/417,197
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 MVSKGEELPTGVVPILVVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT 200
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98.4%; Score 1255; DB 4; Length 379;
Best Local Similarity 98.7%; Pred. No. 4.9e-127;
Matches 236; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICT
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                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1255; DB 3;
Pred. No. 4.6e-127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                           36,513
ER: 6510/102US1
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Patent No. 6518021
                     NAME: Francis, Carol L
REGISTRATION NUMBER: 36,513
REFERENCE/DOCKET NUMBER: 6510
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
TELEFAX: 650-327-321
                                                                                                                                                                                                                                                                                                                                                                                                                    98.4%;
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 98.7
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
US-09-085-305-6
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US-09-417-197-129
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LENGTH: 379
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61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                        1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVFWPT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , OTHER INFORMATION: Description of Artificial Sequence: GFP-HSP27
US-09-513-783A-170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

98.4%; Score 1255; DB 4; Length 459;
Best Local Similarity 98.7%; Pred. No. 6.5e-127;
Matches 236; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                   RESULT 15
U9-09-513-783A-170
; Sequence 170, Application US/09513783A
; Patent No. 6416599
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Ravi
; TITLE OP INVENTION: A System for Cell Based Screening;
; TITLE OP INVENTION: A System for Cell Based Screening;
; CURRENT APPLICATION NUMBER: 15/09/513,783A
; CURRENT FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 180
; SEQ ID NOS: 180
; SEQ ID NO 170
; SEQ ID NO 170
; LENGTH: 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: June 21, 2004, 16:04:05 Job time: 12.7778 secs
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1276
1 MVSKGEELFTGVVPILVELD......VLgGFVTAAGITLGMDELYK
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result/being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 4, Appli	Sequence 4, Appli	Sequence 6, Appli			Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 4, Appli		-	Sequence 4, Appli	Sequence 3, Appli	Sequence 13, Appl
	ID	US-09-887-784-4	US-10-296-953-4	US-10-270-223-6	US-10-257-909A-30	US-10-257-909A-32	US-09-887-784-2	US-10-296-953-2	US-09-920-922-2	US-09-999-745-4	US-09-866-538-4	US-09-797-496B-2	US-09-794-308-4	US-09-865-291-4	US-10-457-982-3	US-10-121-258-13
	DB	6	12	14	14	14	σ	12	σ	σ	10	10	10	10	12	14
	Query Match Length DB	239	239	363	893	1132	239	239	239	239	239	239	239	239	239	239
dР	Query Match	99.2	99.2	99.2	99.2	99.5	98.6	98.6	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4
	Score	1266	1266	1266	1266	1266	1258	1258	1255	1255	1255	1255	1255	1255	1255	1255
	Result No.	1	7	m	4	ß	9	7	8	σ	10	11	12	13	14	15

Sequence 7, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 35, Appli Sequence 31, Appli Sequence 31, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 14, Appli Sequence 15, Appli Sequence 16, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli	equence 9, equence 33, equence 34,
US-10-221-461-7 US-10-100-957A-46 US-10-117-390-2 US-10-378-411-3 US-10-378-411-3 US-10-378-411-3 US-10-370-570-4 US-10-314-861-31 US-09-931-232-1 US-09-931-232-1 US-10-314-861-35 US-10-114-861-35 US-10-114-861-35 US-10-314-861-39 US-10-314-861-39 US-10-318-411-11 US-10-318-411-7 US-10-318-411-7 US-10-318-411-7 US-10-318-411-7 US-10-318-411-7 US-10-318-411-7 US-10-318-411-7 US-10-318-411-7 US-10-318-411-7 US-10-318-411-7 US-10-318-411-7 US-10-318-411-7 US-10-318-411-7 US-10-318-411-7 US-10-318-411-7 US-10-318-411-5 US-10-318-411-5 US-10-318-411-5 US-10-318-411-5 US-10-318-411-5 US-10-318-411-5 US-10-318-411-5 US-10-318-411-5 US-10-318-411-5	-10-389-640- -10-033-717- -10-033-717-
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ALIGNMENTS

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Gaps

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61 LVTTLSYGVQCFSRYPDHWKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120

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181 181

1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT

VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180 121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNPKIRHNIEDGSVQLA 180

DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLGGFVTAAGITLGMDELYK 239 

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WG-10-257-909A-30
Sequence 30, Application US/10257909A
Sequence 30, Application No. US20030187056A1
Sequence 30, US20030187056A1
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Publication No. US20030187056A1
Publication No. US20030187056A1
Publication No. US20030187056A1
APPLICANT: Bernard R. TERRY et al.
TITLE OF INVENTION: Live cell procedures to identify compounds modulating intracellulating of INVENTION: Live cell procedures to identify compounds modulating intracellulating FILE REPERBING: 3759-0125P
CURRENT APPLICATION NUMBER: US/10/257,909A
CURRENT FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                 61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                    121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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US-10-257-909A-30
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99.2%; Score 1266; DB 14;
Best Local Similarity 99.6%; Pred. No. 9.8e-123;
Matches 238; Conservative 0; Mismatches 1;
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TITLE OF INVENTION: AN IMPROVED METHOD TO DETECT INTERACTIONS BETWEEN CELLULAR COMPON
TITLE OF INVENTION: INTERACTIONS BY FLUORESCENCE REDISTRIBUTION.
TITLE OF INVENTION: INTERACTIONS BY FLUORESCENCE REDISTRIBUTION.
FILE REFERENCE: 3759-0126P
CURRENT APPLICATION WIDMER: US/10/270,223
CURRENT FLING DATE: 2002-10-11
NUMBER CF SEQ ID NOS: 12
SOFTWARE: PATENTING DATE: 2002-10-11
SEQ ID NO S: 12
LENGTH: 363
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Best Local Similarity 99.6%; Pred. No. 2.7e-123;
Matches 238; Conservative 0; Mismatches 1;
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Pred. No. 1.5e-123;
                                                                                                                                                          APPLICANT: BJORN, SARA P.
APPLICANT: BJORN, SARA P.
APPLICANT: BAGILARO, LEN
APPLICANT: THASTRUP, OLEN
TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS
FILE REFERENCE: PL0095
CURRENT APPLICATION NUMBER: US/10/296,953
CURRENT PRILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: PA 2000 00953
PRIOR APPLICATION NUMBER: 60/212,681
PRIOR APPLICATION NUMBER: 60/290,170
PRIOR APPLICATION NUMBER: 60/290,170
PRIOR APPLICATION NUMBER: 60/290,170
PRIOR APPLICATION NUMBER: 2001-05-10
PRIOR APPLICATION NUMBER: 2001-05-10
PRIOR APPLICATION NUMBER: PA 2001 00739
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: PA 2001 00739
PRIOR APPLICATION NUMBER: PA 2001 00739
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; ORGANISM: Aequoria Victoria and Human
US-10-270-223-6
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                                                                  Sequence 4, Application US/10296953
Publication No. US20040072995A1
GENERAL INFORMATION:
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ORGANISM: Aequorea victoria
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Best Local Similarity 99.6
Matches 238; Conservative
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SEQ ID NO 4
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APPLICANT: BJORN, SARA P.
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US-09-920-922-2
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                                                                                                                                                                                                                                                                                                        Length 1132;
                                                                                                                                                                                 ; OTHER INFORMATION: Fusion between Aequorea victoria and human
US-10-257-909A-32
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Pred. No. 1e-122;
0; Mismatches 2; Indels
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Patent No. US20020177189A1
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US-10-296-953-2
Sequence 2, Application US/10296953
Publication No. US20040072995A1
GENERAL INFORMATION:
                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 99.2%;
Matches 237; Conservative
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US-09-887-784-2
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US-09-887-784-2
SEQ ID NO 32
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Pred. No. 1e-122;
0; Mismatches 2;
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Best Local Similarity 98.7%; Pred. No. 2.1e-122;
Matches 236; Conservative 1; Mismatches 2;
APPLICANT: PAGLIARO, LEN
APPLICANT: THASTRUP, OLE
TITE OF INVENTION: NOVEL FLUORESCENT PROTEINS
FILE REFERENCE: PLOO95
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Patent No. US20020083488A1
GENERAL INFORMATION:
APPLICANT: Sawano, Asako
ITILE OF INVENTION:
FILE REFERENCE: 11283-01201
CURRENT APPLICATION NUMBER: US/09/920,922
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: JP 2000-237166
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 239
                                                                                               CURRENT APPLICATION NUMBER: US/10/296,953
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: PA 2000 00953
PRIOR FILING DATE: 2000-06-19
PRIOR FILING DATE: 2000-06-19
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2001-06-10
PRIOR FILING DATE: 2001-05-10
PRIOR FILING DATE: 2001-05-10
PRIOR FILING DATE: 2001-05-10
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 2
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Best Local Similarity 99.2%;
Matches 237; Conservative
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US-09-920-922-2
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LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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Sequence 4, Application US/09999745

Patent No. US20020157120A1

GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: Baird, Geoffrey
TILE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
FILE REFERENCE: REGEN1470-1
CURRENT APPLICATION NUMBER: US/09/999,745
CURRENT PILING DATE: 2001-10-23
PRIOR FILING DATE: 1999-05-21
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APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: Campbell, Roder
TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
FILE REFERENCE: REGENIS30-2
CURRENT APPLICATION NUMBER: US/09/866,538
CURRENT APPLICATION NUMBER: US/09/866,538
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.0
; SOFTWARE: Patentin version 3.0
; LENGTH: 239
TYPE: FRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER CF SEQ ID NOS: 67
; SOFTWARE: Patentin version 3.0
; SEQ ID NC 4
; LENGTH: 239
; TYPE: FRT
ORGANISM: Aequorea victoria
US-09-999-745-4
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Best Local Similarity 98.7%;
Matches 236; Conservative
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US-09-866-538-4
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US-09-999-745-4
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FEATURE:
OTHER INFORMATION: Aequorea victoria green fluorescent protein modified as described
OTHER INFORMATION: in specification
US-09-797-4968-2
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Publication No. US20030049597A1
GENERAL INFORMATION:
APPLICANT: Simon, Sanford M.
TITLE OF INVENTION: Chimeric Fluorescent Enzymes and Uses Thereof
FILE REPERBNCE: 600-1-267
FILE REPERBNCE: 2001-267
CURRENT APPLICATION UNMER: US/09/797,496B
CURRENT FILING DATE: 2002-05-24
NUWBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 239
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                                                                     Score 1255; DB 10;
Pred. No. 2.1e-122;
                                                                                                                      1; Mismatches
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US-09-794-308-4
Sequence 4, Application US/09794308
Publication No. US20030170911A1
GENERAL INFORMATION:
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                                                                     Query Match 98.4%;
Best Local Similarity 98.7%;
Matches 236; Conservative
; ORGANISM: Aequorea victoria
US-09-866-538-4
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US-09-797-496B-2
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61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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     181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLGGFVTAAGITLGMDELYK 239
                                DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLGGFVTAAGITLGMDELYK 239
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; Bublication No. US20030059835A1
; Publication No. US20030059835A1
; Publication No. US20030059835A1
; APPLICANT: Tsien, Roger
; APPLICANT: Campbell, Robert
; TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
; TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME
; TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME
; TURRENT APPLICATION NUMBER: US/10/121,258
; CURRENT FILING DATE: 2001-02-04-10
; PRIOR APPLICATION NUMBER: 09/794,308
; PRIOR FILING DATE: 2001-02-26
; PRIOR PILING DATE: 2001-05-24
                                                                                                                                                                     Sequence 3, Application US/10457982

Publication No. US20030212265A1

SERREAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Tsien, Roger Y.
APPLICANT: Hispawaki, Atsushi
APPLICANT: Hopis, Juan
APPLICANT: Hopis, Juan
APPLICANT: Remindton, S. James
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REPERENCE: 07257/071001
CURRENT APPLICATION NUMBER: US/10/457, 982
CURRENT FILING DATE: 2003-06-22
PRIOR PRING DATE: 2000-06-22
PRIOR PLICATION NUMBER: US/09/602,641
PRIOR PLICATION NUMBER: US/09/602,641
PRIOR PLICATION NUMBER: 09/172,063
PRIOR FILING DATE: 1908-10-13
NUMBER OF SEQ ID NOS: 38
SOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 239
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ORGANISM: Aequorea victoria
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Matches 236; Conservative
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NAME/KEY: VARIANT
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APPLICANT: TSIEN, ROGER
APPLICANT: TSIEN, ROGER
APPLICANT: TING, Alice
APPLICANT: TING, Alice
APPLICANT: TING, Jin
TITLE OF INVENTION: EMISSION RATIOMETRIC INDICATORS OF PHOSPHORYLATION
FILE REFERENCE: REGENTISO
CURRENT APPLICATION NUMBER: US/09/865,291
CURRENT APPLICATION NUMBER: 2001-05-24
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Version 3.0
SEQ ID 0.4
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                   APPLICANT: ZACHARIAS, David
APPLICANT: ZACHARIAS, David
APPLICANT: BAIRD, Geoffrey
TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
FILE REFERENCE: REGENIS30
CURRENT APPLICATION NUMBER: US/09/794,308
CURRENT FILING DATE: 2001-02-26
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Pred. No. 2.1e-122;
1; Mismatches 2;
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1; Mismatches
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Publication No. US20030186229A1
GENERAL INFORMATION:
                                                                                                                                                                                                           PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 98.4%;
Best Local Similarity 98.7%;
Matches 236; Conservative
                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Aequorea victoria
US-09-794-308-4
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Matches 236; Conservative
TSIEN, Roger
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SOFTWARE: Patentin Ve
SEQ ID NO 4
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US-09-865-291-4
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                                                        FEATURE:
; OTHER INFORMATION: Enhanced Green Fluorescent Protein (EGPP)
US-10-121-258-13
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 239
TYPE: PRT
TYPE: PRT
CORMAISM: Artificial Sequence
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Search completed: June 21, 2004, 16:09:30 Job time : 34.7778 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

Run on:

June 21, 2004, 15:46:00 ; Search time 10.3333 Seconds

(without alignments) 2224.817 Million cell updates/sec

1 MVSKGEELFTGVVPILVELD.......VLGGFVTAAGITLGMDELYK 239 US-09-887-784-222G Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 Fotal number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.		Query	Length	DB		Cr
-	1233	9.96	238	-	JQ1514	green-fluorescent
7	105	8.2	785	7	H72228	hypothetical prote
٣	92	•	461	~	T06936	
4	91.5	7.2	861	~	H64102	A 1
S	90	7.1	425	~	C97354	hypothetical prote
9	90	7.1	632	~	T06586	Ω
7	œ.	7.0	887	7	E82590	
œ	•	6.9	655	7	D83917	DNA topoisomerase
σ	88	6.9	461	~	S41480	photosystem II chl
10	88	6.9	578	Н	140794	dihydrolipoamide d
11	7.	6.9	370	~	E70390	iron-sulfur cofact
12	87.5	6.9	860	8	AC0582	leucyl-tRNA synthe
13	ζ.	6.9	2222	Н	A36028 ,	ರ
14	87.5	6.9	2573	N	D71614	prot
15	87		1259	7	AE1055	U
16	. 86	6.7	357	~	G81355	tRNA (uracil-5-)-m
17	86	6.7	877	~	H64708	iron-regulated out
18	5	6.7	353	7	E84941	imidazoleglycerol-
19	ů.	6.7	788	-	лругин	DNA-directed DNA p
50	5.	6.7	889	~	JC5576	inter-alpha-trypsi
21	85.5	6.7	1259	7	H65233	ytfN protein - Esc
22	ď.	6.7	1259	~	G91278	hypothetical prote
23	'n.	6.7	1259	~	G86119	
24	85	6.7	281	N	AD2052	hypothetical prote
52	82	٠	459	~	S42647	photosystem II chl
56	85	6.7	459	N	AD2342	photosystem II CP4
27	85	•	9	N	ın	lipoxygenase (EC 1
28	84.5	9.9	613	~	95	tidas
53	•	9.9	888	~	A54280	cell differentiati

glucose dehydrogen	synergohymenotropi	DNA-directed DNA p	IgA Fc receptor pr	IgA Fc receptor pr	hypothetical prote	transcription regu	photosystem II chl	S-layer protein pr	water-stress-induc	nitrogenase (EC 1.	neuraminidase, pro	protective surface	protective surface	probable iron-regu	hypothetical prote
B83911	S68225	JDVLD	A60234	FCSOAG	876853	A97313	S06469	JC4930	S53488	NICLMA	G95153	JC4078	F64102	E71811	D90946
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9.9	6.5	6.5	6.5	6.5	6.5	6.5	6.5	6.5	6.5	6.5	6.5	6.5	6.5	6.5	6.4
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United the Figurescent protein [validated] - hydromeduse (Aequorea victoria)

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A;Residues: 1-861 <TIGR>
A;Cross-references: GB:U32774; GB:L42023; NID:g1573942; PIDN:AAC22581.1; PID:g1573943; T.
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A;Accession: H7228
A;Status: Frelimary
A;Residues: Frelimary
A;Residues: 1-785 <ARN>
A;Residues: 1-785 <ARN>
A;Cross-references: GB:AE001806; GB:AE000512; NID:g4982196; PIDN:AAD36691.1; PID:g498219
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1624
A;Contents: annotation; X-ray crystallography, 1.9 angstroms
C;Comment: This protein is excited by the photoprotein aequorin (see PIR:AQJFNV) emittin
C;Comment: The chromophore of this protein is formed by modification of Ser-dehydro-Tyr-C;Genetics:
G;Genetics:
A;Gene: GFP
A;Introns: 69/3; 167/3
C;Superfamily: green-fluorescent protein
C;Superfamily: green-fluorescent protein
F;65-67/Cross-link: 5-imidazolinone (Ser-Gly) #status experimental
F;66/Modified site: dehydrotyrosine (Tyr) #status experimental
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hardson, D.;
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H72228
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C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Dates: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Datesion: H72228
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hick Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, I
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                                                                                                                                                                                                                  Score 1233; DB 1;
Pred. No. 9.1e-96;
4; Mismatches 4;
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19.7%; Pred. No. 0.9;
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Best Local Similarity 96.6%;
Matches 230; Conservative
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A;Genome: cyanelle
C;Superfamily: photosystem II chlorophyll a-binding protein psbC
C;Keywords: chlorophyll; cyanelle; membrane-associated complex; photosynthesis; photosyst
                                                                                                                                                                                                                                                                             C. Accession: T06936
R. Stirewalt, V.L.; Michalowski, C.B.; Luffelhardt, W.; Bohnert, H.J.; Bryant, D.A. submitted to the EMBL Data Library, July 1995
A. Description: Nucleotide sequence of the cyanelle genome from Cyanophora paradoxa. A; Beference number: Z15840
A; Accession: T06936
A; Accession: T06936
A; Accession: T06936
A; Molecule type: DNA
A; Residues: 1-461 < STI>
A; Residues: 1-461 < STI>
A; Residues: 1-461 < STI>
A; Cossereferences: EMBL: U30821; NID:g1016083; PIDN: AAA81279.1; PID:g1016192
A; Experimental source: strain Pringsheim LB555
C; Genetics:

    Cyanophora paradoxa cyanelle

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photosystem II chlorophyll a-binding protein psbC - Cyanophora paradoxa cyan NiAlternate names: protein CP43
C.Species: cyanalle Cyanophora paradoxa
C.Species: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 26-Aug-1999
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Best Local Similarity 21.4%; Pred. No. 5.5;
Matches 58; Conservative 35; Mismatches
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leucine-tRNA ligase (BC 6.1.1.4) - Haemophilus influenzae (strain Rd KW20)
N;Alternate names: leucyl-tRNA synthetase
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 03-Jun-2002
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 03-Jun-2002
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 03-Jun-2002
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 03-Jun-2002
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 03-Jun-2002
C;Date: 18-Aug-1995 #sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MulD:95350630; PMID:7542800
A;Reference number: A64000; MulD:95350630; PMID:7542800

A,Status: nucleic acid sequence not shown, translation not shown A,Molecule type: DNA

C,Superfamily: leucine-tRNA ligase C,Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

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submitted to the EMBL Data Library, June 1996
A; Description: Identification of a novel family of DNA-binding proteins with two AT-hook
A; Reference number: Z15774
A; Accession: T06586
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-632 < SAT>
A; Cross-references: EMBL:X98740; NID:e995229; PIDN:CAA67292.1; PID:e275185
A; Experimental source: cv. Alaska
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Xylella fastidiosa
C;Date: 18-Mug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Date: 18-Mug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MulD:20365117; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
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A; Residues: 1-887 < SIM>A; Molecule type: DNA
A; Residues: 1-887 < SIM>A; Residues: 1-887 < SIM>A; Residues: 1-887 < SIM>A; Residues: 1-887 < SIM>A; Construction to the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 leucyl-tRNA synthetase XF2176 [imported] - Xylella fastidiosa (strain 9a5c)
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7
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33.3%; Pred. No. 12;
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Best Local Similarity 23.3%; Pred. No. 12;
Matches 49; Conservative 26; Mismatches
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22.2%; Pred. No. 21;
ive 29; Mismatches
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C;Superfamily: leucine-tRNA ligase
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es 44; Conserv
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A; Status: preliminary
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hypothetical protein CAC3702 [imported] - Clostridium acetobutylicum
C;Species 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: C97354
S;Nolling, J.; Barteon, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Baty, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Status: preliminary
                                                                                11;
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A,Residues: 1-425 «KUR»
A,Cross-references: GB:AE001437; PIDN:AAK81622.1; PID:g15026806; GSPDB:GN00168
A,Experimental source: Clostridium acetobutylicum ATCC824
C,Genetics:
A,Gene: CAC3702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
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                                                                                                                                                                                                                                                                           104 DGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADK-QKNGI 162
                                                                                                                                                                                                                                                                                                                                                                                                                    ---KVNFKIRH-------NIEDGSVQLADHYQQNTPIGDGPVLLPDNHYL- 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FSRYPDHMK-----QHDFFKSAMPEGYVQERTIFFKDDGNYKTR-----AEVKFEGD-- 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----TLVNRIELKGIDFKE--DGNILGHKLEYNY------NSH--NVYIMA 155
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DNA-binding protein PD2 - garden pea
C;Species: Pisum sativum (garden pea)
C;Species: Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C;Accession: T06586
R;Sato, N.; Kazuno, A.A.; Ohta, N.; Ohshima, K.
                                                                                                                                                                                          | | | | : | : | : | TGDKLPI-WANFVLMHYGTGAVMAVPAH-DQRDF-----EFAQKYSLPIKQVIAPLA
                                                                                                                                                                                                                                                                                                                            :||: :||:
-----IADKLEKLGV
                                                                                                                                            50 TTGKLPVPWPTLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKD----
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                                                                         Gaps
                                                                             59;
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          Length 861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.1%; Score 90; DB 2; Length 425; Best Local Similarity 24.7%; Pred. No. 7.3; Matches 66; Conservative 31; Mismatches 98; Indels
                                                                             Indels
                                                                         60;
       7.2%; Score 91.5; DB 2; 24.1%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                        365 DEEIDLTKQAFVEHGKLVNSDEFDGKNF--DGAFNG-
                                                                         26; Mismatches
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                                          Best Local Similarity 24.19
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 STQSALSKDPN 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         462 GVKSPINADPN 472
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       Query Match
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A;Cross-references: EMBL:M90639; NID:g289948; PIDN:AAA84148.1; PID:g289949  C;Genetics:	OQBALSKDPNEKR 216     Query Match     6.9%; Score 88; DB 2; Length 461;           :     ::     Best Local Similarity 19.5%; Pred. No. 12;         Gaps 12;       RATCHES 51; Conservative 37; Mismatches 83; Indels 90; Gaps 12;	RESULT 8  DATYCKLILEPICTTGKLPUPWPTLVTTLSYGVOCPSR 74  DB3317  DB3317  DBA topoisomerase IV subunit B BH2140 [imported] - Bacillus halodurans (strain C-125)  DBA topoisomerase IV subunit B BH2140 [imported] - Bacillus halodurans (strain C-125)  DBA topoisomerase IV subunit B BH2140 [imported] - Bacillus halodurans (strain C-125)  DBA topoisomerase IV subunit B BH2140 [imported] - Bacillus halodurans (strain C-125)  DBA topoisomerase IV subunit B BH2140 [imported] - Bacillus halodurans (strain C-125)  DBA topoisomerase IV subunit B BH2140 [imported] - Bacillus halodurans (strain C-125)  DBA topoisomerase IV subunit B BH2140 [imported] - Bacillus halodurans (strain C-125)  DBA topoisomerase IV subunit B BH2140 [imported] - Bacillus halodurans (strain C-125)  DBA topoisomerase IV subunit B BH2140 [imported] - Bacillus halodurans (strain C-125)  DBA 220 DIGGHIMGHARAPERENDARENCRENTSTERN 279  Takens in III shalodurans (strain C-125)  DBA 220 DIGGHIMGHARAPERENDARENCRENTSTERN 279  Takens in III shalodurans (strain C-125)  DBA 220 DIGGHIMGHARAPERENDARENCRENTSTERN 279  Takens in III shalodurans (strain C-125)  DBA 220 DIGGHIMGHARAPERENDARENCRENTSTERN 279  Takens in III shalodurans (strain C-125)  DBA 220 DIGGHIMGHARAPERENDARENCRENTSTERN 279  Takens in III shalodurans (strain C-125)  Takens in III shalodurans (strain C-125)  DBA 220 DIGGHIMGHARAPERENDARENCRENTSTERN 279  Takens in III shalodurans (strain C-125)  DBA 230 DATYCKLILEPICOTOR 179  Takens in III shalodurans (strain C-125)  Takens in III shalodurans (strain C-125)  DA TORDAGARENDARENCRENTSTERN 279  Takens in III shalodurans (strain C-125)  DBA 230 DATYCKLILEPICE IN III shalodurans (strain C-125)  Takens in III shalodurans (strain C-125)  DBA 240 DATE IN INTERNATION CARL STORENTSTERN 279  Takens in III shalodurans (strain C-125)  DBA 250 DATACHARAPEN 279  Takens in III shalodurans (strain C-125)  Takens in III shalodurans (strain C-125)  Takens in III shalodurans (strain C-125)  Takens in III shalodurans (strain C-125)  Takens in III shalodurans (strain C-		,,,,,,	NENUETLEREARILEGARIELY 241  A) Residues: 1-578 «KRU»  A) Cross-references: GB:L31844; NID:g472324; PIDN:AAA21748.1; PID:g472330  C) FUNCTION:	Statement of the EMBL Data Library, May 1993 A) Reference number: 841480  Spattago  Statement of the EMBL Data Library, May 1993 A) Reference number: 841480  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago  Spattago
Qy       108	Qy 200 -HYLSTQSALSKDPNEKR	RESULT 8 D83917 DNA topoisomerase IV subunit C;Species: Bacillus halodural C;Date: 01.Dec-2000 #sequencc C;Accession: D83917 R;Takami, H; Nakasone, K; 7 Nucleic Acids Res. 28, 4317-4 A;Title: Complete genome sequence complete complete genome sequence complete complete genome sequence complete complete genome sequence complete pages and A;Accesion: D89917 A;Scatus: preliminary A;Molecule type: DNA A;Residues: 1-655 cSTO> A;Cross-references: GB:AP00116 A;Experimental source: straif C;Gentics: A;Gene: BH2140 C;Superfamily: DNA topoisomes	Query Match Best Local Similarity 21 Matches 53; Conservative Qy 22 DVNGHKFSVSGB CDb 63 NVTIHKDQSVSVRDB	123	Db 183 NFNVETLSERLREAM QY 158QKNGIKVNFI Db 242 VFFNGESNGIEIEFF QY 213 NE 214 Db 295 NE 296 RESULT 9	S41480 photosystem II chlorophyll ac; Species: chloroplast Chlamm C; Species: chloroplast Chlamm C; Date: 06-Jan-1995 #sequence C; Date: 06-Jan-1995 #sequence R; Cote, M.J.J.; Lemieux, C.; submitted to the EMBL Data L: A; Becription: Identification of Chlamydomonas moewusii. A; Reference number: S41480 A; Accession: S41480

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464 PELASVGLT 472 ---TAAGIT 231

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DNA-directed DNA polymerase (EC 2.7.7.7) II catalytic chain - yeast (Saccharomyces cerev)
NyAlternate names: DNA-directed DNA polymerase II chain A; protein N0825; protein XNL262v
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: A36028; B36028; S60919; S61235; S65121
R;Morrison, A.; Araki, H.; Clark, A.B.; Hamatake, R.K.; Sugino, A.
A;Title: A third essential DNA polymerase in Saccharomyces cerevisiae.
A;Reference number: A36028; MUID:90381771; PMID:2169349
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A; Residues: 1-2222 <SEM>A; Cross-references: EMBL:271538; NID:g1302316; PIDN:CAA96169.1; PID:g1302317; GSPDB:GN00(
A; Cross-references: EMBL:271538; NID:g1302316; PIDN:CAA96169.1; PID:g1302317; GSPDB:GN00(
B; Experimental source: strain S288C
R; Sen-Gupta, M.; Lyck, R.; Fleig, U.; Niedenthal, R.K.; Hegemann, J.H.
Yeast, 12, 505-514, 1996
A; Fitle: The sequence of a 24 152 bp segment from the left arm of chromosome XIV from Sac
A; Reference number: S65111; MUID:96310631; PMID:8740425
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A, Residues: 1214-1216, X', 1218-1221 <MO2>
A, Residues: 1214-1216, X', 1218-1221 <MO2>
B, Sen-Gupta, M.; Lyck, R.; Fleigi, U.; Misdenthal, R.N.; Hegemann, J.M.
Bubmitted to the EMBL Data Library, October 1995
A, Description: The sequence of a 24152 bp segment from the left arm of chromosome XIV for Reference number: $60909
A, Reference number: $60909
A, Reference number: $60909
A, Residues: 1-221 <SEN>
A, Residues: 1-221 <SEN>
A, Residues: 1-221 <SEN>
A, Residues: 1-221 <SEN>
A, Residues: 1-221 <SENS
A, Residues: 1-221 <SENS
A, Residues: 1-221 <SENS
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A, Residues: 1-221 <SENS
A, Residues: 1-221 <SENS
A, Residues: 1-221 SENS
A, Residues: 1-221 
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A;Cross-references: EMBL:X92494; NID:g1045236; PIDN:CAAG3235.1; PID:g1045247
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Accession: A36028
A,Molecule type: DNA
A,Residues: 1-222 cMOR>
A,Cross-references: GB:M60416; GB:M36724; NID:g171408; PIDN:AAA88711.1; PID:g171409
A,Accession: B36028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.
                                                                                                                                                                                         A;Cross-references: GB:AL513382; PIDN:CAD05125.1; PID:g16501899; GSPDB:GN00176 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 TIGKLPVPWPTLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 TGEEIPV-WAANFVLMEYGTGAVMAVPGH-DQRD-YEFASKYGLTIKPVILAADGSEPDL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           371 SEQALTEKGULFNSGEPDGLAFEAAFNAIADKL-----AEKGVGERKVNYRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 RAEVKFEGDTLVNRIBLKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----NIEDGSVQLADHYQQNTPIGDGPVLLPDNHYL-STQSALSKDP
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A; Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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6.9%; Score 87.5; DB
Best Local Similarity 23.3%; Pred. No. 29;
Matches 42; Conservative 21; Mismatches
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A;Gene: SGD:POL2; DUN2; MIPS:YNL262w
                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: leucine-tRNA ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 H-----
                                A,Accession: AC0582
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-860 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S65121
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A;Residues: 1-370 <AQF>
A;Cross-references: GB:AE000720; NID:g2983529; PIDN:AAC07111.1; PID:g2983536; GB:AE00065
A;Experimental source: strain VFS
C;Genetics:
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C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 07-Dec-1999
C;Accession: E70390
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 392, 353-358, 1998
Affile: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: E70390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                     IELKGIDFKEDG---NILGHKLEYNYNSHNVYIMADKQKN--GIKVNFKIRHNIEDGSVQ 178
                                                                                                                                                                                                                LADHYQQNT----PIGD--GPVLLPDNHYLSTQSALSKD----PNEKRDHMVLGGFV--- 225
                                                                                                                                                                                                                                                                       347 CKVTRIEQGEDGLKVSFIGDKGEESIDVEKVLIAVGRRSNIEGLDVE-KIGVKTEGGSII 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGKLP-----VPWPTLVTTLSYGVQCFSRYPDHMKQ-HDFFKSAMPEGYVQERTIFFKDD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 NGKRSGTENVVGILSLAKALEIIVSNFSRYQEQLKKLRDLFENLLLEA-LPDAQIVGKDA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 GNYKTRAEV---KFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283 ERSPSISSVIMPKFFGAEIVNKLSEKGIYCSTGSACLSGEYEPNKHMLKMGFSQEKALRM 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGEELFTGVV----PILVELD----GDVNGHKF-SVSGEG----EGDATYGKLTLKFICT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary; nucleic acid sequence not shown; translation not shown
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C;Keywords: phosphortein; pyridoxal phosphate; sulfurtransferase
F;195/shiding site: pyridoxal phosphate (Lys) (covalent) #status predicted
F;318/Active site: Cys (cysteine persulfide intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        iron-sulfur cofactor synthesis protein nifS - Aquifex aeolicus N;Contains: L-cysteine sulfurtransferase (EC 2.8.1.-)
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25.4%; Pred. No. 9.8;
tive 30; Mismatches
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Local Similarity 25.4% nes 49; Conservative

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Query Match

A;Gene: nifSl

51

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VRFSFGLLNKEEE 355 162 IKVNFKIRHNIED 174

343

RESULT 12

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Search completed: June 21, 2004, 16:02:00 Job time: 11.3333 secs
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Matches
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Probable exported protein ytfN [imported] - Salmonella enterica subsp. enterica serovar

probable exported protein ytfN [imported] - Salmonella enterica serovar

C;Species: Salmonella enterica subsp. enterica serovar Typhi

A;Note: this species has also been called Salmonella typhi

A;Note: this species has also been called Salmonella typhi

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C;Accession: AE1055

R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

K;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A;Authors: Parry, C; Quail, M.; Rutherford, C; Simmonds, M.; Skelton, J.; Stevens, K.;

A;Authors: Parry, C; Quail, M.; Pilo: 11671608
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A, Cross-references: GB. AE001396; GB. AE001362; NID: g3845188; PIDN: AAC71881.1; PID: g384519
A, Experimental source: clone 3D7
C, Genetics:
A, Gene: PFE0460c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 NVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            883 LPKSFPETYFFTLENGKKLYLSYPCSMLNYRVHQKFTNHQYQELKDPLNYIYETHSENTI 942
                                                                                                                                                                                                                                                                                                100 FFKDDGNYKTR--AEVKFEGDTLVNR-----IELKGIDFKEDGNILGHKLEYNYN 147
                                                                                                                                                                                                                                                                                                                               A;Accession: D71614
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                          99
                                                                                                                                                                                                        54 LPVPWP-TLVTTLSYGVQCFSRYPDHM-----KQHDFFKSAMPEGYV----QERTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
A;Cross-references: SGD:S0005206; MIPS:YNL262w
A;Map position: 14L
C;Superfamily: DNA-directed DNA polymerase II
C;Keywords: DNA binding; nucleotidyltransferase; nucleus; zinc finger
                                                                                                                                                             31;
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6.9%; Score 87.5; DB 2; Length 2573;
Best Local Similarity 26.2%; Pred. No. 1.2e+02;
Matches 34; Conservative 30; Mismatches 53; Indels 13
                                                                                                           Query Match
Best Local Similarity 28.2%; Pred. No. 1e+02;
Matches 37; Conservative 14; Mismatches 49; Indels 31.
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                                                                                                                                                                                                                                                                                                                                                                                               148 S--HNVYIMAD 156
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237 TYLKRERDYM 246
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1042 AFGLKARLTGDL------KVAQDKQ--GLGLNGQI--NIPDGRFRA---YGQ 1080
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A,Accession: AE1055
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1259 AAR>
A;Cross-references: GB:AL513382; PIDN:CAD06890.1; PID:gl6505538; GSPDB:GN00176
C;Genetics:
A;Gene: ytEN
C;Superfamily: ytEN protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 SRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKT---RAEVKFEGDTLVN-----RIE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 LKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQ 185
                                                                                                                                                                                                                                                                                                                                                                13 VPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLSYGVQCF
                                                                                                                                                                                                                                                                                                                                                                                                                     957 VPPMVRLD-----VSPDVVFDATPSLFTL-----DGRVDVPWARIVV---
                                                                                                                                                                                                                                                                                                                68;
                                                                                                                                                                                                                                                  6.8%; Score 87; DB 2; Length 1259;
23.2%; Pred. No. 53;
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                                                                                                                                                                                                                                                                                                                70; Indels
                                                                                                                                                                                                                                                                                                                34; Mismatches
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nes 52; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

June 21, 2004, 15:42:24; Search time 6.44444 Seconds (without alignments) 1931.085 Million cell updates/sec Run on:

US-09-887-784-222G 1276 1 MVSKGEELFTGVVPILVELD......VLGGFVTAAGITLGMDELYK 239 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt 42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P42212 aequorea vi			Q9pbg8 xylella fas			Q8zqz6 salmonella	P21951 saccharomyc	homo sa	candida	xylella		Q9pp92 campylobact							Q98qp0 mycoplasma		-			Q7vnf0 haemophilus				-	-		4935	P46024 haemophilus
SUMMARIES		GFP AEQVI	PSBC CYAPA	SYL HAEIN	SYL_XYLFA	PSBC_CHLEU	SYL_SALTI	SYL_SALTY	DPOE YEAST	AC2L_HUMAN	CP51_CANGA	SYL XYLFT	VIT4 CAEEL	TRMA_CAMJE	HIS7 BUCAI	ADAS HUMAN	DPOL_HPBHE	ITH3_MESAU	YTFN_ECOLI	YC03_KLEPN	PEPF MYCPU	SYL_SHEON	LAGC_DICDI	SET7_HUMAN	GRBE_RAT	SYD HAEDU	BAG STRAG	PSBC_SYNY3	SLAP_BACLI	AMPA_WIGBR	NIFD_CLOPA	ADAS CAVPO	D152 HAEIN	D151_HAEIN
	Jength DB	238 1	461 1	861 1	879 1	461 1	860 1	860 1	2222 1	689 1	533 1	879 1	1603 1	357 1	353 1	658 1	788 1	886 1	1259 1	504 1	613 1	859 1	888 1	366 1	538 1	589 1	1164 1	472 1	874 1	1	٦	9	795 1	7
d	Query Match Length	97.1	7.2	7.2		6.9	•	٠	6.9	•	٠	6.8	6.9	6.7	6.7	6.7	6.7	6.7	6.7	6.7	•		9.9	•	•		•		•		•			•
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P23865 escherichia 092405 asperdillus	P28840 rattus norv 032629 haemophilus p19424 hacillus en	Q58743 methanococc Q99nbl mus musculu	P91679 drosophila 042918 schizosacch	O25443 helicobacte Q8xbn8 escherichia	
PRC_ECOLI	NECI_RAT D153_HAEIN GIN BACSE	YD48 METJA AC2L MOUSE	OPT1_DROME AMY2_SCHPO	TRMB_HELPY SYL_ECO57	SYL_ECOL6
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682	752	336	737	393 860	860
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# ALIGNMENTS

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SEQUENCE
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                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                         X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

MEDLINE-99238303; PubMed=10220315;

A Elsiager M.A., Wachter R.M., Hanson G.T., Kallio K., Remington S.J.;

Structural and spectral response of green fluorescent protein
variants to changes in pH.";

L Blochemistry 38:226-5301(1999).

-!- FUNCTION: Bnergy-transfer acceptor. Its role is to transduce the blue chemiluminescence of the protein aequorin into green fluorescent light by energy transfer; Fluoresces in vivo upon receiving energy from the Ca(2+)-activated photoprotein aequorin. Absorbs light maximally at 395 nm and exhibits a smaller absorbance peak at 470 nm. The fluorescence emission spectrum peaks at 500 nm with a shoulder at 540 nm.

-!- SUBUNIT: Monomer.

-!- TISSUE SPECIFICITY: Photocytes.
      X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF MUTANT WITH YELLOW EMMISSION
             MEDLINE=98455509; PubMed=9782051; Wachter R.M., Elsliger M.A., Kallio K., Hanson G.T., Remington S.J.; "Structural basis of spectral shifts in the yellow-emission variants of green fluorescent protein.";
                                                                                                                                                                                                                                                                                                                                                                             EMBL; M62654; AAA27722.1; -.
EMBL; M62653; AAA27721.1; -.
EMBL; L29345; AAA58246.1; -.
EMBL; K96418; CAA65278.1; -.
                                    of green fluorescent process
Structure 6:1267-1277(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JAN-03.
28-AUG-02.
10-APR-02.
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18FP; 07-JUL-97
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16MA;
16MB;
16MC;
16ME;
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F0B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTILSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VTTFSYGVQCFSRYPDHMKQHDFPKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NRIBLKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VSKGBELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
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                                                                                                                             5-imidazolinone (Ser-Gly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26886 MW; EA5A6F21FBFB6E05 CRC64;
                                                                                                                                         3-DIDEHYDROTYROSINE
PDB; ZEMD; 20-AUG-97.
PDB; ZEMN; 20-AUG-97.
PDB; ZEMN; 20-AUG-97.
PDB; ZEMO; 20-AUG-97.
InterPro; IPR009017; GFP_like.
InterPro; IPR000786; Green_fl_protein.
Pfam; PF01353; GFP; 1.
                                                                                PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl_protein; 1.
Luminescence; 3D-structure.
                                                                                                                                                      X P R O G H R S Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 97.9
Matches 233; Conservative
                                                                                                                                                                                                                                                                                           217
238 AA;
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328 YLMRSPSGEIIFGGETM--
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                                                                                                                                                                                                                                                                                                       STANDARD;
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623
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861 AA;
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P43827;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 YKTRA---EVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIK 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 GHKFSVSGEGEGDATYGKLTLKFICTTGKL-----PVPWP--TLVTT----LSYGV--- 69
181 HYQQNTPIGDGPVLLPDNHYLSTQSALSXDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-UTEX LB 555 / Pringsheim;
Loeffelhardt W., Stirewalt V.L., Michalowski C.B., Annarella M.,
Loeffelhardt W., Stirewalt V.L., Mewmann-Spallart C.,
Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.;
"The complete sequence of the cyanelle genome of Cyanophora paradoxa:
the genetic complexity of a primitive plastid.";
[In] Schenk H.E.A., Herrmann R., Jeon K.W., Mueller N.E.,
Schwemmler W. (eds.);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bryant D.A.;
"Nucleotide sequence of the cyanelle DNA from Cyanophora paradoxa.";
Plant Mol. Biol. Rep. 13:327-332(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -I- FUNCTION: The 43 kDa protein (p6) is a component of the core of photosystem II. It is a chlorophyll binding protein.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Cyanelle thylakcid membrane.
-!- SIMILARITY: Belongs to the psbB / psbC family.
                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Photosystem II 44 kDa reaction center protein (P6 protein) (CP43).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Photosynthesis; Photosystem II; Thylakoid; Chlorophyll; Cyanelle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotism and Symbiosis, pp.40-48, Springer-Verlag, Heidelberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stirewalt V.L., Michalowski C.B., Loeffelhardt W., Bohnert H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.2%; Score 92; DB 1; Length 461;
21.4%; Pred. No. 3;
                                                                                                                                                                                                                                                                                                                             Eukaryota; Glaucocystophyceae; Cyanophoraceae; Cyanophora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----QCFSRYPDHMKQHDFFKSAMPE-GYVQERTIFFKDD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 461 AA; 50402 MW; 62664E239E13B9C1 CRC64;
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tive 35; Mismatches
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InterPro; IRR005869; Photo44.
InterPro; IRR00932; PSIIprot.
TIGRFAMS; TIGR01153; psbC; 1
                                                                                                                                                           01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last seq
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U30821; AAA81279.1; -.
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                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                 Cyanophora paradoxa.
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                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2762;
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                                                                                                                                                                                                                                                                                                            Cyanelle
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--RFWDTRAPWLEPLRGANGLD 364
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                                                                                                                                    164 VNFKIRHNIEDGSVQLADHYQQNTPIGD----GPVLLPDN--HYLSTQSALSKDPNEKRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Relachman R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutron G., Fitzhugh W., Fields C.A., Gocayne J.D., Scort J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.E., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Venter J.C., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aminoacy1-tRNA synthetase; ProteIn biosynthesis; Ligase; ATP-binding;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 34, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS).
                                                                                                                                                                                                                                                                  365 LT-KIKYDIQPWQERRAABYMTHAPLGSLNSVGGVATEINSVNYVSPRSWLS----
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
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622 ATP (BY SIMILARITY).
97750 MW; EB93304F6B4CBFB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     235
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InterPor | IPR0013102; Leu-tRNASyntla.
InterPor | IPR0013102; LRNA-syntla.
InterPor | IPR001412; LRNA-syntla.
InterPro; IPR001412; LRNA-syntla.
InterPro; IPR001412; LRNA-syntla.
InterPro; IPR00131; ENRA-syntla.; I.
PRINTS; PR00189; TRNASYNTHLEU.
IIGRFAMS; TIGR00396; LeuS_bact; I.
PROSITE; PR00181; AA TRNA_LIGAE.
IIGRFAMS; TIGR00396; AA TRNA_LIGAE.
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IIGRFAMS; TIGR00396; AB TRNA_LIGAE.
IIGRFAMS; TIGR003
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STRAIN-Rd / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
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475 VAFSGTGSPIKTDPEWRK 492
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hes 44; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydomonas eugametos.
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641
                                                                                                                                                                                                                                               Complete proteome.
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                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                 Query Match
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PSBC_CHLEU
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                             11;
                                                          103
                                                                                     314 TGDKLPI-WVANFVLMHYGTGAVMAVPAH-DQRDF-----EFAQKYSLPIKQVIAPLA 364
                                                                                                                                            365 DEEIDLTKQAFVEHGKLVNSDEFDGKNF--DGAFNG------IADKLEKLGV 408
                                                                                                                                                                       -----NIEDGSVQLADHYQQNTPIGDGPVLLPDNHYL- 202
                                                                                                                                                                                        Mindounistandard N. Aruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Arruda P., Baia G.S., Baptista C.S., Alvarenga R., Alves L.M.C., Arruda P., Baia G.S., Baptista C.S., Barandon M.H., Bonaccoral E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa Meto C.M., Carrer M., Coldand G.M., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Fraga J.S., Franco M.C., Frohme M., Furlan L.R., Gandian M.L., Kemper E.L., Kitajima J.P., Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., M. Marchael A.M.B.N., Madeira H.M.F., Marchool J.B., Marchael B.C., Myaki C.Y., Monteliar O.L., Andraca E.C., Myaki C.Y., Monteliar D.C., Marchael B.C., Myaki C.Y., Monteliar D.Y., Marchino C.L., Marchael B.C., Myaki C.Y., Monteliar D.Y., Nobrega F.G., Nunes L.R., Oliveira M.C., de Oliveira M.A., Persinento A.L.T.O., Netto L.E.S., Manni A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A., Badeira H.A., Br., Persina G.A.G., Persinento A.L.T.O., Netto L.E.S., Ade Slova A.J.M., Ada Silva M.A., Madiania W.J., de Rosa A.J.M., Ada Silva M.A., Cata S.H., Marchiner D.C., Rodrigues V., de Rosa A.J.M., Ada Silva M.A., Verjovski A.M., da Silva M.A., Verjovski A.M., da Silva M.A., Verjovski A.M., The genome sequence of the plant pathogen Xylella fastidiosa."; https://doi.org/10.0000
                                                          50 TIGKLPVPWPTLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKD----
                                                                                                                 104 DGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADK-QKNGI
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                         16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEE-2003 (Rel. 41, Last annotation update)
LEUCY1-RNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS).
LEUS CR XF2176.
Xylella fastidiosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                             29;
  Length 861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP +
                             Indels
                             909
  DB 1;
                                                                                                                                                                                                                                                                                                                                 879 AA
 7.2%; Score 91.5; D 24.1%; Pred. No. 7; iive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diphosphate + L-leucyl-tRNA(Leu).
SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                          ---KVNFKIRH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xanthomonadaceae; Xylella.
Query Match
Best Local Similarity 24.18
Matches 46; Conservative
                                                                                                                                                                                                                                 203 STOSALSKDPN 213
                                                                                                                                                                                                                                                            462 GVKSPINADPN 472
                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Q9PBG8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 MADKQKNG-IKVNFKIRHNIEDGSVQLADHYQQNTPI------GDGPVLLPDN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP, ME 00049; -; 1.

InterPro; IRR002300; Leu-tRNAsyntla.

InterPro; IRR001300; LRNA-syntla.

InterPro; IRR001412; tRNA-syntla.

InterPro; IRR001412; tRNA-syntli.

InterPro; IRR003008; ValRS_IIERS_edit.

Pfam; PF00113; TRNA-syntla.

PRINTS; PR00198; TRNASYNTHLEU.

TIGRFAMs; TIGR00366; leus bact; 1.

PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.

Aminoacyl-tRNA_synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 TTGKL PVPWPTLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         378 STWEPDVWRDWYADKTR---EFE---LINSABFDGLDYQDAFEVLAERFE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 -----KTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of
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01-0CT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Photosystem II 44 kDa reaction center protein (P6 protein) (CP43)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Turmel M., Mercier J.P., Cote M.J.J.;

"Group I introns interrupt the chloroplast psaB and psbC and the mitochondrial rrnL gene in Chlawdomonas.";

Nucleic Acids Res. 21:524-2550(1993).

--- FUNCTION: The 43 kba protein (p6) is a component of the core photosystem II. It is a chlorophyll binding protein.

--- SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales;
Chlamydomonadaceae, Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 879;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                637 641 "XMSKS" REGION.
640 640 ATP (BY SIMILARITY).
879 AA; 99796 MW; 9FDCCB9920922919E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      461 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.2%; Preα. ν...
-:ve 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "HIGH" REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.0%; Score 89.5;
22.2%; Pred. No. 10
                                                                                                                                                                                                                     EMBL; AE004031; AAF84975.1; ALT_INIT.
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MEDLINE=94077731; Pubmed=7504814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 -HYLSTQSALSKDPNEKR 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  280 FUNTAYPSEFYGPTGPEASQAQAFTFLVRDQRLGANVASAQGPTGLGKYLMRSPTGEIIF 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GNYKTRA---EVKF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          340 GGET-----MRFWDFR------GPWCEPLRGPNGLDLN-KLKNDIQPW 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 SVQLADHYQQNTPIGD----GPVLLPDN--HYLSTQSALSKDPNEKRDHMVLGGF---- 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   376 QERRAAEYMTHAPLGSLNSVGGVATEINAVNFVSPRSWLA-----TSHFVLGFFFFVGH 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 DATYGKLTLKFICTTGKL----PVPWP--------TLVTTLSYGVQCFSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00421; PSII; 1.
TIGRFAMs; TIGR01153; psbC; 1.
Photosynthesis; Photosystem II; Thylakoid; Chlorophyll; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
LEUS OR STY0699 OR T2219.
Salmonella typhi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar_Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 6.9%; Score 88; DB 1; Length 461; Similarity 19.5%; Pred. No. 6.4; 51; Conservative 37; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                461 AA; 50559 MW; 03DEA75510B4C38B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 YPDHMKQHDFFKSAMPE-GYVQERTIFFKDD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      860 AA
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                                                                                                                                                                                                                 EMBL; M90639; AAA84148.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            430 LWHAGRARAAAGFEKGIDRV 450
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STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
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                                                                                                                                                                                                                                                 PIR; S41480; S41480.
InterPro; IPR005869; Photo44.
InterPro; IPR000932; PSIIprot.
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Q8ZBHS;
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
and CT18.";
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McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
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InterPro; IPR002302; Leu-tRNAsyntla.

InterPro; IPR001302; Leu-tRNAsyntla.

InterPro; IPR001312; TRNA-synt_la.

InterPro; IPR001312; TRNA-synt_la.

PRINTS; PR00133; TRNA-synt 1; 1.

PRINTS; PR00139; TRNA-synt 1; 1.

PRINTS; PR00139; TRNA-synt 1; 1.

PR0SITE; PS00178; AA TRNA LIGASE 1; 1.

PR0SITE; PS00178; AA TRNA LIGASE 1; 1.

Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                J. Bacteriol. 185:2330-2337(2003).
-!- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP +
diphosphate + L-leucyl-tRNA(Leu).
-! SUBCELJULAR LOCATION: Cytoplasmic.
-!- SUBCELJULAR Belongs to class-I aminoacyl-tRNA synthetase family.
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
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522 ATP (BY SIMILARITY).
96940 MW; 2F95E480BBABE33C4 CRC64;
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21; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AL627267; CAD05125.1; -.
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Matches 42; Conservative
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Q8ZQZ6;
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                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                        Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                     CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP + diphosphate + L-leucyl-tRNA(Leu). SUBCELLULAR LOCATION: Cytoplasmic. SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
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01-AUJ-1991 (Rel. 19, Last sequence update)
10-OCT-2003 (Rel. 19, Last annotation update)
10-OCT-20103 (Rel. 12, Last annotation update)
DNA polymerase epsilon, catalytic subunit A (EC 2.7.7.7) (DNA polymerase II subunit A).
POLJ-3N DNN2 ON YNL262W OR NO825.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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MEDLINE=90381771; PubMed=2169349;
Mortison A., Araki H., Clark A.B., Hamatake R.K., Sugino A.;
Mathird essential DNA polymerase in S. cerevisiae.";
Cell 62:1143-1151(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.9%; Score 87.5; DB 1; Length 860; 23.3%; Pred. No. 15;
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ATP (BY SIMILARITY)
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21; Mismatches
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                                                                                      Nature 413:852-856(2001)
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P21951;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate + {DRA} (N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 LPVPWP-TLVTTLSYGVQCFSRYPDHM------KQHDFFKSAMPEGYV----QERTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      883 LPKSFPETYFFTLENGKKLYLSYPCSMLNYRVHQKFTNHQYQELKDPLNYIYETHSENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOUBLINE CONSISTS OF FIVE SUBUNITS (200 kDa, 80 kDa, 34 kDa, 30 kDa, 8ND 29 kDa).

SUBCELLULAR LOCATION: Nuclear.

SUBCELLULAR LOCATION: Nuclear.

N-TERMINAL HALF OF THE PROTEIN, WHILE THE C-TERMINUS IS NECESSARY FOR COMPLEXING SUBUNITS B AND C.

MISCELLANEOUS: In eukaryotes there are five DNA POlymerases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Mismatches 49; Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "DNA polymerase II, the probable homolog of mammalian DNA polymerase epsilon, replicates chromosomal DNA in the yeast Saccharomyces cerevisiae.";
                                        MEDLINE=96310631; PubMed=8740425; Sen-Gupta M., Lyck R., Fleig U., Niedenthal R.K., Hegemann J.H.; Sen-Gupta M., Lyck R., Fleig U., Niedenthal R.K., Hegemann J.H.; The sequence of a 24,152 bp segment from the left arm of chromosome with from Saccharomyces cerevisiae between the BNI1 and the POL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alpha, beta, gamma, delta, and epsilon which are responsible for different reactions of DNA synthesis.
-!- SIMILARITY: Belongs to the DNA polymerase type-B family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R Germonilne; Lawley.

R SGD; SO05206; POL2.

R GO; GO:0005206; POL2.

R GO; GO:0000731; P:DNA repair synthesis; IMP.

R InterPro; IPR006134; DNA_pol_B.

R InterPro; IPR006134; DNA_pol_B.

R InterPro; IPR006134; DNA_pol_B.

R InterPro; IPR006135; DNA_pol_B.

R Pfam; PF001104; DNA_pol_B; 1.

DR Pfam; PF001104; DNA_pol_B = xco; 1.

SMART; SM00486; POLBc; 1.

DR PROSITE; PS00116; DNA_POLYMERASE B; FALSE_NEG.

RW Transferase; DNA-directed DNA_polymerase; DNA replication;

Transferase; DNA-directed DNA_polymerase;

RW Transferase; DNA-directed DNA_polymerase;

RW Transferase; DNA_directed DNA_polymerase;

RW Transferase;

RW Transfe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBO J. 11:733-740(1992).
-!- FUNCTION: DNA POLYMERASE II PARTICIPATES IN CHROMOSOMAL DNA
REPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Araki H., Ropp P.A., Johnson A.L., Johnston L.H., Morrison A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 2222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                644 644 M -> I (IN POL2-9 TS MUTANT).
710 710 p -> S (IN POL2-18 TS MUTANT).
2222 AA; 255669 MW; CBCDDEZAB147D65B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.9%; Score 87.5; 28.2%; Pred. No. 46
                                                                                                                                                                                                                                                                                                                                                                                                                                        TEMPERATURE SENSITIVE MUTANTS.
MEDLINE=92164663; PubMed=1537345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M60416; AAA88711.1; -. EMBL; X92494; CAA63235.1; -. EMBL; Z71538; CAA6159.1; -. PIR; A36028; A36028. Germonline; 143268; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                               (east 12:505-514 (1996)
STRAIN=S288c / FY1679
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)

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TISSUB-Brain, and Testis;

WEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=1247, Med=1247; Med=1247;

MEDLINE-22388257; PubMed=12477;

MEDLINE-22482; Med=12477;

Med=12482; Med=12477;

Med=12482; Med=12477;

Med=12482; Med=12477;

Med=12482; Med=12477;

Med=12482; Med=12477;

Med=12482; Med=12477;

Med=12482; Med=12477;

Med=12482; Med=12477;

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Med=12482; Med=12477;

Med=12482; Med=12477;

Med=12482; Med=12477;

M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21638749; PubMed=11780052;
MEDLINE=21638749; PubMed=11780052;
MeDLINE=21638749; PubMed=11780052;
Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
Deloukas P., Matthews L.H., Ashurst J., Babbage A.K., Bagguley C.L.,
Bailey J., Barlock K.P., Bates K.N., Beard L.M., Beare D.M.,
Bailey O.P., Blad C.P., Bladey S.E., Bridgeman A.M., Brown A.J.,
Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
Blington A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
Blington A., Coville G.J., Heath P.D., Ho S., Holden J.L., Howden P.J.,
Hurkle B., Hunt A.R., Hunt S.E., Jekosch K., Johnson D.,
A Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
Harkle B., Hunt A.R., Hunt S.E., Jekosch K., Johnson D.,
Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lavlor S.,
Lehvaeslaino M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
Mille S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
B. Skuce C.D., Smith M.L., Scott C.E., Sehra H.K., Showhkeen R., Sims S.,
Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.W.,
Milchead S.L., Whittaker P., Willey D.L., Williams L.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                AC2L HUMAN STANDARD; PRT; 689 AA.
Q9NUB1; Q8LV99; Q8N214; Q96J11; Q96JX6; Q9NU28;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
Acctyl-coentayme A synthetase 2-like, mitochondrial precursor (BC 6.2.1.1) (Acctate--CoA ligase 2) (Acctyl-CoA synthetase 2-ACAS2L OR KIAA1846.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                               1000 SDIFKVFLEGD 1010
                      148 S--HNVYIMAD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 414:865-871(2001)
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                            AC2L_HUMAN
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SEQUENCE OF 169-689 FROM N.A. (ISOFORM 1).

TISSUB-Placenta, and Tongue;

Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,

Ninomiya K., Wagatsuma M., Kikawa E., Omura Y., Abe K., Kamihara K.,

A Katsuta N., Sarc K., Tanikawa M., Yamazaki M., Irie R., Sato H.,

Yamamoto J., Isono Y., Kawai-Hio, Y., Saito K., Nishikawa T.,

Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,

Kikuchi H., Murakawa K., Takahashi. Fujii A., Oshima A., Sugiyama A.,

Kikuchi H., Murakawa K., Takahashi. Fujii A., Oshima A., Sugiyama A.,

Kawakami B., Ota T., Hayashi K., Sugiyama T., Otsuki T., Ishibashi T.,

Rawai Y., Wakamatsu A., Kanehori K., Suzuki Y., Sugano S.,

Kawai Y., Wakamatsu A., Kanehori K., Isogai T.;

"NEDO human CDNA sequencing project."

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- CAUTION: Ref.1 (CAB81884) sequence differs from that shown due to erroneous gene model prediction.
-!- CAUTION: Ref.3 sequence differs from that shown due to a frameshift in position 250 and numerous sequencing errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21245130; PubMed=11347906;
Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XX. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 8:95-95(201).
- FUNCTION: Converts acetate to acetyl-CoA so that it can be used for exidation through the tricarboxylic cycle to produce ATP and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          t peptide; Alternative splicing.
MITOCHONDRION (POTENTIAL).
ACETYL-COENZYME A SYNTHETASE 2-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CO(2) (By similarity).
-!- CATALYTIC ACTIVITY: ATP + acetate + CoA = AMP + diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acetyl-CoA.
-!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note=No experimental confirmation available;
-!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V -> M (IN REF. 2; AAH39261)
V -> M (IN REF. 2; AAH44588)
G6E84E39302AD08B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Missing (in isoform 2).
/FTId=VSP_007249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 336-689 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q9NUB1-2; Sequence=VSP_007249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=09NUB1-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, BC039261, AAH39261.1, EMBL, BC04588, AAH44588.1, EMBL, AX027817, BAB5390.1, ALT_INIT. EMBL, AX092295, BAC03853.1, ALT_SEQ. EMBL, AB058749, BAB47475.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL035661; CAB75500.1; -. EMBL; AL080312; CAB81884.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:16091; ACGASZL.
InterPro; IPR000873; AMP-bind.
Pfam; PF00501; AMP-binding; 1.
BROSITE; PS00455; AMP_BINDING; 1.
Ligase; Mitochondrion; Transit per
TRANSIT 136 MITOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74856 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 2
488 4
689 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              £ami]
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InterPro; IPR001128; Cytochrome P450.
                                                                                      METAL
CONFLICT
                                                                                                                                   SEQUENCE
                                                                                                                    CONFLICT
                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S F F F W KW D R S S S F F F F S S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                   69 VQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRA----EVKFEGDTLVNRIE 125
                                                                           68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96161286; PubMed=8593007; Geber A., Hitchcock C.A., Swartz J.E., Pullen F.S., Marsden K.E., Geber A., Hitchcock C.A., Swartz J.E., Pullen F.S., Marsden K.E., Kwon-Chung K.J., Bennett J.E., "Deletion of the Candida glabrata ERG3 and ERG11 genes: effect on cell "Deletion of the Candida glabrata ERG3 and antifungal susceptibility.";
                                                                        FTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLSYG
                                                                                                       473 FFGIVPVLMDEKGSV------VEGSNVSGALCIS------QAWPGMARTI---
                                                                                                                                                      CATALYTIC ACTIVITY: Obtusifoliol + 3 O(2) + 3 NADPH = 4-alpha-methyl-5-alpha-ergosta-8,14,24(28)-trien-3-beta-ol + formate + NADP(+) + 3 H(2)O.
PATHWAY: Ergosterol biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=ATCC 2001;
MEDLINE=95081364; PubMed=7989540;
Burgener-Kairuz P., Zuber J.P., Jaunin P., Buchman T.G., Bille J.,
                                                                                                                                                                                                                                                                                                   CP51_CANGA STANDARD; PRT; 533 AA.
P50855; Q02312;
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2003 (Rel. 42, Last annotation update)
Cytochrome P450 51 (EC 1.14.13.70) (CYPLI) (P450-LIAI) (Sterol 14-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lanosterol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Torulopsis (Candida) glabrata in clinical specimens by specises specific nested PCR amplification of a cytochrome P-450 lanosterol-alpha-demethylase (LLA1) gene fragment.";
J. Clin. Microbiol. 32:1902-1907(1994).
-: FUNCTION: Catalyzes C14-demethylation of lanosterol which is critical for ergosterol biosynthesis. It transforms lanostero into 4,4-dimethyl choleste-8,14,24-triene-3-beta-ol (By
                                                                                                                                                                                                                                                                                                                                                                                      alpha-demethylase) (Lanosterol 14-alpha demethylase) (P450-14DM)
                                                                                                                                                                                                                                                                                                                                                                                                                     Candida glabrata (Yeast) (Torulopsis glabrata).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                              52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Rapid detection and identification of Candida albicans and
                 DB 1; Length 689;
                                            36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrob. Agents Chemother. 39:2708-2717(1995).
                                            16; Mismatches
               6.8%; Score 87;
24.1%; Pred. No. 1
                                                                                                                                                                                              126 LKGIDFKEDGNILGHKL 142
                                                                                                                                                                                                                           ----- NISGHRL 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L40389; AAB02329.1; -. EMBL; S75389; AAB32679.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 60-473 FROM N.A.
                                              33; Conservative
                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=5478;
                                                                                                                                                                                                                                                                                                                                                                                                          ERG11 OR CYP51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rossier M.;
                                                                                                                                                                  511
                                                                                                                                                                                                                           554
                 Query Match
                                            Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 GHEFIFNAKLADVSAEAAYSHL-------TTPVFGKGVIYDCPNHRLM 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-22421331; PubMed=12533478; Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B., van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B., Moon D.H., Miyaki C.Y., Furlan L.R., Canatgo L.E.A., da Sliva A.C.R., Moon D.H., Takita M.A. Lemos B.G.M., Machado M.A., Ferro M.T.T., da Sliva F.R., Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M., Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J., Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E., Marino C.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M., Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V., Baia G.S., Penille R.C., Ferro J.A., Formighieri E.F., Kishi L.T., de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G., Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 GHKFSVS---GEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLSYGVQCFSRYPDH--M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 KQHDFFKSAM-PEGYV-----QERTIFFKDDGNYKTRAEVKFEGDTLVNRIBLKGIDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 BOKKFVKGALTKEAFVRYVPLIAEEIYKYFRNSKNFKINENNSGIVDVMVSQPEM--TIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 KEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 TASRSLIGKEMRDKLDTDFAYLYSDLDKGFTPINF-VFPNLPLEHYRKRDHAQQAIS---
                                                                                                                                                            472 IRON (HEME AXIAL LIGAND) (BY SIMILARITY)
64 I -> M (IN REF. 2).
473 I -> T (IN REF. 2).
61305 MW, A0506C17507E6EF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Bacteriol. 185:1018-1026(2003).
-!- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP + diphosphate + L-leucyl-tRNA(Leu).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR SYNthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS).
LEUS OR PD1230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pierce's
                                                        PROSITE; PS00086; CYTOCHROME P450; 1.
Electron transport; Oxidoreductase; Monooxygenase; Membrane; Heme;
Sterol biosynthesis; NADP.
                                                                                                                                                                                                                                                                                                                                                                                                                  49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xylella fastidiosa (strain Temeculal / ATCC 700964).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                          6.8%; Score 86.5; DB 1; Length 533; 21.4%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Comparative analyses of the complete genome sequences of disease and citrus variegated chlorosis strains of Xylella
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                          81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       879 AA
                                                                                                                                                                                                                                                                                                                                                                                                                  32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------GTYMSLIKERREKND 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 GPVLLPDNHYLSTQSALSKDPNEKRD 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xanthomonadaceae; Xylella.
                                                                                                                                                                                                                                                                                                                                                                                                                  44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                   64
473
Pfam; PF00067; p450; 1
PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                                          533 AA;
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=183190;
                                                                                                                                                                                                              64
                                                                                                                                                                                                                                          473
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Q87<u>C</u>65;
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[1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Q9PP92;
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TRMA_CAMJE
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Matches
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  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 TIGKLPVPWPTLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNY-- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------KTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 MADKQKNG-IKVNFKIRHNIEDGSVQLADHYQQNTPI-------GDGPVLLPDN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      378 STWEPDVWRDWYADKTR---EFE---LINSAEFDGLDYQGAFEVLAERFE------
                                                                                                                                                                                                                        Pfam; PF00133; tRNA-synt 1; 1.
PRINTS; PR0098; TRNASYNTHLEU.
TIGRPAMs; TIGR00396; leuS bact; 1.
PROSITE; PS00178; AA TRNA_LIGASE 1; 1.
Aminoacy1-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-71 FROM N.A.

MEDLINE=85269643; PubMed=4022780;
Spieth J., Denison K., Kirtland S., Cane J., Blumenthal T.;
"The C. elegans vitellogenin genes: short sequence repeats in the promoter regions and homology to the vertebrate genes.";
Nucleic Acids Res. 13:5283-5295(1985).
-I- FUNCTION: Precursor of the egg-yolk proteins that are sources of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-282 FROM N.A.
Blumenthal T., Spieth J., Zucker E.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                      "KMSKS" REGION.
ATP (BY SIMILARITY).
4C2EE01B8FDC497E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1603 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.8%; Score 86.5; D
22.2%; Pred. No. 18;
tive 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                       "HIGH" REGION
                                                                                                         EMBL; AEVLIGO.; -: 1.
INCEPPO; IPRO02302; Leu-ERNASyNTIA.
INCEPPO; IPRO02302; Leu-ERNASYNTIA.
INCEPPO; IPRO01412; ERNA-SYNTI.
INCEPPO; IPRO01412; ERNA-SYNTI.
INCEPPO; IPRO09008; ValRS, ILERS_edit.
                                                                                            EMBL; AE012557; AA029080.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 -HYLSTQSALSKDPNEKR 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                475 VAFSGTGSPIKTDPEWRK 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIT4_CAEEL STANDARD; 1
P18947; Q9BPP3;
01-NOV-1990 (Rel. 16, Created)
10-OCT-2003 (Rel. 42, Last seqn
10-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                 879 AA; 99823 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vitellogenin 4 precursor.
                                                                                                                                                                                                                                                                                                                                                       55
641
640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEOUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108
                                                                                                                                                                                                                                                                                                                                                                      SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 LAVNGQEVVKSETRAKVTFVEESKINR-EIK-----KVSGPKEEIVYSMENEKLIEQ 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 -----NYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMAD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEG-YVQERTIF---FKDDG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                     -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUB SPECIFICITY: Synthesized in Caenorhabditis only by 32 cell building the incestine of adult hermaphroditic individuals; they are cotranslationally secreted into the body cavity and subsequently taken up by the gonad.
-!- SIMILARITY: Contains 1 VWFD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Campylobacter jejuni.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
methyltransferase) (RUMT).
TRMA OR CU0831C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 1603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 Y -> V (IN REF. 3).
169 L -> V (IN REF. 2).
187 EVAYT -> RSELH (IN REF. 2).
275 T -> S (IN REF. 2).
AA; 186307 MW; E303170325BC99BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 KQKNG-----IKVNFKIRHNIEDGSVQLADHYQQNTP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309 FYKOGDKAEVNPFKAİEIEQKV-EQLEEIFROIOEH-EQNTP 348
nutrients during embryonic development (Potential).
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POTENTIAL.
VITELLOGENIN 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A43084; A43084.
Wormbep; F59D8.2; CE26817.
InterPro; IPR001747; Lipid transprt_N.
InterPro; IPR001846; WWF D.
Pfam; PF01347; Vitellogenin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WWFD.
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                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AC024137; AAK09074.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M11498; AAA28163.1; -. EMBL; X02754; CAA26531.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.48;
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SMART; SM00216; VWD; 1.
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es 52; Conserv
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MEDLINE=20445173; PubMed=10993077;
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000116;
01-NOV-1997
01-NOV-1997
15-MAR-2004
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ADAS_HUMAN
셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 KQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKF--EGDTLV------NRIELKG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDFKED------GNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIE 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 LDFADEKICAFMPRLLEYLRQDNKLKEKL-----FGVEFLTTKQE--LSITLLYHKNIE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 EKHSFIKKYFKEFYTKDFKLFASKDKHYRTRAELSFYHENDTLFYAMFDPKSKKKYIIEY 73
                                                                                                                                                                                                                                                                                                                          -1- FUNCTION: Catalyzes the formation of 5-methyl-uridine at position 54 (M-5-U54) in all tRNA (By similarity).
-1- CAPTALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-homocysteine + tRNA containing thymine.
-1- SIMILARITY: Belongs to the RNA MSU methyltransferase family. TrmA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
             MEDLIKE 20150912; PubMed=10688204; Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C., Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Quail W.K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Quail W.K., Rajandream M.Y., Rutherford K.M., van Vliet A.H.M., Whitehead S., Barrell B.G., Treveals hypervariable sequences." Ireveals hypervariable sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
18-stidine biosynthesis bifunctional protein hisB [Includes: Histidinol-phosphatase (EC 3.1.3.15); Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19) (IGPD)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    symbiotic bacterium).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.7%; Score 86; DB 1; Length 357;
24.8%; Pred. No. 6.9;
tive 18; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
BY SIMILARITY.
, CEC5328347CEE497 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AL139076; CAB73096.1; -. PIR; G81355; G81355. HAMAP; MF_01011; -; 1. InterPro; IPR001051; SAM bind. InterPro; IPR001566; TrmA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    315 315 B
357 AA; 42276 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterobacteriaceae; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 24.8
Matches 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subfamily.
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P57203;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 GIKVNFKIRHNIE-----DGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEK 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 TLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIF---FKDDGNYKTRAEVKF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TESFPLODFS--TAHLFMLSVFRS---EGVIFDDILICPHFLDDDCVCRKPKIKMIEPWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 ETKVSIKVWLDLEETSKIDTGVKFFDHMLEQLSVHSGICM-----NISVQGDLDID----
And the sequence of the endocellular bacterial symbiont of aphids shipmens sp. APS.";

"Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS.";

Nature 407:81-86(2000).

-!- CATALYTIC ACTIVITY: D-erythro-1-(imidazol-4-yl)glycerol 3-phosphate = 3-(imidazol-4-yl)-2-oxopropyl phosphate + H(2)O.

-!- CATALYTIC ACTIVITY: L-histidinol-phosphate + H(2)O = L-histidinol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 164 HISTIDINOL-PHOSPHATASE.
165 353 IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE.
353 AA; 40835 MW; 903BE7E53AD8DAAO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61; Gaps
                                                                                                                                                                                                                                                                             -!- PATHWAY: Histidine biosynthesis; sixth step.
-!- PATHWAY: Histidine biosynthesis; eighth step.
-!- SUBCELLUTAR LOCATION: CYCOpleamic (By similarity).
-!- SIMILARITY: In the N-terminal section; belongs to the histidinol-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00954; IGP DEHYDRATASE 1; 1.
PROSITE; PS00955; IGP DEHYDRATASE 2; 1.
Histidine biosynthesis; Multifunctional enzyme; Lyase; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                      phosphatase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 -DHHTIEDTGIVLGEALLQALGKKNGLSRFGFYLPMDE 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 imidazoleglycerol-phosphate dehydratase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.7%; Score 85.5; DE 24.3%; Pred. No. 7.5; tive 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD002282; IGPD; 1.
TIGRPAMS; TIGRO162; HAD-SF-IIIA; 1.
TIGRPAMS; TIGRO1261; hisb Nerm; 1.
TIGRPAMS; TIGRO1656; HistIdinol-ppas; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP; MF_01022; -; 1.
InterPro; IPR006549; HAD-SF-IIIA.
InterPro; IPR0065954; HisB N.
InterPro; IPR006543; HistIdinol-phos.
InterPro; IPR000807; IGPD.
Pfam; PF00475; IGPD.
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Best Local Similarity 24.33
Matches 53; Conservative
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1. Biol. Chem. 273:10296-10301 (1998).
2. -- CATALYTIC ACTIVITY: 1-acyl-glycerone 3-phosphate + a long-chain acid anion.
3. Cohector: FAD.
2. -- STBUNIT: May be part of an heterotrimeric complex composed of DAP-C.
3. SIBULIT: May be part of an heterotrimeric complex composed of DAP-C.
3. SIBULIT: May be part of an heterotrimeric complex composed of DAP-C.
3. SIBULITAR LOCATION: PEROXISOMAL. LOCALIZED TO THE INNER ASPECT
3. SIBULITAR LOCATION: PEROXISOMAL. LOCALIZED TO THE INNER ASPECT
3. SIBULITAR LOCATION: PEROXISOMAL. LOCALIZED TO THE INNER ASPECT
3. SIBULITAR LOCATION: PEROXISOMAL. LOCALIZED TO THE INNER ASPECT
3. SIBULITARIES Defects in AGPS are the cause of rhizomelic chondrodysplasia punctara. type 3 (RCDP3) [MIM:600121]. RCDP3 is an autosomal recessive disease characterized by rhizomelic shortening of the upper extremities, severe growth and mental retardation and cataract.
3. SIMILARITY: BELONGS TO THE FAD-BINDING OXIDOREDUCTASE/TRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                      MEDLINE=97330864; PubMed=9187299; de Vet E.C.J.M., van den Bosch H.; de Vet E.C.J.M., van den Broek B.T.E., van den Bosch H.; "Nucleotide sequence of human alkyl-dihydroxyacetonephosphate synthase cDNA reveals the presence of a peroxisomal targeting signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALKYLDIHYDROXYACETONEPHOSPHATE SYNTHASE
                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
   peroxisomal precursor
Alkyldihydroxyacetonephosphate synthase, peroxisomal precurso (EC 2.5.1.26) (Alkyl-DHAP synthase) (Alkylglycerone-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 658;
                                                                                                                                                                                                                                                                                                                                MEDLINE=98221159; PubMed=9553082;
de Vet E.C.J.M., Ijlst L., Oostheim W., Wanders R.J.A.,
van den Bosch H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R -> H (in RCDP3).
/FTId=VAR 005002.
0E97AE86B513DF32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MICROBODY (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.7%; Score 85.5; 1
24.2%; Pred. No. 16;
                                                                                                                                                                                                                                                                                 Biochim. Biophys. Acta 1346:25-29(1997).
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Genew; HGNC:327; AGPS.
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658
8
419
                                                                                                                                                                                                                                                                                                                 VARIANT RCDP3 HIS-419.
                                                                      sapiens (Human).
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Best Local Similarity
Matches 45; Conserv
                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                       NCBI_TaxID=9606;
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419
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                   (EC 2.5.1.;
synthase).
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                                                                      Homo
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10;

Gaps

60; Indels 59;

22; Mismatches

45; Conservative

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239 TSVSYGLMC-----PADETRIISLDTSQMNRILWVDENNLTAHVEAGITGQELER 289
                                                                                                                                                        179
                                                                                                                                                                                                                                                                                                                         180 ADHYQQNTPIG-----DGPVLL--PDNHYLSTQSALSKDPNEKRDHMVLG-----GFVT 226
63 TTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVN 122
                                                                                                                                                                                                                                    290 QL-----KESGYCTGHEPDSLEFS----TVGGWVSTRASGMKKN--IYGNIED----L 332
                                                                                                                                                                                                                                                                                                                                                                                                 333 VVHIKMVTPRGIIEKSCQGPRMSTGPDIH-------HFIMGSEGTLGVIT 375
                                                                                                                                                            123 RIELKGIDFKEDGNILGHK----LEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: June 21, 2004, 15:55:25 Job time: 7.55556 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

June 21, 2004, 15:45:30 ; Search time 30.6667 Seconds (without alignments) 2458.984 Million cell updates/sec

Run on:

US-09-887-784-222G 1276 1 MVSKGEELFTGVVPILVELD......VLGGFVTAAGITLGMDELYK 239 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

1017041 seqs, 315518202 residues Searched:

1017041

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL 25:* Database

sp_archea:*
sp_bacteria:*
sp_fungl:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mcanelle:*
sp_organelle:* 

sp plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*

sp_archeap:*

Pred..No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		•			SUMMERTES		
1		Query	* Duery			,	
Score		Match	Length	DB	ΩI	Description	ption
1235		96.8	238	N	Q8GHE2	Q8ghe2	azotobacter
1232		96.6	238	ഹ	093125	093125	aequorea vi
1230		96.4	238	~	Q8GHE4	Q8ghe4	
1229		96.3	238	7	QBGHE3	08ghe3	azotobacter
1197	_	93.8	238	'n	Q17105	017105	aequorea vi
1182		92.6	238	ഹ	017106	017106	aequorea vi
1077		84.4	238	Ŋ	QBWTC6	Q8wtc6	aequorea ma
1073		84.1	238	'n	Q8WP95	Q8wp95	aequorea ma
1069		83.8	238	Ŋ	Q8WTC4	Q8wtc4	aequorea ma
1067		83.6	238	വ	QBWTD0	Q8wtd0	
1066		83.5	238	ഹ	QBWTC8	Q8wtc8	aequorea ma
1066		83.5	238	Ŋ	Q8WTC9	Q8wtc9	
1064		83.4	238	ហ	Q8WTC7	Q8wtc7	
1062	٠.	83.2		īΟ	Q8WTC5	Q8wtc5	
252.5		19.8		ιU	Q95UA7	Q95ua.7	montastraea
252.5		19.8		Ŋ	Q7Z0WS	Q7z0w5	montastraea

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61 9 62 VITLSYGVQCFSRXPDHMKQHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTLV 121

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Q963f5 montastraea Q8t6u0 dendronepht Q7z0w9 montastraea Q8i6i8 trachyphyll Q9u6y3 clavolaria	Q7z0w4 montastraea Q8mu48 montastraea Q8t5f1 montastraea Q7z0w6 montastraea Q7z0w7 montastraea	agaricia agaricia montastra montastra		Q95p04 goniopora t Q86lv8 meandrina m Q9b1y9 renilla mue Q95vt0 montastraea Q95vt6 montastraea Q916y8 discosoma s Q716s certanthus Q8t6y radianthus Q8t5f0 scolymia cu Q9u6y7 discosoma s
	5 Q720W4 5 Q8MU48 5 Q8TSF1 5 Q720W6 5 Q720W			5 Q95P04 5 Q86LV8 5 Q98LV9 5 Q96V0 5 Q916X8 5 Q3168 5 Q815F0 5 Q815F0
225 236 225 225 266	225 224 225 227 234		222 222 222 232 232 44	221 233 233 233 233 333
19.2 19.2 18.8 18.7	18.2 18.2 16.8	16.5	16.22	
247 244.5 242.5 240 238.5	233 232 214 214	212.5 210 210 209 209	206.5 206.5 206.5 205.5 205.5	203.5 203.5 203.5 202.2 201.5 198.5 198.5
11 18 19 20 21	22 23 24 25 26	78888		W W W & & & & & & & & & & & & & & & & &

## ALIGNMENTS

T 1  28GHE2 PRELIMINARY; PRT; 238 AA.  98GHE2;  01-MAR-2003 (TrEMBLrel. 23, Created)  01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  01-MAR-2003 (TrEMBLrel. 25, Last annotation update)  Green fluorescence protein.  9.289GFP.  Azotobacter.  Azotobacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  Recteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  ROBILTAXID=354;  [1]  ROBILTAXID=354;  [1]  ROBILTAXID=354;  [1]  ROCCUTENCE FROM N.A.  SEQUENCE FROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUENCE; PROM N.A.  SEQUE	138; 0; Gaps
T.1 26GHEZ PRELIMINARY; PRT; 238 AA. 26GHEZ; 01-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 25, Last annotation update) 01-CCT-2003 (TrEMBLrel. 25, Last annotation update) 03-OCT-2003 (TrEMBLrel. 25, Last annotation update) 04-OCT-2003 (TrEMBLrel. 25, Last annotation update) 05-OCT-2003 (TrEMBLrel. 25, Last annotation update) 05-OCT-2003 (TrEMBLrel. 25, Last annotation update) 06-OCT-2003 (TrEMBLrel. 25, Last annotation update) 07-OCT-2003 (TrEMBLRel. 25, Last annotation update) 08-OCT-2003 (TremBLRel. 26, Last annotation update) 08-OCT-2003 (TremBLRel. 26, Last annotation update) 08-OCT-2003 (TremBLRel. 26, Last annotation update) 08-OCT-2003 (TremBLRel. 26, Last annotation update) 08-OCT-2003 (TremBLRel. 26, Last annotation update) 08-OCT-2003 (TremBLRel. 26, Last annotation update) 08-OCT-2003 (TremBLRel. 26, Last annotation update) 08-OCT-2003 (TremBLRel. 26, Last annotation update) 08-OCT-2003 (TremBLRel. 26, Last annotation update) 08-OCT-2003 (TremBLRel. 26, Last annotation update) 08-OCT-2003 (TremBLRel. 26, Last annotation update) 08-OCT-2003 (TremBLRel. 23, Last annotation update) 08-OCT-2003 (TremBLRel. 23, Last annotation update) 08-OCT-2003 (TremBLRel. 23, Last annotation update) 08-OCT-2003 (TremBLRel. 23, Last annotation update) 08-OCT-2003 (TremBLRel. 23, Last annotation update) 08-OCT-2003 (TremBLRel. 23, Last annotation update) 08-OCT-2003 (TremBLRel. 23, Last annotation update) 08-OCT-2003 (TremBLRel. 23, Last annotation update) 08-OCT-2003 (TremBLRel. 23, Last annotation update) 08-OCT-2003 (TremBLRel. 23, Last annotation update) 08-OCT-2003 (TremBLRel. 23, Last annotation update) 08-OCT-2003 (TremBLRel. 23, Last annotation update) 08-OCT-2003 (TremBLRel. 23, Last annotation update) 08-OCT-2003 (TremBLRel. 23, Last annotatio	Length 238; Indels
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OGGHEZ  PRELIMINARY;  PRT;  20  OGGHEZ;  O1-MAR-2003 (TERMELTE1. 23, Last sequention-2003 (TERMELTE1. 23, Last sequention-21-2003 (TERMELTE1. 25, Last annotagree fluorescence protein.  O1-CCT-2003 (TERMELTE1. 25, Last annotagreent fluorescence protein.  Azotobacter vinelandii.  Bacteria; Proteobacteria; Gammaproteoba Pseudomonadacee; Azotobacter.  NCBI_TAXID=354;  [1]  SEQUENCE FROM N.A.  STRAIN=DSN289;  Noranyi P., Berenyi M., Burg K.;  NCCCUTTENCE Of green fluorescence prote Azotobacter.  "Occurrence of green fluorescence prote GO; Go:0006091; P:energy pathways; IEA.  EMBL; AF324408; AAN86140.1;  EMBL; AF324408; AAN86140.1;  EMBL; AF324408; Green_fl_protein.  PRINTS; PRO1329; GFLUORESCENT.  PRODOM; PRO13756; Green_fl_protein; 1.  SEQUENCE 238 AA; 26914 NW; F84840FF	N
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T.1 208GHE2; 00-MAR-2003 (TEMBLEE) 01-MAR-2003 (TEMBLEE) 01-MAR-2003 (TEMBLEE) 01-OCT-2003 (TEMBLEE) Green fluorescence pro 2289GFP. Azotobacter vinelandii Bacteria; Proceobacter Pseudomonadaceae; Azot NCBL TaxID=354; [1] SEQUENCE FROM N.A. STRAIN=DSM228; STRAIN=DSM2289; "Occurrence of green f Azomonas and Azotobact Submitted (NOV-2000) V. EMBL; AF324408; AAN861 GO:0006091; Prener InterPro; IPR009017; G InterPro; IPR009017; G InterPro; IPR009017; G Ffan, PF01329; GFLUOP PRODOM; PF013756; GFLEOP	Query Match Best Local Similarity Matches 232; Conserv
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61 VTTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
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Microbiology 0:0-0(1996).
Bissp: U73901; AAB18957.1; -.
HSSP; P42212; 1BFP.
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MEDIINE=96305137; PubMed=8707053;
Oranack B.P., Valdivia R.H., Falkow S.;
"FACS-optimized mutants of the green fluorescent protein (GFP).";
Gene 173:33-38(1996).
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=6100;
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InterFro; IPR009017; GFP_like.
InterFro; IPR007086; Green_fl_protein.
Pfam; PF01353; GFP; Green_fl_protein.
PRINTS; PR01229; GFLUORESCENT.
PRODOM; PD013756; Green fl_protein; 1.
SEQUENCE 238 AA; 26840 MW; A28622809A9DEA60 CRC64;
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Green fluorescent protein mutant 3.
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                                                                                                                                                                                                                                                                                                      Cocurrence of green fluorescence protein in diazotrophic bacteria Acomansa and Azotobacter.";

**Cocurrence of green fluorescence protein in diazotrophic bacteria Azomansa and Azotobacter.";

**Submitted (NOV-2000) to HE EMBL/GenBank/DDBJ databases.

EMBL; AF324405; AAN86137.1; --

GO; GO:0006091; P:energy pathways; IEA.

InterPro; IPR009017; GFP-like.

InterPro; IPR009017; GFP-like.

PERM: PF0153; GFP: 1.

PRINTS; PR01229; GFUORESCENT.

PERM: PD013756; Green fl protein; 1.

SEQUENCE 238 AA; 26902 MW; 15FE9B9C5B4F6B89 CRC64;
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                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azomonas.
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Pseudomonadaceae; Azotobacter.
NCBI_TaxID=354;
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InterPro; IPR00901; GFP like.
InterPro; IPR000786; Green fl_protein.
Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
ProDom; P013756; Green fl_protein, 1.
SEQUENCE 238 AA; 26887 MW; BOE1616BD2AF6188 CRC64;
01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Green fluorescence protein.
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Last sequence update)
Last annotation update)
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Aequorea victoria (Jellyfish).
Eukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Leptomedusae,
Aequoreidae, Aequorea.
NCBI_TaxID=6100;
                                                                                                                                                                                                                                                                                       Subdiving J. N., Campbell A.K.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; X83560; CAA58790.1; -..
PIR; JS0692; JQ1514.
HSSP; P42212; IBFP.
GO, GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IPR0090786; Green_fl_protein.
                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                  Green fluorescent protein (Fragment)
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
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93.8%; Score 1197; DB 5; Length 238;
Best Local Similarity 93.7%; Pred. No. 2.4e-91;
Matches 223; Conservative 6; Mismatches 9; Indels
Pred. No. 5.4e-94;
2; Mismatches 5; Indels
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Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, X83959; CAA58789.1; -.
PIR; JS0692, JQD514.
HSSP; P42212; JGFL.
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR000786; Green_fl_protein.
PF01353; GFP; I.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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ProDom; PD013756; Green fl protein; 1.
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97.18;
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Q17105;
01-NOV-1996 (TrEMBLrel. 01,
                       Matches 231; Conservative
Best Local Similarity
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Q17106
ID Q1710
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62 VITLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERIFFKDDGNYKTRAEVKFEGDTLV 121
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Li S.J., Xia N.S.;
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
                                                                                                                            Query Match 92.6%; Score 1182; DB 5; Length 238; Best Local Similarity 92.9%; Pred. No. 4.2e-90; Matches 221; Conservative 7; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Colorful mutants of green fluorescent protein from Aequorea
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF415431; AAL33916.1; -.
EMBL; AF4050001; P:energy pathways; IEA.
InterPro; IPR009017; GFP lik.
InterPro; IPR000786; Green_fl_protein.
                                                                                         238 AA; 26867 MW; BD4648262D8EABD4 CRC64;
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Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl_protein; 1.
SEQUENCE 238 AA; 26867 MW; BD464826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=GFPAm, and GFPdnaxm;
Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Qin Y.X., Pang S.Q.,
Li S.J., Xia N.S.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AY013824; AAK02062.1;
EMBL, AY013821; AAK02059.1;
GO, GC:0006691; P:energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IPR009086; Green_fl_protein.
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Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
MCBI_TaxID=147615;
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81.5%; Pred. No. 4.6e-81;
ive 20; Mismatches 24; Indels (
                                                                                            Length 238;
                                                                                       84.4%; Score 1077; DB 5; Length 2
81.9%; Pred. No. 2.2e-81;
ive 20; Mismatches 23; Indels
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ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 27049 MW; 8185D0E5E529012B CRC64;
PRINTS, PR01229; GFLUORESCENT.
ProDom, PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 27015 MW; 6B8FD75E88926903 CRC64;
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Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25,
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62 VTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
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Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.
Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                       Aequorea macrodactyla.
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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Eukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Leptomedusae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           macrodactyla.", Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF495431; AAL33918.1; -
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR000786; Green_fl_protein.
Pf01353; GFP; 1.
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ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 26956 MW; 75521EAFOCEBA73A CRC64;
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121 NRIELKGMDFKEDGNILGHKLEYNFNSHNVYIMPDKANNGLKVNFKIRHNIEGGGVOLAD 180
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Li S.J., Xia N.S.;
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Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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81.1%; Pred. No. 1.8e-80;
ive 20; Mismatches 25; Indels
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AR435428; AAL33313.1;
GO, GO.000691; P:energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IPR0090786; Green_fl_protein.
Pfam; PF01353; GFLUORESCENT.
ProDom; PD013756; Green_fl_protein; 1.
SEQUENCE 238 AA; 27031 MW; 5F80Al9C19DC584D CRC64;
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QBWTC9
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
VCBI_TaxID=147615;
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                                                                                                                                                                                                                                                                                                                                 Length 238;
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF435429; AAL33914.1; ...

R GO; GO:0006091; P:energy pathways; IEA.

R InterPro; IPR009017; GFP_like.

R InterPro; IPR007086; Green_£1_protein.

R Pfam; PF01353; GFP; 1.

R PRINTS; PR01229; GFLUORESCENT.

R PRINTS; PR01229; GFLUORESCENT.

R PRODOM; PD013756; Green_£1_protein; 1.
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                 EMBL, AF435421, AAL33912.1, -.
GO, GO: 0006091, P:energy pathways; IEA.
InterPro; IPR0009017, GFP_like.
InterPro; IPR000786, Green_fl_protein.
PRINTS; PR01239, GFUORSECENT.
PRODM; P013756, Green fl_protein; 1.
SEQUENCE 238 AA; 26997 MW; 5F80A192173CB84D CRC64;
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81.1%; Pred. No. 1.8e-80;
tive 20; Mismatches 25;
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81.1%; Pred. No. 1.5e-80;
iive 20; Mismatches 25;
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Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.O.,
Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 81.9%; Pred. No. 3.8e-80;
Matches 195; Conservative 17; Mismatches 26; Indels
                                                                           Luo W.K., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 238;
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF435432; AAL33917.1; -.
EMBL, AF435432; P:energy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR0090786; Green_fl_protein.
Pfam; PF01353; GFP; 1...
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Submitted (CGT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF435430; AAL33915.1; -...
EMBL; AF435430; AAL33915.1; -...
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR0009017; GFP_like.
InterPro; IPR000786; Green_fl_protein.
PRINTS; PR01229; GFLUORESCENT.
PRODOM; PD013756; GFLORESCENT.
PRODOM; PD013756; Green fl_protein; 1.
SEQUENCE 238 AA; 27002 MW; BD5BA2982264C018 CRC64;
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ProDcm; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 27018 MW; 75521EA5534E573A CRC64;
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Last annotation update)
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SEQUENCE FROM N.A.
STRAIN=GFPxm191uv;
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                                                               62 VITLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
                                                                                                                                                  122 NRIBLKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
182 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLGGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                 12 VVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKF.ICTTGKLPVPWPTLVTTLSYGVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cyan fluorescent protein (Fragment).
Montastraca cavernosa (great star coral).
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia; Pavilna; Favildae; Montastraea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 225;
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Ralkowski P.G., Sun Y.;

Ralkowski P.G., Sun Y.;

Montastraea cavernosa fluorescent protein.";

Lymotastraea cavernosa fluorescent protein.";

Lymotastraea cavernosa fluorescent protein.";

Robin G. (SEP-2001) to the EMBL/GenBank/DDBJ databases.

Robin ANGS460; AALI17905-1;

R GO; GO:0006091; P:energy pathways; IEA.

R GO; GO:0006091; P:energy pathways; IEA.

R InterPro; IPR007086; Green_fl_protein.

R Pfam; PF01353; GFP; 1.

RR Pfam; PF01353; GFLUORESCENT.

R ProDom; PD013756; Green_fl_protein; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.8%; Score 252.5; DB 5; ilarity 31.1%; Pred. No. 4.8e-13; Conservative 43; Mismatches 82;
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Database :							

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Enhanc	Abr40352 Human amı Aaq65781 Amino aci		-	~	Aay54349 Amino aci	4.		Aab85900 A. victor	Aab31171 Amino aci	Aag66198 A. victor		Aae14599 Aequorea	Aae34958 Aequorea	Aag79829 Green flu	Abr83616 Green flu	Ada38074 Aequorea	Abu63204 Aequorea	Adc18358 EGFP (enh	Abw00914 Aequorea	Ade28570 Enhanced	Abm79011 Enhanced	Aag68319 Jellyfish	Aau99804 Biomembra
SUMMARIES	AAE17518	ABK40352 AAG65781	AAG65782	AAE17517	AAB22882	AAY54349	AAY79584	AAB50804	AAB85900	AAB31171	AAG66198	ABG94444	AAE14599	AAE34958	AAG79829	ABR83616	ADA38074	ABU63204	ADC18358	ABW00914	ADE28570	ABM79011	AAG68319	AAU99804
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Score	1272	1272	1272	1264	1261	1261	1261	1261	1261	1261	1261	1261	1261	1261	1261	1261	1261	1261	1261	1261	1261	1261	1261	1261
Result No.	, n	7 M	4	ហ	ø	7	89	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Novel fluorescent protein in in vitro assay for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution, has a green fluorescent protein with F64L and E222G

WPI; 2002-098224/13. N-PSDB; AAD28163.

Claim 9; Page 37; 41pp; English.

mutation.

Aaw97451 Wild-type	Aau99803 Biomembra	Aau99802 Biomembra	Aau99800 Biomembra	Aau99801 Biomembra	Aau99807 Biomembra	Aay50142 Green flu	Aab24252 EGFP-MODC	Aaul0888 EGFP-MODC	Ade28562 EGFP/ hum	Ade28564 EGFP/ hum	Ade28568 EGFP/ hum	Ade28566 EGFP/ hum	Aab22860 GFP-DEVD-	Aay79638 Caspase-3	Abg94422 Recombina	Aay42181 EGFP/DRM	Abr83620 HUB1-GFP	Aay54359 GFP mutan	Abr83621 RUB1-GFP
AAW97451	AAU99803	AAU99802	AAU99800	AAU99801	AAU99807	AAY50142	AAB24252	AAU10888	ADE28562	ADE28564	ADE28568	ADE28566	AAB22860	AAY79638	ABG94422	AAY42181	ABR83620	AAY54359	ABR83621
~	ß	S	2	ß	Ŋ	m	٣	ß	7	7	7	7	ო	m	ß	~	9	m	9
265	268	270	272	273	280	281	281	281	286	289	290	290	294	294	294	308	320	323	323
0.66	99.0	99.0	0.66	0.66	0.66	0.66	0.66	0.66	0.66	99.0	0.66	0.66	0.66	0.66	0.66	0.66	0.66	0.66	0.66
1261	1261	1261	1261	1261	1261	1261	1261	1261	1261	1261	1261	1261	1261	1261	1261	1261	1261	1261	1261
56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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/note= "Wild type Glu substituted with Gly; This corresponds to position 222 in the wild type protein"
                                                                                                                                                                    /note= "Wild type Phe substituted with Leu; This
corresponds to position 64 in the wild type protein"
Misc-difference 223
                                                                                                Jellyfish; green fluorescent protein, GFP; protein redistribution, cellular function; genetic reporter; mutant; Stoke's shift; mutein.
                                                                             Enhanced F64L-E222G jellyfish green fluorescent protein mutant.
                                                                                                                                                            Key Location/Qualifiers
Misc-difference 65
                                                                                                                                                                                                                                                                                                                                                                            Thastrup 0;
                    ¥
                  AAE17518 standard; protein; 239
                                                                                                                                                                                                                                                                                                       19-JUN-2000; 2000DK-0000953.
20-JUN-2000; 2000US-02126B1P.
10-MAY-2001; 2001US-0290170P.
                                                                                                                                                                                                                                                                                    18-JUN-2001; 2001WO-EP006848
                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                            Bjorn SP, Pagliaro L,
                                                                                                                                                                                                                                                                                                                                                        (BIOI-) BIOIMAGE AS.
                                                                                                                             Aequorea victoria.
Synthetic.
                                                                                                                                                                                                                                             WO200198338-A2
                                                           22-APR-2002
                                                                                                                                                                                                                                                                27-DEC-2001.
                                      AAE17518;
RESULT 1
AAE17518
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BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

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The invention relates to a fluorescent protein derived from green fluorescent protein (GFP) or its analogue. The GFP containing mutations at red, and E22G has a bigger compared to other GFP's making it very cultable for high throughput screening due to better resolution. The fluorescent protein is useful in invitro assays for measuring protein kinase activity, or for measuring protein calcistribution. The fluorescent protein tags in transgenic animals, living and fixed cells; organelle tags, secretion marker and genetic reporter. The fluorescent protein is also useful as a cell or organelle integrity marker, a marker to be used in cell morphology, as transfection marker. The fluorescent protein is also used in setul as a cell or organelle integrity marker, a marker to be used in combination with fluorescence activated cell sorting (FACS). The novel proteins can also be used as reporters to monitor live or dead biomass of organisms, such as fungi. The fluorescent protein is also useful as markers in transcriptional and translational fusions for performing transposons encoding the fluorescent protein are useful for screening promoters and for tagging plasmids and chromosomes. The fluorescent protein engineered into the genome of a phage is useful for designing diagnostic tool. The present sequence is a DNA encoding cenhanced F64L-B222G jellyfish green fluorescent protein (GFP) mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLIGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.8%; Score 1272; DB 5; Length.239;
llarity 99.6%; Pred. No. 1.5e-122;
Conservative 1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; heterologous conjugate; intracellular protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human amino acid sequence SEQ ID NO: 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABR40352 standard; protein; 363 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2001; 2001DK-00001433.
11-OCT-2001; 2001US-0328896P.
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nes 238; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 239 AA;
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The invention relates to a novel cell, comprising three heterologous conjugates (HC), a first HC (HC1) comprising an anchor protein that specifically binds to an internal structure within the cell conjugated to an internal structure within the cell conjugated to an interactor protein (IP) of type A, a second HC (HC2) comprising IP of type B conjugated to a first protein of interest, and a third HC (HC3) comprising a second protein of interest conjugated to detectable group. The cell is useful for detecting if a compound disrupts or induces the interaction between two intracellular proteins. The cell is also useful for screening compounds that modulate the interaction between two intracellular proteins. The present sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLIGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel cell for identifying modulators of protein interaction, contains a first conjugate comprising anchor protein, second conjugate having type interactor protein and third conjugate with detectable group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ll nervous system; antiinflammatory; cytostatic; nootropic; ischemic; osteopathic; GFP; green fluorescent protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPMPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MVSKGBELFTGVVPILVBLDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                            Length 363;
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                                                                                                                                                                                                                                                                                                                                                                                            Score 1272; DB 6;
Pred. No. 2.8e-122;
1; Mismatches 0;
                                                                                                                             Disclosure; Page 112-113; 118pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG65781 standard; protein; 893 AA.
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29-MAY-2000; 2000DK-00000849.
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                                                                                                                                                                                                                                                                                                                                                                                            Match 99.8%;
Local Similarity 99.6%;
les 238; Conservative
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            WPI; 2003-430211/40.
N-PSDB; ACC72604.
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                                                                                                                                                                                                                                                                                                                                                                Sequence 363 AA;
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fusion protein.
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Matches
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Thastrup O, Almholt DC;

Bjorn SP,

Scudder KM,

Praestegaard M;

BR, Terry

(BIOI-) BIOIMAGE AS

WPI; 2001-611727/70. N-PSDB; AAI66853.

11-APR-2001; 2001WO-DK000264. 17-APR-2000; 2000DK-0000651. 29-MAY-2000; 2000DK-00000849.

25-OCT-2001.

```
The invention relates to determining, if a compound, is a dislocator of PDE4. The method comprises testing if the compound removes PDE4 spots, which may optionally be induced by a Roliptam-like reference compound, and testing if it inhibits the catalytic activity of the PDE4, where the compound is a dislocator of PDE4, if it removes PDE spots and if it does not inhibit the catalytic activity of PDE4. The method is useful for identifying compounds useful for the treatment of diseases of the central nervous system such as depression and for the treatment of inflammatory disease, respiratory diseases, chronic obstructive pulmonary disease (COPD), including asthma, chronic bostructive pulmonary disease conductors shock, toxic shock syndrome, systemic lupus erthematosis, psoriasis, bone resorption diseases, reperfusion injury, cancer and HIV compound with affinity for the catalytic site on intracellular distribution of the PDE for the preparation of a medicament. The present
                                                                                                                           Determining if a compound is a dislocator of PDE4 for identifying compounds for treating CNS and inflammatory disease comprises identifying compounds which remove PDE4 spots.
  Bjorn SP, Thastrup O, Almholt DC;
                                                                                                                                                                                                                  Example 1; Page 156-160; 160pp; English.
Scudder KM,
                                                                 WPI; 2001-611727/70
                                                                                       N-PSDB; AAI66852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 893 AA;
                        Praestegaard M;
    BR.
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    Terry
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655 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGGGGGDATYGKLTIKFICTTGKLPVPWPT 714
                                                                                                                                                              LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                             715 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 774
                                                                                                                                                                                                                                            VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                    1 MVSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                               Gaps
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0
Score 1272; DB 4; Length 893;
Pred. No. 1.1e-121;
1; Mismatches 0; Indels C
        99.8%;
99.6%;
                        Best Local Similarity 99.6
Matches 238; Conservative
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Amino acid sequence of HSPDE4A4-E222G fusion protein.
          AAG65782 standard; protein; 1132 AA
                                (first entry)
                                07-JAN-2002
                     AAG65782;
    RESULT
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PDE4; central nervous system; antiinflammatory; cytostatic; nootropic; autoimmune; ischemic; osteopathic; GFP; green fluorescent protein;

Aequorea victoria. Homo sapiens

fusion protein.

WO200179526-A2

Enhanced F64L jellyfish green fluorescent protein mutant.

22-APR-2002 (first entry)

SEXEXEX

AAE17517 standard; protein; 239 AA

AAE17517

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The invention relates to determining, if a compound, is a dislocator of PDE4. The method comprises testing if the compound removes PDE4 spots, which may optionally be induced by a Rolipram-like reference compound, and testing if it inhibits the catalytic activity of the PDE4, where the compound is a dislocator of PDE4, if it removes PDE spots and if it does not inhibit the catalytic activity of PDE4. The method is useful for compound suseful for the reatment of diseases of the central nervous system such as depression and for the treatment of inflammatory disease such as joint inflammation, Crohn's disease, inflammatory bowel compounds useful for the treatment of inflammatory disease, respiratory diseases, chronic obstructive pulmonary bowel compound synchia systemic lupus erthematosis, candetoxic shock toxic shock syndrome, systemic lupus erthematosis, psoriasis, bone resorption diseases, reperfusion injury, cancer and HIV compound with affinity for the catalytic site on intracellular distribution of the PDE for the preparation of a medicament. The present sequence represents the amino acid sequence of a HSPDE444-E222G fusion
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                                                                                                                                                                                                                                                                                                                  Determining if a compound is a dislocator of PDE4 for identifying compounds for treating CNS and inflammatory disease comprises identifying compounds which remove PDE4 spots.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 99.8%; Score 1272; DB 4; Length 1132; Best Local Similarity 99.6%; Pred. No. 1.5e-121; Matches 238; Conservative 1; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 162-167; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1132 AA;
셤
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121

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The invention relates to a fluorescent protein derived from green fluorescent protein (GFP) or its analogue. The GFP containing mutations at FedL and E222G has a bigger compared to other GFP's making it very suitable for high throughput screening due to better resolution. The fluorescent protein is useful in invitro assays for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution. The fluorescent protein tags in transgenic animals, living and fixed cells; organelle tags, secretion marker and genetic reporter. The fluorescent protein is also useful as a cell or organelle integrity marker, a marker to be used in combination with fluorescence activated and as a marker to be used in combination with fluorescence activated cells sorting (FACS). The novel proteins can also be used as reporters to monitor live or dead biomass of organisms, such as fungi. The fluorescent protein is also useful as markers in transcriptional and translational tusions for performing transposons encoding the fluorescent protein are useful for screening promoters and for tagging plasmids and chromosomes. The fluorescent protein engineered into the genome of a phage is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel fluorescent protein in in vitro assay for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution, has a green fluorescent protein with F64L and E222G mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             designing diagnostic tool. The present sequence is enhanced F64L
                                                                                                                                                       /note= "Wild type Phe substituted with Leu; This corresponds to position 64 in the wild type protein"
Jellyfish, green fluorescent protein, GFP, protein redistribution, cellular function, genetic reporter; mutant, Stoke's shift, mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1264; DB 5; Length 239;
Pred. No. 1e-121;
1; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ellysish green fluorescent protein (GPP) mutant
                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 35; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thastrup
                                                                                                                                                                                                                                                                                                                                19-JUN-2000; 2000DK-00000953.
20-JUN-2000; 2000US-02126B1P.
10-MAY-2001; 2001DK-00000739.
10-MAY-2001; 2001US-0290170P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.2%;
99.2%;
                                                                                                                                                                                                                                                                                           18-JUN-2001; 2001WO-EP006848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pagliaro L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2:002-098224/13.
                                                                                                                                                                                                                                                                                                                                                                                                                            (BIOI-) BIOIMAGE AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                            Aequorea victoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDE; AAD28162
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                                                                                                                                        Misc-difference
                                                                                                                                                                                                                 WO200198338-A2
                                                                                                                                                                                                                                                       27-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bjorn SP,
                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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The invention relates to systems, methods and reagents for cell-based screening or detection of compounds which affect particular biological functions. The methods of the invention utilise fluorescent biodetector collected which, when acted on by a compound of interest, cause an alteration in the cellular distribution of at least the fluorescent alteration in the cellular distribution of at least the fluorescent collects. The one embodiment, the biosensors comprise hear shock proteins or alteration in the cellular distribution of at least the fluorescent protein (e.g., jellyfish green fluorescent protein (e.g., jellyfish green fluorescent protein can be used to detect protease or another embodiment biodetector proteins can be used to detect protease another embodiment biodetector fusion proteins comprise one or more callular localisation signal. The latter two protease, and at least one cellular localisation signal. The latter two components may be from heterologous sources. Due to the protease, or may be from heterologous sources. Due to the callular localisation signal the cell. Once acted on by the protease of interest, the region of the cell. Once acted on by the protease of interest, the fluorescent protein to be directed to a different cellular sequence. The second localisation signal attached to the fluorescent protein to be directed to a different cellular comparatment after cleavage of the protease recognition sequence. The change in distribution of the fluorescent protein can be detected using imaging methods with a high degree of spatial resolution. The methods and imaging methods with a high degree of spatial resolution.
                                                                                                                                                                                                                                                                                                  Biodetector protein; fusion protein; recognition site; cellular targetting sequence; cellular localisation; fluorescent protein; protease activity detection; toxin detection; cellular stress detection; drug discovery; cell based screening.
                   DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLIGFVTAAGITLGMDELYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Automated cell-based characterization of toxin by contacting cells containing luminescent reporter molecules with test substance and
                                                                                                                                                                                                                                                                Enhanced green fluorescent protein (EGFP), SEQ ID NO:46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 11; Fig 29A; 336pp; English
                                                                                                                                              AAB22882 standard; protein; 239 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0122152P.
99US-0123399P.
99US-00352171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-FEB-2000; 2000WO-US004794.
                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Giuliano KA, Kapur R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CETT-) CETTOWICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analyzing optically.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-594086/56.
                                                                                                                                                                                                                                                                                                                                                                                                                  Aequorea victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAA93373
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                         AAB22882;
      181
                                                                                                                                 AAB2288
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Gaps

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Conservative

237;

Matches

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1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTKFICTTGKLPVPWPT 1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT

9

LVITLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTL 120

61

g à g à,

121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQROGIKVNFKIRHNIEDGSVQLA 180

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cellular activities and to screen compounds which modulate these example, may be used for the screening of compounds which modulate these apoptosis, while biosensors containing a recognition site for caspase, for appoptosis, while biosensors containing other protease recognition sites may be used for the detection of proteolytic toxins (such as anthrax lethal factor). The method provides improved target validation and candidate compound optimisation by combining many cell screening formats with fluorescence-based molecular reagents and computer-based feature extraction, data analysis and automation, resulting in increased quantity and speed of data collection and faster evaluation of drug candidates. Sequences AAB22881-B22885 represent fluorescent proteins which may used as components of biosensor fusion proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                        LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                   VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLIGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biosensors of the invention can be used to investigate a wide range of
                                                                                                                                                                                                                                                                                                                             1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                                           1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fluorescent protein; green fluorescent protein; emission intensity; fluorescence; pH detection; pH sensor; EGFP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of the mutant green fluorescent protein EGFP.
                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                              Length 239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "wild type Phe substituted with Leu"
                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                            99.0%; Score 1261; DB 3;
98.7%; Pred. No. 2.1e-121;
iive 2; Mismatches 1;
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UNIV OREGON STATE.
                                                                                                                                                                                                                                                                            236; Conservative
                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                                                                 Sequence 239 AA;
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13-OCT-1998;
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                                                                                                                                                                                                                                                Query Match
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protein based on the Aequorea green fluorescent protein (GFP). The emission intensity changes as pH varies between 5 and 10 of the present protein are novel. The functional engineered fluorescent proteins show reversible changes in fluorescence over physiological pH ranges. They can also be used for determining the pH of samples and cells. The polynucleotides can also be used to produce transgenic animals. The fluorescent protein pH sensors can be delivered to cells in the form of polynucleotides encoding the protein sensor fused to a targeting signal. The targeting signal directs the expression of the protein sensors to restricted cell locations. This makes it possible to measure the pH of a precisely defined cellular region or organelle
                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                         New functional engineered green fluorescent proteins, used for measuring the pH in biological samples and cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLIGFVTAAGITLGMDELYK 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MVSKGBELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                     engineered fluorescent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protease; biosensor; EGFP; signal peptide; cell screening; assay;
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                                                                                                                                                                                                                                                                                                                                                                                        Length 239;
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                                                                                                                                                                                                                                                                                                                                                                                       99.0%; Score 1261; DB 3; 98.7%; Pred. No. 2.1e-121; ive 2; Mismatches 1;
                                                                                                                                                       sequence represents a functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Olson K,
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                                                                                                                         Disclosure; Page 9; 89pp; English
Wachter RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY79584 standard; peptide; 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US025431.
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Matches 236; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CELL-) CELLOMICS INC.
Tsien RY, Llopis J,
                             WPI; 2000-116540/10.
N-PSDB; AAZ45642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGFP signal domain
                                                                                                                                                                                                                                                                                                                                                           Sequence 239 AA;
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Aequorea victoria; jellyfish; fluorescent protein indicator; greer. fluorescent protein; GFP; linker moiety; sensor; calmcdulin-binding domain; mutant; mutein.
                                                                                                                                                                                                                                                                                                          Jellyfish GFP mutant EGFP.
                                                                                                                                                               Best Local Similarity
Matches 236; Conserv
    WPI; 2000-365644/31
                                                                                                                                                  Sequence 239 AA;
         N-PSDB; AAA27573
                                                                                                                                                                                                                                                                                                                                                  WO2001071565-A2
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                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                   RESULT 9
AAB50804
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The present sequence is a fluorescnet protein used in the construction of a fluorescent protein indicator. The indicator comprises a sensor polypeptide that is responsive to a chemical, biological, electrical or physiological parameter, and a fluorescence protein functional group. The sensor polypeptide is operatively inserted into the fluorescent moiety. The fluorescent indicator is useful for detecting the presence of a response inducing member in a sample. The method involves contacting the sample with the indicator and detecting a change in fluorescence, in polypeptide. The novel fluorescent proteins are advantageous due to their reduced size as compared to the FRET (fluorescence resonance energy
                                                                                                                                                                                                                                                                                             Novel fluorescent proteins comprising a sensor protein inserted into them, useful for measuring the response of a sensor biological, chemical, electrical or physiological parameter in vivo or in vitro.
                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 24; 94pp; English.
17-MAY-2000; 2000WO-US013684.
                                                  99US-00316919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transfer) -based sensors
                                                                                                                                (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                  Baird GA;
                                                                                                                                                                                                                             WPI; 2001-032017/04.
N-PSDB; AAC90488.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 239 AA;
                                                        21-MAY-1999;
21-MAY-1999;
                                                                                                                                                                                     Tsien RY,
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                                                                                                                                                                                                                                                The present sequence is that of the EGFP signal domain, which can be included in novel recombinant protease biosensors (PBS) of the invention. The PES (see AAY79618-54) comprise: a first domain (see AAY79579-87) comprising at least 1 detectable polypetide signal such as the present comprising at least 1 asset 1 asset 1 asset 1 asset 1 asset 1 protease recognition site, and a third domain (see AAY79633-623) comprising at least 1 reactent target sequence. A recombinant nucleic comprising at least 1 reactent target sequence. A recombinant nucleic acid (see AAA27627-43) encoding the PB, an expression vector, and a contacting a nost cell are also claimed. A claimed method for genetically engineered host cell are also claimed. A claimed method for contacting a host cell that possesses the recombinant PB with a test compound, and determining the PB distribution in the host cell, where compound, and determining the PB distribution in the host cell, where compounds that modify protease activity in a host cell include the compounds that modify protease activity in a host cell include the compounds that modify protease activity in a host cell include the recombinant PB with a test recombinant PB with a test recombinant ps. or the vector, or the vector or the vector or the vector or changes in the PB is useful in high content screens to detect in vivo activition of enzymatic activity, and to identify specific activity based or claavage of a known recognition motif
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                                                                                                             Recombinant nucleic acid encoding a protease biosensor useful for fluorescence based cell and molecular biochemical assays for drug discovery comprising three operably linked nucleic acid sequences
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98.7%; Pred. No. 2.1e-121;
iive 2; Mismatches 1;
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                                                                                                                                                                                                                        Claim 14; Fig 29A; 218pp; English
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                                                                                                                                                           VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                            DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLIGFVTAAGITLGMDELYK 239
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                                                                                                                                                                                                                             61 LVTTLTYGVQCFSRYPDHMKQHDFPKSAMPBGYVQERTIFFKDDGNYKTRAEVKFEGDTL
                                                 1 MVSKGBELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                    Melanin concentrating hormone receptor; MCHR; MCH; chimeric; fusion; fluorescent polypeptide; orexigenic; anabolic; food intake; GFP; green fluorescent protein.
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                        A. victoria green fluorescent protein (GFP) and linker sequence.
                           ö
Length 239;
                           Indels
 99.0%; Score 1261; DB 4;
98.7%; Pred. No. 2.1e-121;
iive 2; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                 AAB85900 standard; protein; 239
                                                                                                                                                                                                                                                                                                                                                                    30-NOV-2001 (first entry)
     99.0
Best Local Similarity 98.7
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aequorea victoria
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07-JUN-1999;
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                                                                                                                                                                                      The invention provides melanin concentrating hormone (MCH) receptor (MCHR) chimeric and fusion proteins. The MCHR chimeric proteins comprise MCHR polypeptide regions from different species. The MCHR fusion protein comprise MCHR polypeptide region and a fluorescent polypeptide region protein joined directly, or via a linker, to the carboxy side of the MCHR polypeptide region. The MCHR fusion proteins can be expressed by standard recombinant methodology. MCH action promotes feeding (orexigenic) and up regulation of MCH activity stimulates food intake. The present sequence represents a A. victoria green fluorescent protein (GFP) and a linker
                                                                                                                                                                                                                                                                                                                                                                                                    LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                              Fusion proteins comprising melanin concentrating hormone receptor peptides and fluorescent proteins, useful for identifying appetite
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                                                                                                                                                                                                                                                                                                                       Length 239;
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of a green fluorescent protein (GFP).
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                                                                                                                                                                                                                                                                                                                      Score 1261; DB 4;
Pred. No. 2.1e-121;
2; Mismatches 1;
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                                                                                                                                                                     Claim 2; Page 14; 71pp; English.
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                    14-MAR-2001; 2001WO-US008071
                                       15-MAR-2000; 2000US-0189698P
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 98.7%;
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                         (MERI ) MERCK & CO INC
                                                                                                 WPI; 2001-565791/63,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aequorea victoria.
                                                                                                         N-PSDB; AAH47304.
                                                                                                                                                                                                                                                                                                   Sequence 239 AA;
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20-SEP-2001
                                                                                                                                                  stimulants.
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                                                                             Marsh DJ;
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death rate of a micro-organism within a predetermined time period in a desired environment. The method comprises introducing at least two reporter genes encoding luminescent and/or fluorescent products into the micro-organisms, incubating the micro-organism within the desired environment, and detecting luminescence and/or fluorescence after a predetermined time period. Use of two different markers within a micro-organism enables the differentiation between growth and death rates. The method is used to assess the growth rate and death rate of a micro-organism within a predetermined time period in a desired environment. The present sequence represents a green fluorescent protein (GFP), and is encoded by a plasmid which encodes luminescent and fluorescent proteins, and is and is used in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                             Assessing growth and death rates of a micro-organism in a desired environment, by introducing 2 reporter genes encoding luminescent and fluorescent products and detecting luminescent fluorescence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The specification describes a method for assessing the growth
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98.7%; Pred. No. 2.1e-121;
ive 2; Mismatches 1;

    A. victoria green fluorescent protein (EGFP).

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99FI-00001296
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Best Local Similarity 98.7
Matches 236; Conservative
                                                                                                                                                                                                                                                     2001-061737/07
                                                                                                                                                                            Lilius E, Virta M;
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                                                                 (LILI/) LILIUS E. (VIRT/) VIRTA M.
                                                                                                                                                                                                                                                                                               N-PSDB; AAC86954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 239 AA;
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17-SEP-1999;
        29-OCT-1999;
01-DEC-1999;
                                                           Giuliano K,
                                                                                                                                dentifiers.
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                                                                                                                                                                                                                                                                                 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                             The invention relates to a gene encoding proteins having cyan-green fluorescence characteristic and having a function of showing stable fluorescence characteristic in acid region. A method for the preparation of a cyan-green fluorescent protein is provided which involves a transformant transformed by a recombinant vector comprising the gene, where the transformed is cultured and the protein is collected from the culture. The present sequence represents the A. victoria green fluorescent protein (EGFP)
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                                                                                                                                                                                                                                                                                                                                                    DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLIGFVTAAGITLGMDELYK 239
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                                                                                                                                                                                                                                               MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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                                                                                                                                                                                                             Length 239;
                                                                                                                                                                                                              Score 1261; DB 5;
Pred. No. 2.1e-121;
                                                                              gene encoding cyan-green fluorescent protein.
                                                                                                                                                                                                                               2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                  ABG94444 standard; protein; 239
                                                                                                Example; Page 14; 20pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0031271.
99US-0122152P.
99US-0123399P.
99US-00352171.
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   04-AUG-2000; 2000JP-00237165
                     04-AUG-2000; 2000JP-00237165.
                                     (RIKA ) RIKAGAKU KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                        Local Similarity 98.7
les 236; Conservative
                                                      WPI; 2002-299190/34.
                                                                N-PSDB; ABL40628
                                                                                                                                                                                               Sequence 239 AA;
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27-FEB-1998;
26-FEB-1999;
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12-JUL-1999;
31-AU3-1999;
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                                                                                                                                                                                                                                 Matches
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The invention describes methods of automated detection, classification and identification comprising treating cells containing luminescent reporter molecules (I) in array of locations with a test substance, where (I) are detectors, classifiers or identifiers, imaging cells in each clocation to obtain luminescent signals and converting optical information into digital data to interpret presence of toxins in the test substance. The method are useful for detection of toxins chosen from proteases, ADP-cribosylating toxins, cytotoxic phospholipases, and exfoliative toxins. Three classes of cell-based luminescent reporter molecules such as detectors, classifiers and identifiers are described and serve as creporters of toxic threat agents. The first two levels of characterisation ensure a rapid readout of toxin class without contains the ability to detect many new mutant toxins or dissect several complex mixtures of known toxins. This is the amino acid sequence of a protease biosensor related signal sequence used in the cell-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLIGFVTAAGITLGMDELYK 239
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                                                                                                                                                                                                                                                                                                                                                                                      of
                                                                                                                                                                                                                                                                                                                                                   Automated cell-based toxin detection, classification, and/or identification by treating cells involves use of three classes luminescent reporter molecules such as detectors, classifiers o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1261; DB 5;
Pred. No. 2.1e-121;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 10; Fig 29A; 214pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE14599 standard; protein; 239
99US-00398965.
99US-00430656.
99US-0168408P.
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Best Local Similarity 98.7
Matches 236; Conservative
                                                                                                                                                                                                                  Kapur R;
                                                                                                                                                                                                                                                                           WPI; 2002-634730/68.
                                                                                                                          GIULIANO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aequorea victoria.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     screening system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 239 AA;
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The invention relates to a method for mutagenesis that comprises synthesising a mutated strand and a complementary strand by use of synthesising a mutated strand and a comprises a DNA synthesis in which one cor megaprimers. The method basically comprises a DNA synthesis in which one cor more primers that have a nucleotide sequence containing at least one cor more primers that have a nucleotide sequence containing at least one and then subjected to an elongation reaction using a thermostable high-correct then subjected to an elongation reaction using a thermostable high-correct the elongated terminus are ligated by means of a thermostable DNA ligase to synthesise a circular DNA containing the primers; a digestion in which the step of DNA synthesis is repeated several fines to amplify the DNA containing the primers and then, a least DNAs other than the amplified circular DNA are digested into several fragments obtained in the step of DNA synthesis in which, with the several fragments obtained in the step of digestion as megaprimers, the megaprimers are annealed to the circular DNA synthesised above, followed by an elongation reaction performed using the thermostable high-fidelity DNA polymerase. The method is useful for mutagenesis, particularly for introducing centain mutations at certain sites of the nucleotide sequence. The present method is simple, and annealed contain sites of the mutagenesis present sequence is somether and an annealed contain sites of the nucleotide sequence. The present sequence is somether and an annealed contain contain the sequence is an annealed to be an annealed to the contain mutations at the sequence of a present sequence is somether and an annealed contain contain the sequence is an annealed to the sequence. The present sequence is
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note= "Wild-type GFP Met-Ser are replaced with Met-Val-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aequorea victoria enhanced green fluorescent protein (EGFP) used for mutagenesis in an exemplification of the invention. The EGFP is derived by altering the green fluorescent protein (GFP) sequence of Aequorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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                                                                                                                                  "GFP Phe64 is replaced by Leu"
                                                                                                                                                                                  "GFP Ser65 is replaced by Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.0%; Score 1261; DB 5; 98.7%; Pred. No. 2.1e-121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 13-14; 31pp; English.
                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                         03-AUG-2001; 2001EP-00306650
                                                                                                                                                                                                                                                                                                                                                                       04-AUG-2000; 2000JP-00237166
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                                                                                                                                                                                     /note=
                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miyawaki A, Sawano A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-208112/27.
                                                                                                                                                          Misc-difference 66
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                                                                                                                                                                                                                                                                                                                                                                                                                (RIKE ) RIKEN KK.
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                                         Misc-difference
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                                                                                                               Misc-difference
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es 236;
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181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLIGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                     detection; phosphatase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kinase/phosphatase in samples, has donor molecule, phosphorylatable domain, phosphoaminoacid binding domain, and acceptor molecule, in operative linkage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel chimeric phosphorylation indicators, useful for detecting
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                                                                                                                                                                                                                   Aequorea victoria enhanced green fluorescent protein (EGFP).
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                                                                                                                                                                                                                                                                      kinase; enhanced green fluorescent protein; EGFP.
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                                                                                                                                                                                                                                                   Phosphorylation indicator; fluorescent protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Col 56-57; 38pp; English.
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                                                                                                                AAE34958 standard; protein; 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                        24-MAY-2001; 2001US-00865291.
                                                                                                                                                                                                                                                                                                                                                                                                         24-MAY-2002; 2002WO-US016955.
                                                                                                                                                                                   (first entry)
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nes 236; Conservative
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                                                                                                                                                                                                                                                                                                      Aequorea victoria.
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                                                                                                                                                                                  28-MAY-2003
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181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 239

Search completed: June 21, 2004, 15:54:11 Job time: 47.1111 secs

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121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNYYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLIGFVTAAGITLGMDELYK 239
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Sequence 3, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 21, Appli
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Sequence 6, Appli
Sequence 129, Appli
Sequence 129, Appli
Sequence 127, Appli
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Sequence 127, Appli
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Sequence 125, App
Sequence 2, Appli
Sequence 6, Appli
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Sequence 46, Appl
                                                                                 (without alignments)
965.630 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                          1 MVSKGEELFTGVVPILVELD......VLiGFVTAAGITLGMDELYK 239
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/cgm2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgm2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgm2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgm2_6/ptodata/2/iaa/PcTWS_COMB.pep:*
/cgm2_6/ptodata/2/iaa/PcTWS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-513-78A-46

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US-09-920-922-2

US-09-062-102-1

US-09-172-063-21

US-09-172-063-21

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US-09-171-197-129

US-09-417-197-113

US-09-417-197-197

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US-09-417-197-65

US-09-417-197-65

US-09-417-197-65

US-09-417-197-125
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                                                                                                                                                                                                     389414 segs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                  US-09-887-784-222I
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Maximum DB seq length: 200000000
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; Sequence No. 6150176
; Patent No. 6150176
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Hiyawaki, Atsushi
; APPLICANT: Macher, Rebekka M.
; APPLICANT: Wacher, Rebington, S. James
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: FLUORESCENT PH OF A BIOLOGICAL SAMPLE
; CURRENT APPLICATION WINBER: US/09/172,063
; CURRENT FILING DATE: 1998-10-13
; CURRENT FILING DATE: 1998-10-13
; CURRENT FILING DATE: 1998-6-09
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH. 239
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Pred. No. 1.9e-127;
2; Mismatches 1;
US-08-818-252-2

US-08-818-253-4

US-08-818-253-4

US-09-417-197-75

US-09-417-197-71

US-09-417-197-119

US-09-417-197-114

US-09-417-197-143

US-09-417-197-143

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US-09-417-197-43
US-09-417-197-117
US-09-417-197-119
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Best Local Similarity 98.7%;
Matches 236; Conservative
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ORGANISM: Aequorea victoria
       LOCATION: (0)...(0)
OTHER INFORMATION: EGFP
    NAME/KEY: VARIANT
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Pred. No. 1.9e-127;
2; Mismatches 1; Indel8
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RESULT 2
UG-09-513-783A-46
; Sequence 46, Application US/09513783A
; Patent Nc. 6416559
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.; APPLICANT: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening; TITLE OF INVENTION: 97-022-L1
; CURRENT FPLICATION NUMBER: US/09/513,783A
; CURRENT FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Taien, Roger Y.
APPLICANT: Baird, Geoffrey
TITLE O: INVENTION: FLUORESCENT PROTEIN INDICATORS
FILE REFERENCE: 07257/073001
CURRENT APPLICATION NUMBER: US/09/316,919
CURRENT PILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
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Pred. No. 1.9e-127;
2; Mismatches 1;
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Patent No. 6469154
GENERAL INFORMATION:
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Best Local Similarity 98.7%;
Matches 236; Conservative
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; ORGANISM: Aequorea victoria
US-09-316-919-4
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Best Local Similarity 98.7
Matches 236; Conservative
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APPLICANT: Teien, Roger Y.
APPLICANT: Mignawki, Atsushi
APPLICANT: Midpawki, Atsushi
APPLICANT: Midpawki, Atsushi
APPLICANT: Machter, Rebekka M.
APPLICANT: Wachter, Rebekka M.
APPLICANT: Ranington, S. James
ITILE OF INVENTION: WESCENT PROTEIN SENSORS FOR
ITILE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/071001
CURRENT APPLICATION NUMBER: 08/09/602,641
CURRENT FILING DATE: 2000-06-22
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 239
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98.7%; Pred. No. 1.9e-127;
tive 2; Mismatches 1;
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APPLICANT: Sawano, Asako
TITLE OF INVENTION: METHOD FOR MUTAGENESIS
FILE REFERENCE: 11283-012001
CURRENT APPLICATION NUMBER: US/09/920,922
CURRENT FILING DATE: 2001-08-02
PRIOR PILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 9
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                                                                                                                                                                                                                                                  Sequence 3, Application US/09602641 Patent No. 6608189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Aequorea victoria FEATURE:
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Best Local Similarity 98.7
Matches 236; Conservative
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RESULT 8
US-09-513-783A-2
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                    JS-09-364-946-1
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APPLICANT: Li, Xianqiang
TITLE OF INVENTION: Rapidly Degrading GFP-Fusion Proteins and Methods
TITLE OF INVENTION: 0 Use
FILE REFERENCE: D6100
CURRENT APPLICATION NUMBER: US/09/062,102
CURRENT APPLICATION NUMBER: US 60/060,855
EARLIER APPLICATION NUMBER: US 60/060,855
EARLIER FILING DATE: 1997-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Sequence of the EGFP-MODC422-461 fusion protein.; Patent No. 6130313
US-09-062-102-1
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98.7%; Pred. No. 2.4e-127;
iive 2; Mismatches 1;
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09062102
Patent No. 6130313
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: artificial sequence
                                                                     ORGANISM: Aequorea victoria
                                                                                                                                             Best Local Similarity 98,7
Matches 236, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 98.7
Matches 236; Conservative
                                 LENGTH: 239
TYPE: PRT
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US-09-062-102-1
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LENGTH: 281
                                                                                      US-09-920-922-2
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                                                                  APPLICANT: Kain, Steve
APPLICANT: Kain, Steve
APPLICANT: Li, Xianqiang
TITLE OF INVENTION: Rapidly Degrading GFP-Fusion Proteins and Methods
TITLE OF INVENTION: OF USE
FILE REPERENCE: D6100CIP/D2
CURRENT APPLICATION NUMBER: US/09/364,946
CURRENT FILING DATE: 1999-07-30
EARLIER PAPLICATION NUMBER: US 09/191,233
EARLIER PAPLING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 14
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Best Local Similarity 98.7%; Pred. No. 2.6e-127;
Matches 236; Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1261; DB 4;
Pred. No. 2.4e-127;
2; Mismatches 1;
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Sequence 2, Application US/09513783A
Sequence 2, Application US/09513783A
Sequence 2, Application US/09513783A
GENERAL INFORMATION:
APPLICANT: Giuliano, Kenneth A.
TITLE OF INVENTION: A System for Cell Based (FILE REFERENCE 97-022-L1)
CURRENT PELLION UNMER: US/09/513,783A
CURRENT PELLING DAITE: 2000-02-25
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 294
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Sequence 1, Application US/09364946 Patent No. 6306600
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: artificial sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 98.7%;
Matches 236; Conservative
                                                    GENERAL INFORMATION
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US-09-364-946-1
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FEATURE:
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                                                                     61 LVTTLTYGVQCFSRXPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                      121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                                                                                                                           1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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APPLICANT: Myawaki, Atsushi
APPLICANT: Logis, Juan
APPLICANT: Myawaki, Juan
APPLICANT: Remington, S. James
APPLICANT: Remington, S. James
APPLICANT: Remington, S. James
APPLICANT: Remington, S. James
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MARASHRING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/071001
CURRENT FPLING DATE: 1998-10-13
EARLIER APPLICATION NUMBER: 09/094,359
EARLIER FILING DATE: 1998-06-09
NUMBER OF SEQ ID NOS: 38
SOFTWARN: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.0%; Score 1261; DB 3; Length 323; 98.7%; Pred. No. 3e-127; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                             ; Sequence 21, Application US/09172063; Patent No. 6150176; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (0)...(0)
; OTHER INFORMATION: GT-EGFP
US-09-172-1)63-21
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Best Local Similarity 98.77
Matches 236; Conservative
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US-09-172-063-21
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LENGTH: 323
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Sequence 21, Application US/09602641; Patent No. 6608189; GENERAL INFORMATION: APPLICANT: Taien, Roger Y. APPLICANT: Miyawaki, Acsushi APPLICANT: Llopis, Juan

RESULT 10 US-09-602-641-21

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61 LVTTLSYGVQCFSRXPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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Malignant Cancer Cells by Delivery of N-Terminal
Interleukin-1-Alpha Pro-Piece Polypeptide
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APPLICANT: Wachter, Rebekka M.
APPLICANT: Remington, S. James
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
TITLE OF INVENTION: WASSURING THE PH OF A BIOLOGICAL SAMPLE
CURRENT APPLICATION NUMBER: US/09/602,641
CURRENT FILING DATE: 1000-06-22
PRIOR PILING DATE: 1998-10-13
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 323
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Pred. No. 3e-127;
2; Mismatches 1; Indels
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OMPRATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,305
FILING DATE: 29-MAY-1998
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dovett, David H.
APPLICANT: Lovett, David H.
APPLICANT: Lovett, David H.
TITLE OF INVENTION: Selective Induction of TITLE OF INVENTION: Malignant Cancer Celtring OF INVENTION: Interleukin-1-Alpha NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bozicevic & Reed, LLP STREET: 285 Hamilton Ave, Suite 200
CITY: Palo Alto
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Patent No. 6191269
GENERAL INFORMATION:
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Best Local Similarity 98.7%;
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Aequorea victoria
                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: VARIANT
CCATION: (0) ... (0)
COTHER INFORMATION: GT-EGFP
US-09-602-611-21
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APPLICANT: OCCUPATION: et al.
TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An IT TITLE OF INVENTION: On A Cellular Response
FITE SEPERANCE: 3759-0110P
CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patentin version 3.0
SEQ ID NO 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 LVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 315
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                                                                 321 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWVLLEFVTAAGITLGMDELYK 379
                                  181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLIGFVTAAGITLGMDELYK 239
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                                                                                                                                                                                                      ; Sequence 48, Application US/09800170; Patent No. 6481667; GENERAL INFORMATION: APPLICANT: Kinsella, Todd; TITLE OF INVENTION: TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES; FILE REFERENCE: A-68614-1/DJB/RMS/RMK; CURRENT APPLICATION NUMBER: US/09/800,170; CURRENT APPLICATION NUMBER: US 60/187,130; PRIOR APPLICATION NUMBER: US 60/187,130; PRIOR FILING DATE: 2000-03-06; NUMBER OF SEQ ID NOS: 90; NUMBER OF SEQ ID NOS: 90; SOFTWARE: PatentIn version 3.1; SEQ ID NO 48
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Best Local Similarity 98.7%; Pred. No. 4.7e-127;
Matches 236; Conservative 2; Mismatches 1;
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US-09-800-170-48
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Best Local Similarity
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US-09-800-170-48
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; Patent No. 6518021
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP, et al.
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An
; TITLE OF INVENTION: On A Cellular Response
; FILE REFERENCE: 3759-0110P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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US-09-417-197-129
                                                                                                                                                                                                                                                                                                                                                                                                           Score 1261; DB 3;
Pred. No. 3.6e-127;
2; Mismatches 1;
ATTORNEY/AGENT INFORMATION:
NAME: Francis, Carol L
REGISTRATION NUMBER: 65.0/102US1
REFERENCE/DOCKET NUMBER: 65.0/102US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
TELEPAK: 650-327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT FILING DATE: 1999-10-07
WUMBER OF SEQ ID NOS: 143
SOFTWARE: PATENTIN VEYBION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                             99.0%;
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                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 98.7
Matches 236; Conservative
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US-09-085-305-6
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Best Local Similarity
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US-09-417-197-129
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LENGTH: 379
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US-09-513-783A-170
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99.0%; Score 1261; DB 4; Length 459;

Best Local Similarity 98.7%; Pred. No. 5.1e-127;

Matches 236; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                         ; Sequence 170, Application US/09513783A; Sequence 170, Application US/09513783A; Patent No. 6416959; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.; APPLICANT: Kapur, Ravi; TITLE OF INVENTION: A System for Cell Based Screening; FILE REFERENCE: 97-022-11; CURRENT APPLICANTON VIMBER: US/09/513,783A; CURRENT FILING DATE: 2000-02-25; NUMBER CF SEQ ID NOS: 180; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: FRT
ORGANISM: Artificial Sequence
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US-09-513-783A-170
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Search completed: June 21, 2004, 16:04:03 Job time: 12.7778 secs

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SEQ ID NO 4
LENGTH: 239
TYPE: PRT
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Sequence 6, Appli
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Sequence 2, Appli
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Sequence 4, Appli
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1940.117 Million cell updates/sec
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Sequence 4, Al
Sequence 3, Al
Sequence 13,
                                                                                               June 21, 2004, 15:54:20 ; Search time 34.7778 Seconds
                                                                                                                                                                                              1 MVSKGEELFTGVVPILVELD......VLiGFVTAAGITLGMDELYK
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/ Ggn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/ Ggn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/ Ggn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
/ Ggn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
/ Ggn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
/ Ggn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
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/ Ggn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
/ Ggn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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4 US-10-270-223-6
4 US-10-257-909A-30
US-10-257-909A-32
US-10-296-953-2
US-10-296-953-2
US-09-999-745-4
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US-09-794-308-4
US-09-865-291-4
US-10-457-982-3
US-10-121-258-13
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                                                                                                                                                                                                                                                                                 1163542 seqs, 282313646 residues
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Gapop 10.0 , Gapext 0.5
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1274
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Match Length DB
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## ALIGNMENTS

61 LVTTLSYGVQCFSRYPDHMKQHDFPKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120 61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120 121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVQLA 180 1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGGGDATYGKLTKRICTTGKLPVPWPT 60 1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT 60 181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLIGFVTAAGITLGMDELYK 239 Gaps ö Query Match 99.8%; Score 1272; DB 9; Length 239; Best Local Similarity 99.6%; Pred. No. 2.2e-124; Matches 238; Conservative 1; Mismatches 0; Indels Sequence 4, Application US/09887784
Patent No. US20020177189A1
GENERAL INFORMATION:
APPLICANT: BOONN, Same et al
TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS
FILE REFERENCE: 3759-0115P
CURRENT FILING DATE: 2001-06-19
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.0 ORGANISM: Aequoria Victoria 181

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ures to identify compounds modulating intracellulationsphodiesterase (PDE) enzymes
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Sequence 32, Application US/10257909A

Sequence 32, Application US/10257909A

Sequence 32, Application US/2030187056A1

GENERAL INFORMATION:
TITLE OF INVENTION: distribution of phosphodiesterase (PDE) enzymes

TITLE OF INVENTION: USA-0125P

TITLE OF INVENTION: 01257,909A

CURRENT APPLICATION NUMBER: US/10/257,909A

CURRENT FILING DATE: 2002-10-17

NUMBER OF SEQ ID NOS: 36

SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bernard R. TERRY et al.
TITLE OF INVENTION: Live cell procedures to ide
TITLE OF INVENTION: Live cell procedures
FILE REFERENCE: 3759-0125P
CURRENT APPLICATION NUMBER: US/10/257, 909A
CURRENT FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 36
SOFTWARE FEASTSEQ for Windows Version 3.0
LENGTH: 893
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 30, Application US/10257909A, Publication No. US20030187056A1, GENERAL INFORMATION:
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Publication No. US20030143634A1

GENERAL INRORMATION:

APPLICANT: BLOIMAGE A/S

TITLE OF INVENTION: AN IMPROVED METHOD TO DETECT INTERACTIONS BETWEEN CELLULAR COMPON

TITLE OF INVENTION: INTRACTIONS BY FLUORESCENCE REDISTRIBUTION.

FILE REPERENCE: 3759-0126P

CURRENT APPLICATION NUMBER: US/10/270,223

CURRENT PILLIOR DATE: 2002-10-11

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin version 3.1
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Pred. No. 2.2e-124;
1; Mismatches 0;
                                       Sequence 4, Application US/10296953
; Publication No. US20040072995A1
; GENERAL INFORMATION:
APPLICANT: BOORN, SARA P.
APPLICANT: PAGLIARO, LEN
FILE REFERENCE: PL0095 FLUORESCENT PROTEINS
FILE REFERENCE: PL0095 FLUORESCENT PROTEINS
FILE REFERENCE: PL0095 PAIOR APPLICANTION NUMBER: US/10/296,953
CURRENT APPLICANTION NUMBER: US/10/296,953
CURRENT FILING DATE: 2000-06-19
PRIOR FILING DATE: 2000-06-19
PRIOR FILING DATE: 2000-06-10
PRIOR FILING DATE: 2001-05-10
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: RA 2001 00739
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: RA 2001 00739
PRIOR SEQ ID NOS: 24
SOFWWARE: PATCHING DATE: 2001-05-10
FRIOR SEQ ID NOS: 24
SSOFWWARE: PATCHING VEY: 2.1
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; ORGANISM: Aequoria Victoria and Human
US-10-270-223-6
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Best Local Similarity 99.6%;
Matches 238; Conservative
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US-10-296-953-4
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Best Local Similarity 99.6
Matches 238; Conservative
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TYPE: FRT
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                                                                                               ; OTHER INFORMATION: Fusion between Aequorea victoria and human
US-10-257-909A-12
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                                                                                                                                     Score 1272; DB 14;
Pred. No. 2e-123;
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Patent No. US20020177189A1

GENERAL INFORMATION:

TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS

FILE REFERENCE: 3759-0115P

CURRENT APPLICATION NUMBER: US/09/887,784

CURRENT FILING DATE: 2001-06-19

NUMBER: OF SEQ ID NOS: 24

SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                  1; Mismatches
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Publication No. US/20040072995A1
GENERAL INFORMATION:
                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                        Query Match
Best Local Similarity 99.6%;
Matches 238; Conservative
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US-09-887-784-2
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LENGTH: 239
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US-10-296-953-2
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SEQ ID NO 32
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61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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Pred. No. 3.1e-123;
APPLICANT: BJORN, SARA P.

APPLICANT: PAGLIARO, LEN

JAPLICANT: THAGTURP, OLE

TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS
FILE REFERENCE: PL0095
CURRENT APPLICATION NUMBER: US/10/296,953
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: PA 2000 00953
PRIOR FILING DATE: 2000-06-19
PRIOR FILING DATE: 2000-06-19
PRIOR PILING DATE: 2000-06-10
PRIOR PILING DATE: 2001-05-10
PRIOR PLING DATE: 2001-05-10
PRIOR PLING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: PA 2001 00739
PRIOR PILING DATE: 2001-05-10
PRIOR PILING DATE: 2001-05-10
SOFTWARE: PACHELIAND VUMBER: PA 2001 00739
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PACHELIN VET: 2.1

SEQ ID NO 2
LENGTH: 239
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Patent No. US20020083488A1
GENERAL INFORMATION:
APPLICANT: Miyawaki, Atsushi
APPLICANT: Sawano, Asako
TITLE OF INVENTION: METHOD FOR MUTAGENESIS
FILE REFERENCE: 11283-012001
CURRENT FILING DATE: 2001-08-02
PRIOR PILING DATE: 2000-04
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO. 539
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Best Local Similarity 98.7%;
Matches 236; Conservative
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US-10-296-953-2
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US-09-920-922-2
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Indels

Score 1261; DB 10; Pred. No. 3.1e-123; 2; Mismatches 1;

Length 239;

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1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT

1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT

180

121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNYYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180

VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA

121

181 DHYQQNTFIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLIGFVTAAGITLGMDELYK 239 

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Query Match
Best Local Similarity 98.7%;
Matches 236; Conservative
; ORGANISM: Aequorea victoria
US-09-866-538-4
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Sequence 4. Application US/09999745

GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: Taien, Roger Y.
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
TITLE REFERENCE: RECEN1470-1
CURRENT APPLICATION NUMBER: US/09/999,745
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 09/316,920
PRIOR APPLICATION NUMBER: 09/316,920
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin version 3.0
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Pred. No. 3.1e-123;
2; Mismatches 1;
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Best Local Similarity 98.7%;
Matches 236; Conservative
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ORGANISM: Aequorea victoria
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LENGTH: 239
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OTHER INFORMATION: Aequorea victoria green fluorescent protein modified as described OTHER INFORMATION: in specification
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Sequence 2, Application US/09797496B

Bublication No. US20030049597A1

GENERAL INFORMATION:
APPLICANT: Simon, Sanford M.
APPLICANT: Chen, Yu

TITLE OF INVENTION: Chimeric Fluorescent Enzymes and Uses Thereof FILE REFERENCE: 600-1-267

CURRENT APPLICANTION NUMBER: US/09/797,496B

CURRENT FILING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin version 3.1

SEQ ID NO 2
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; Publication No. US20030170911A1
; GENERAL INFORMATION:
; APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 99.0%; Score 1261; DB 10;
Best Local Similarity 98.7%; Pred. No. 3.1e-123;
Matches 236; Conservative 2; Mismatches 1;
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ORGANISM: Artificial Sequence
US-09-797-496B-2
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US-09-794-308-4
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APPLICANT: REGENTA OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TSIEN, ROGER
APPLICANT: TSIEN, ROGER
TITLE OF CAMPBELL ROBER
TITLE OF THE TREENING FLUORESCENT PROTEINS
FILE REFERENCE: REGENIS30-2
CURRENT APPLICATION NUMBER: US/09/866,538
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN Version 3.0
SEQ ID NO 4
LENGTH: 239
TYPE: PRI

Sequence 4, Application US/09866538 Publication No. US20030032088A1 GENERAL INFORMATION:

RESULT 10 US-09-866-538-4

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181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLIGFVTAAGITLGMDELYK 239
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                                                                                                                                                                Sequence 3, Application US/10457982; Publication No. US20030212265A1; GENERAL INFORMATION:
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Matches 236, Conservative
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NAME/KEY: VARIANT
LOCATION: (0)...(0)
OTHER INFORMATION: EGFP
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Fublication No. US20030186229A1

GENERAL INFORMATION:

APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA

APPLICANT: TING, Alice

APPLICANT: TING, Alice

APPLICANT: ZHANG, Jin

TITLE OF INVANTION: EMISSION RATIOMETRIC INDICATORS OF PHOSPHORYLATION

FILE REFERENCE: REGENISSO

CURRENT APPLICATION NUMBER: US/09/865,291

CURRENT FILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 42

SOFTWARE: Patentin version 3.0

SEQ ID NO 4
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APPLICANT: TSIEN, ROGER
APPLICANT: ZACHARIAS, David
APPLICANT: BAIRD, Geoffrey
TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
FILE REPERENCE: REGENISSO
CURRENT APPLICATION NUMBER: US/09/794,308
CURRENT FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 25
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                                                                                                                                                                                       PatentIn version 3.0
                                                                                                                                                                                                                                                                       ; ORGANISM: Aequorea victoria
US-09-794-308-4
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181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 239
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; Sequence 13, Application US/10121258
; Publication No. US20030059835A1
; GENERAL INFORMATION:
    APPLICANT: Tabin, Roger
; APPLICANT: Campbell, Robert
; APPLICANT: Campbell, Robert
; TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
; TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME
; TITLE REFERENCE: UCO93.1CP2CP1
; CURRENT APPLICATION NUMBER: US/10/121,258
; CURRENT FILING DATE: 2002-04-10
; PRIOR FILING DATE: 2001-02-26
; PRIOR FILING DATE: 2001-05-24
; FRIOR FILING DATE: 2001-05-24
                                                                                                                                                                                                                                                                                           GAPPLICANT: Tsien, Roger Y.

APPLICANT: Tsien, Roger Y.

APPLICANT: Miyawaki, Atsushi
APPLICANT: Llopis, Juan
APPLICANT: Machter, Rebekka M.
APPLICANT: Wachter, Rebekka M.
APPLICANT: Wachter, Rebekka M.
APPLICANT: Remington, S. James
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
TILE REFERENCE: 0725/071001
CURRENT APPLICATION NUMBER: US/10/457,982
CURRENT APPLICATION NUMBER: US/09/602,641
PRIOR FILING DATE: 2003-06-09
PRIOR FILING DATE: 1998-10-13
PRIOR PRICATION NUMBER: 09/172,063
PRIOR PRICATION NUMBER: 09/172,063
PRIOR SPLICATION NUMBER: 1998-10-13
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 239
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121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                                                                                              Query Match

99.0%; Score 1261; DB 14; Length 239;
Best Local Similarity 98.7%; Pred. No. 3.1e-123;
Matches 236; Conservative 2; Mismatches 1; Indels 0
) NUMBER CF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FATURE:
; OTHER INFORMATION: Enhanced Green Fluorescent Protein (EGFP)
US-10-121-258-13
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Search completed: June 21, 2004, 16:09:28 Job time : 34.7778 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

June 21, 2004, 15:46:00 ; Search time 10.3333 Seconds Run on:

(without alignments) 2224.817 Million cell updates/sec

US-09-887-784-222I

1274
1 WVSKGEBLFTGVVPILVBLD......VLiGFVTAAGITLGMDBLYK 239 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	green-fluorescent	hypothetical prote		u		Ē	protective surface	protective surface	iron-sulfur cofact	leucyl-tRNA synthe	cellulase (EC 3.2.	DNA-directed DNA p	hypothetical prote	dihydrolipoamide d	tRNA (uracil-5-)-m	DNA-directed DNA p	inter-alpha-trypsi	hypothetical prote	S-layer protein pr	hypothetical prote	u	imidazoleglycerol-	photosystem II chl	DNA-directed DNA p	IgA Fc receptor pr		ptogamin	nitrogenase (EC 1.	neuraminidase, pro
SUMMAKIES	ID	JQ1514	H72228	H64102	T06586	E82590	D83917	JC4078	F64102	E70390	AC0582	S29043	A36028	D71614	140794	G81355	ЭДОГНН	JC5576	AD2052	JC4930	C97354	A99552	E84941	T06936	JDVLD	A60234	FCSOAG	JH0414	NICLMA	G95153
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oh	Query Match	97.3	8.2	•	7.1	7.0	6.9			6.9	•	6.9	6.9		6.8	6.8	6.7	6.7	6.7	6.7	9.9		9.9	٠	9.9		•		6.5	•
	Score	1239	104	91.5	90	89.5	88.5	88.5	88.5	87.5	•	87.5	87.5	87.5	87	98	85.5		82	82	84.5	•	84	84	83.5	83.5	83.5	83	82.5	82.5
	Result No.	-	7	m	4	2	9	7	ω	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote hypothetical prote	carboxy-terminal p	proprotein convert	alpha-amylase homo	lipoxygenase (EC 1	water-stress-induc	synergohymenotropi	hypothetical prote	hypothetical prote	hypothetical prote		- 2			hypothetical prote
D90946 H85794	A41798	KXRTC1	T39539	T11852	S53488	S68225	S76940	T27856	T13674	T13673	SYECL	H90713	D85564	G86643
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682 682	682	752	774	865	263	310	355	471	734	743	860	860	860	1983
6.4 4.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.3	6.3	6.3	6.3
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# ALIGNMENTS

	RESULT 1
	JQ1514
	green-tluorescent proctein (validated) - hydromedusa (Aequorea Victoria) C.condios: homiorea victoria
	C.japetares Aequoted victoria C.japetares Agrangued Hagmience revision 03-Dec-1999 #fext.change 23-Mar-2001
	C; Accession: JS0692; JQ1514; PQ0335; S48693; S51330; S51331
	R; Prasher, D.C.; Eckenrode, V.K.; Ward, W.W.; Prendergast, F.G.; Cormier, M.J.
	gene 111, 229-233, 1992
	A;iltie: Filmary Structure of the Aequorea victofia green-filmorescent procein. A;Reference number: JQ1514; MUID:92175527; PMID:1347277
	A;Accession: JS0692
	A Molecule UVDe: DNA
	A;Cross-references: GB:M62654; NID:q55662; PIDN:AAA27722.1; PID:q155663
	A;Accession: JQ1514
	A; Molecule type: mRNA
	A; WeBildues: 1-99, F', 101-140, L', L', 144-7418', V', 220-238 e, KMAD. B. Cross-references: CB MK2543' NID. A15460, PINN. RAA27721 1: PID. 0155661
	A; Molecule type: protein
	A;Residues: 46-64;74-122;132-151;154-183;185-200 <pra3></pra3>
	Rinouye, S.; Tsuji, F.I.
	FEBS Lett. 351, 211-214, 1994
	A;Title: Evidence for redox forms of the Aequorea green fluorescent protein.
	A;Kererence number: S48693; MULD:943644/0; PMLD:8082/6/
	A. ACCESSION STRONG A. ACCESSION STRONG A. ACCESSION STRONG A. C. A. A. A. A. A. A. A. A. A. A. A. A. A.
	A.V.Cacus, presimilary A.W.Social Frys. mbnz
	A.Residues: 1-24, 'O'. 26-156,'P',158-171,'K',173-238 <ino></ino>
	A; Cross-references: GB:L29345; NID:g606383; PIDN:AAA58246.1; PID:g606384
	R,Watkins, J.N.; Campbell, A.K.
	submitted to the EMBL Data Library, January 1995
	A,Reference number: S51330
	A; Accession: S51330
	A; Molecule type: mRNA
	A;KESIQUES: 1-12, V, 1-2-24, V, 20-44, N, 40-125, G, 1-35-120, F, 1-35-121, R, 1-13-221, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13-121, R, 1-13
	Astronomental source: clone dipl
	A; Accession: S51331
	A; Molecule type: mRNA
	A;Residues: 1-24,'Q',26-29,'R',31-83,'L',85-153,'G',155-156,'P',158-171,'K',173-208,'Q','
	A; Cross references: EMB1: X83960; NID: 9634010; PIDN: CAAS8790:1; PID: 9634011
	A) EXPERIMENTED SOURCE: CLONE GIP.  D.Vang F. Moss T. C. Dhilling It C.N.
٠	submitted to the Brookhaven Protein Data Bank, August 1996
	A;Reference number: A65692; PDB:1GFL
	A; Contents: annotation; X-ray crystallography, 1.9 angetroms, residues 'A', 2-79,'R', 81-95
	A, Note: engineered sequence based on J01514, cloned and expressed in Bacherichia Coli
	K; Yang, F; Moss, Let, Fullips U., G.N. Nat Richechnol 14 1246-1251 1996
	A.Title: The molecular structure of green fluorescent protein.
_	A; Reference number: A58953; MUID:98294543; PMID:9631087

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GVKSPINADPN 472
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Best Local S:
Matches 46;
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A,Accession: H7228
A,Actatus: Frelimary
A,Molecule type: DNA
A,Residues: 1-785 <ARN>
A,Cross-references: GB.AE001806; GB:AE000512; NID:g4982196; PIDN:AAD36691.1; PID:g498219
C,Genetics:
A,Gene: TM1624
A;Contents: annotation; X-ray crystallography, 1.9 angstroms
C;Comment: This protein is excited by the photoprotein aequorin (see PIR:AQJFNV) emittin
C;Comment: The chromophore of this protein is formed by modification of Ser-dehydro-Tyr-C;Genetics:
A;Gene: GFF
A;Introns: 69/3; 167/3
A;Introns: 69/3; 167/3
C;Superfamily: green-fluorescent protein
C;Keywords: chromoprotein; luminescence
F;65-67/Crcss-link: 5-imidazolinone (Ser-Gly) #status experimental
F;66/Modified site: dehydrotyrosine (Tyr) #status experimental
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chardson, D.;
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: H72228
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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hypothetical protein TM1624 - Thermotoga maritima (strain MSB8)
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Pred. No. 3.2e-96;
5; Mismatches 3;
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30; Conservative
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Best Local Similarity
Matches 46; Conserv
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Best Local S:
Matches 230
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Cispecies: Pisum sativum (garden pea)
Cispecies: Pisum sativum (garden pea)
Cipate: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
Cipate: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
Cipate: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
Cipate: 23-Apr-1999 #sequence_revision of A. Ohshima, K.
Submitted to the EMBL Data Library, June 1996
A. Description: Identification of a novel family of DNA-binding proteins with two AT-hook
A. Description: Identification of a novel family of DNA-binding proteins with two AT-hook
A. A. A. Secsion: To658
A. A. Secsion: To658
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     leucine-tRNA ligase (EC 6.1.1.4) - Haemophilus influenzae (strain Rd KW20) NiAlternate names: leucyl-tRNA synthetase (Species: Haemophilus influenzae (Species: Haemophilus influenzae C; Species: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 03-Jun-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 TTGKLPVPWPTLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKD----
Haemophilus influenzae (strain Rd KW20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: leucine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.1%; Score 90; DB 2; Length 632; Best Local Similarity 23.3%; Pred. No. 12; Matches 49; Conservative 26; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 DEEIDLTKQAFVEHGKLVNSDEFDGKNF--DGAFNG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.2%; Score 91.5; I
Local Similarity 24.1%; Pred. No. 14;
ies 46; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-binding protein PD2 - garden pea
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איז די מאייסטר עד יייישייחרות להואסטיים איז איים הייים איז די רושיים אוז איז איז איז איז איז איז איז איז איז אי	
50t 70t	Kidaduli, n.; Nakabule, n.; takaki, i.; Maello, s.; Sabaki, k.; Mabui, N.; Fuji, F.; Eitan Nucleic Acids Res . 28, 4317-4331, 2000 N.Titlo. Complete concess of the alkalishilis hastarium basillus halodurane and s
468 LKGIEPTDNSTLLDEKFENALGNKILKEISNPRHDVESANHSTHNKOVTVSHQKAIETNN	A. Reference number: A83650; MUID:20512582; PMID:11058132 A. Accession: D83917
	A;Status: preliminary A;Wolecule type: DNA
Db 528 QSQVEDVAKKNIQDDSKPSEESLHKADKYR 557	
RESULT 5 882590	C;Genetics: A;Gene: BH2140 C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B
leucy1-tRNA synthetase XF2176 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Species: Xylella fastidiosa C;Species: Xylella fastidiosa	
C;Accession: B82590 R;anonymous, The Xvlella fastidiosa Consortium of the Organization for Nucleotide Semier	Matches 53; Conservative 37; Mismatc
Nature 406, 151-157, 2000 A/Title: The genome sequence of the plant pathogen Xylella fastidiosa. A.Paference number: A87515. MITEL 20165117. DMID. 1041014	Qy 22 DVNGHKFSVSGEGEGDATYGKLTLKFI
A; Note: for a complete list of authors see reference number A59328 below A; Accession: E82590	Qy 60 TLVTTLSYGVQCFSRYPDHMKQHDFPKSAMPEGYVQERTIFFKDDG
A;Status: preliminary A;Molecule type: DNA	Db 123
Ajresidues: 1-88/ SIM> Ajross-references: GB:AE004031; GB:AE003849; NID:g9107309; PIDN:AAF84975.1; GSPDB:GN001 A:Experimental source: strain 9a5c	OY 106NYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADK 157
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H	Db 183 NFNVETLSERLREAAFLLKGLKIELVDL
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000	δ
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigh	Db 242 VFF
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B. A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F., M.; Miracca, B.C.; Miyaki, C.Y.; P.G.; Mines I.R.; Oliveira, M.C.; de Oliveira, M.C.; de Oliveira, R.C.; Dialmieri, D.A.	Oy 213 NE 214 Dh 295 NE 296 Dh 295 NE 296
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir	
M.; Isunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A;Reference number: A59328	RESULT 7 JC4078
A; Contents: annotation C; Genetics:	protective surface antigen D-15 precursor - Haemophilus influenzae (type b) C.Species: Haemophilus influenzae
A;Gene: XF2176 C;Superfamily: leucine-tRNA ligase	AlVariety: type b C:Date: 30-0101-1995 #sequence_revision 14-Jul-1995 #text_change 29-Sep-1999
Query Match 7.0%; Score 89.5; DB 2; Length 887; Best Local Similarity 22.2%; Pred. No. 21:	C;Accession: 00-47/0 R;Flack, 15. Loosmore, S.; Chong, P.; Thomas, W.R. Gene 156, 97-99, 1995
ative 29; Mismatches 68; Indels 57; Gaps 10;	A/Title: The sequencing of the 80-kDa D15 protective surface antigen of Haemophilus influate A.Reference number: JC4078; MJID:95255676; PMID:7737523
Qy 50 TTGKLPVPWPTLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNY 107	A;Accession: JC4078 A;Modecule type: DNA A;Modecule type: DNA
108KTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNVNSHNVYI 153	A.Cross-references: GB:113961; NID:g537447; PIDN:AAA85645.1; PID:g537448 A.Experimental source: type b
	C,Superfamily: protective surface antigen D-15 C,Keywords: surface antigen
199	F.1-19/Domain: signal sequence #status predicted <sig> F;20-797/Product: protective surface antigen D-15 #status predicted <wat></wat></sig>
Db 430RQGRGQRRVNYRLRDWGVSRQRYWGCPIPVIYCPTCGAVPVPEDQLPVILPEN 482 Qy 200 -HYLSTQSALSKDPNEKR 216	Query Match 6.9%; Score 88.5; DB 2; Length 797; Best Local Similarity 21.9%; Pred. No. 22; Matches 48; Conservative 30; Mismatches 78; Indels 63; Gaps 11;
:     :   Db 483 VAFSGTGSPIKTDPEWRK 500	65 LSYGVQCFSRYPDHMKQHDFRSAMPEGYVQERTI :   :   :   : :   : : :   : : : : : :
RESULT 6	
D83917 DNA topoisomerase IV subunit B BH2140 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans	Qy 100 FFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNS 148
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C;Accession: D83917	Qy 149 HNVYIMADKQK-NGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLL 196

Query Match Best Local Similarity 25.4%; Score 87.5; DB 2; Length 370; Best Local Similarity 25.4%; Pred. No. 9.9; Matches 49; Conservative 30; Mismatches 91; Indels 23; Gaps 8;  Qy 4 KGEELFTGVVPILVELDGDNOGHKE-SVSGEGEGDATYGKLTLKFICT 50 Db 164 KGVPLLTDAVQAIGKIPIELKNISYATFSGHKFHAIKGSGFLYISDEANYEPLIVGGGQE 223  Qy 51 TGKLPVPWPTLYTLSYGVQCFSRYPDHMKQ-HDFFKSAMPEGYVQETIFFKDD 104 Db 224 NGKRSGTENVVGILSLAKALEIIVSNFSRYQEQLKKIRDLEA-LPDAQIVGKDA 282	Man, Y	C; Date: 09-NOV-Z001 #Sequence_revision 09-NOV-Z001 #Text_Canage is-NOV-Z002 C; Accession: ACOS82 R; Parkhill, J: Dougan, G: James, K.D:; Thomson, N.R.; Pickard, D:; Wain, J:, Churcher, K.; Moule, S: O'Gaora, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S: Moule, S: O'Gaora, P.  Nature 413, 848-852, 2001 A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; A; Cersion: A; C: Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Reference number: ABOS02; MUID:21534947; PMID:11677608 A; Reference number: ABOS02; MUID:21534947; PMID:11677608 A; Residues: 1-860 *PAR> A; Residues: 1-860 *PAR> A; Conser-references: GB:AL513382; PIDN:CAD05125.1; PID:g16501899; GSPDB:GN00176 C; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A;	Qy 50 TTGKLPVPWPTLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKT 109  Db 314 TGEEIPV-WAANFVLMEYGTGAVMAVPGH-DQRD-YEFASKYGTTIKPVILAADGSEPDL 370  Qy 110 RAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYSHNYYIMADKQKGIKKVNFKIR 169  Db 371 SEQALTEKGVLFKSGEFBCALFRAFNAIADKLARGVGGEKKVNYKLR 418  Qy 170 HNIEDSCALSKDD 212
Db 543 RNLYIQSMKFKGNGIKTNDFDFSFGMYNSLNRGYFPTKGVKASLG-GRVTI  Qy 197 PDNHYLSTQSALSKDPNBKRDHMVLIGFVTAAGITLG 233  Db 594 PGSDNKYYKLSADVQGFYPLDRDHLWVVSAKASAGYANG 632  RESULT 8  RESULT 8  F64102  protective surface antigen D-15 - Haemophilus influenzae (strain Rd KWZ0)  C; Species: Haemophilus influenzae  C; Date: 18 - Aug-1995 #sequence_revision 18 - Aug-1995 #text_change 18 - Sep-1998	Eigheischmann, R.D.; Adame, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlava, G.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; weidm, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Puhrmann, J.L.; Geoghagen, N.S.; Science 269, 496-512, 1995 A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Ven A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A6400; MUID:95350630; PMID:7542800 A;Reference number: acid sequence not shown; translation not shown A;Residues: 1-808 <tigr> A;Residues: 1-808 <tigr> A;Cossereferences: GB:L42023; TIGR:HI0917 C;Superfamily: protective surface antigen D-15 C;Keywords: surface antigen</tigr></tigr>	Ouery Match Best Local Similarity 21.9%; Pred. No. 23; Matches 48; Conservative 30; Mismatches 78; Indels 63; Gaps Qy 65 LSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQE	RESULT 9 E70390 iron-sulfur cofactor synthesis protein nifs - Aquifex aeolicus N;Contains: L-cysteine sulfurtransferase (EC 2.8.1) C;Species: Aquifex aeolicus C;Species: Aquifex aeolicus C;Species: Aquifex aeolicus C;Date: 08-May-1998 #text_change 07-Dec-1999 C;Accession: E70390 R;Deckert, 3:, Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graha: V;Deckert, 353-358, 1998 A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeoli: A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: E7039 A;Accession: E7039 A;Accession: E7039 A;Accession: A000; MUID:98196666; PMID:9537320 A;Accession: DNA A;Residues: 1-370 <aqf> A;Cross-references: GB:AE000720; NID:g2983529; PIDN:AAC07111.1; PID:g2983536; A;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Superfamily: nitrogen fixation protein nifs C;Superfamily: nitrogen fixation protein nifs C;Superfamily: nitrogen fixation protein nifs C;Superfamily: hyridoxal phosphate; sulfurtransferase C;Keywords: phosphoprotein; pyridoxal phosphate; sulfurtransferase F;195/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted</aqf>

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A;Molecule type: DNA
A;Residues: 1-2222 <SEW>
A;Cross-references: EMBL:271538; NID:g1302316; PIDN:CAA96169.1; PID:g1302317; GSPDB:GNO00
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                                                                                                                                                                                                                                                                                                                                                            A, Experimental source: strain S288C
R;Sen-Gupta, M.; Lyck, R.; Fleig, U.; Niedenthal, R.K.; Hegemann, J.H.
Yeast 12, 505-514, 1996
A;Title: The sequence of a 24 152 bp segment from the left arm of chromosome XIV from Sac
A;Reference number: S65111; MUID:96310631; PMID:8740425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein PFB0460c - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Accession: D71614
R;Gardner, M.J; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; Pertea, M.; Salzbergy, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.; Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Readus: 1-221 (SEF)
A;Cross-references: EMBL:X22494; NID:q1045236; PIDN:CAA63235.1; PID:q1045247
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 FFKDDGNYKTR--AEVKFEGDTLVNR-----IELKGIDFKEDGNILGHKLEYNYN 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 VQERTIFFKD--DGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYN--YNSH 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 LKKETILCKDIKSGSNDPMDEISLFKDDMVDDKELK--DFEKSSLKIKNKEVYNFIYNKM 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 NVYIMADKOKNGIKVNFKIRHNIEDGSVOLADHYQQNTPIGDGPVLLPDNHYLSTQSALS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66
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A;Molecule type: DNA
A;Residues: 1-2573 <GAR>
R.Sen-Gupta, M.; Lyck, R.; Niedenthal, R.K.; Fleig, U.N.; Hegemann, J.H. submitted to the Protein Sequence Database, April 1996
A;Reference number: S63235
A;Moleonite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 LPVPWP-TLVTTLSYGVQCFSRYPDHM-----KQHDFFKSAMPEGYV----QERTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            883 LPKSFPETYFFTLENGKKLYLSYPCSMLNYRVHQKFTNHQYQELKDPLNYIYETHSENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: DNA-directed DNA polymerase II
C;Keywords: DNA binding; nucleotidyltransferase; nucleus; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 6.9%; Score 87.5; DB 1; Length 2222; Local Similarity 28.2%; Pred. No. 1e+02; nes 37; Conservative 14; Mismatches 49; Indels 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2573;
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Best Local Similarity 26.2%; Pred. No. 1.2e+02;
Matches 34; Conservative 30; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics:
A;Gene: SGD:POL2; DUN2; MIPS:YNL262w
A;Cross-references: SGD:SO005206; MIPS:YNL262w
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Best Local S:
Matches 37
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A; Rocession: S29043
A; Residues: 1.941 < CZA
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A; Ribitai, T.; Yamane, T.; Hidaka, T.; Kuyama, K.; Suzuki, A.; Ashida, T.; Ozaki, K.; Itc
C; Biochem. 122; 683-685; 193
A; Title: Crystallization and preliminary X-ray analysis of a truncated family A alkaline
A; Reference number: PC4404; MUID: 98060488; PMID: 9399567
A; Reference number: PC4404
A; Rolecule type: protein
A; Residues: 228-584 < SHI>
A; Residues: 228-584 < SHI>
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MA-directed DNA polymerase (EC 2.7.7.7) II catalytic chain - yeast (Saccharomyces cerew NyAlternate names: DNA-directed DNA polymerase II chain A; protein N0825; protein YNL262 C; Species: Saccharomyces cerevisiae
C; Species: Saccharomyces cerevisiae
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C; Accession: A5028; B36029; S63235; S65121
R; Morrison, A.; Araki, H.; Clark, A.B.; Hamatake, R.K.; Sugino, A.
Cell 62, 1143-1151, 1990
A; Title: A third essential DNA polymerase in Saccharomyces cerevisiae.
A; Reference number: A36028; MUID:90381771; PMID:2169349
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A, Residues: 1-222 < MOR>
A, Residues: 1-222 < MOR>
A, Cross-references: GB:M60416; GB:M36724; NID:g171408; PIDN:AAA88711.1; PID:g171409
A, Accession: B36028
A, Molecule type: protein
A, Residues: 1214-1214, X', 1218-1221 < MO2>
B, Rolecule type: Drotein
A, Residues: 1214-1214, X', 1218-1221 < MO2>
B, Ren-Gupta, M.; Lyck, R.; Pleig, U.; Niedenthal, R.N.; Hegemann, J.M.
B, Sen-Gupta, M.; Lyck, R.; Pleig, U.; Niedenthal, R.N.; Hegemann, J.M.
A, Description: The sequence of a 24152 bp segment from the left arm of chromosome XIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       319
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                                                              A; Reference number: $29043; MUID: 91037937; PMID: 2230718
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1 Similarity 20.3%; Pred. No. 33;
49; Conservative 33; Mismatches
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A;Molecule type: DNA
A;Residues: 1-2221 <SEN>
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             C;Genetics:
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2. Bacteriol. 176, 3614-3630, 1994
A;Title: Biochemical and molecular characterization of the Clostridium magnum acetoin de
A;Reference number: 140789; MUID:94266715; PMID:8206840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Description: catalyzes the oxidation of dihydrolipoamide to lipoamide using NAD A; Pathway; acetoin dehydrogenase enzyme system C; Superfamily: Alcaligenes dihydrolipoamide dehydrogenase; dihydrolipoamide dehydrogenase; Keywords: PAD; flavoprotein; lipoamide; NAD; oxidoreductase; redox-active disulfide F;5-77/Domain: lipoyl/biotin-binding homology <LPB> clps, 77/Fomain: beta-alpha-beta RAD nucleotide-binding fold F;112-561/Domain: dihydrolipoamide dehydrogenase homology <DLD> F;287-315/Region: beta-alpha-beta NAD nucleotide-binding fold
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C.Species: Campylobacter jejuni
C.Species: Campylobacter jejuni
C.Species: Campylobacter jejuni
C.Species: Jandar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C.Accession: G81355
R.Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillint
R.Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.W.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A,Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp.
A,Reference number: A81250, MUID:20150912; PMID:10688204
A,Recession: G81355
A,Status: p:eliminary
A,Residues: 1-357 < PAR>
A,Residues: 1-357 < PAR>
A,Residues: 1-357 < PAR>
A,COSS-references: GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB73096.1; PID:g696827
A,Experimental source: serotype O2, strain.NCTC 11168
                                                                                                                                                                                                                                                                                          dihydrolipoamide dehydrogenase (EC 1.8.1.4) [validated] - Clostridium magnum N;Alternate names: 2-oxoglutarate dehydrogenase complex chain E3; acetoin dehydrogenase hydrogenase complex chain E3; S-complex 50K chain C;Species: Clostridium magnum C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000 C;Accession: I40794
184 NLHIKENKKKDEKEKKNKIHNNDENNNM----IYYKNI---DKTHYILDNNVVHILNDIN 236
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A;Molecule type: DNA
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--GNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIE 173
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                                                                                               Query Match 6.8%; Score 86; DB 2; Length 357; Best Local Similarity 24.8%; Pred. No. 13; Matches 30; Conservative 18; Mismatches 39; Indels
                                                                                                                                                                                                                                     80 KOHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKF--EGDTLV---
A;Gene: trmA; Cj0831c
C;Keywords: methyltransferase; S-adenosylmethionine
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

June 21, 2004, 15:42:24; Search time 6.44444 Seconds (without alignments) 1931.085 Million cell updates/sec Run on:

US-09-887-784-222I Title:

1 MVSKGEELFTGVVPILVELD........VLiGFVTAAGITLGMDELYK BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Perfect score: Sequence:

239

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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### ALIGNMENTS

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Rouwendal G.J.A., Mendes O., Wolbert E.J.H., de Boer A.D.; "Enhanced expression in tobacco of the gene encoding green fluorescent protein by modification of its codon usage."; plant Mol. Biol. 33:989-999(1997).
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                                                                                                                                                                                                          Aequorea victoria (Jellyfish).
Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=6100;
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lcrystal structure of the Aequorea victoria green fluorescent
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MEDLINE-92175527; PubMed=1347277;
Prasher D.C., Eckenrode V.K., Ward W.W., Prendergast F.G.,
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Inouye S., Tsuji F.I.;
Agguorea green fluorescent protein. Expression of the ger
fluorescence characteristics of the recombinant protein.";
FEBS Lett. 341:277-280(1994).
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Ormoe M., Cubitt A.B., Kallio K., Gross L.A., Tsien R.Y.,
Remington S.J.;
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"The molecular structure of green fluorescent protein.";
Nat. Biotechnol. 14:1246-1251(1996).
GFP_AEQVI STANDARD; PRT; 238 AA. P42212; Q17104; Q27903; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Green fluorescent protein.
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green-fluorescent protein.";
Biochemistry 32:1212-1218(1993).
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5-imidazolinone (Ser-Gly).
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PDB; ZEMO; 20-AUG-97.
InterPro; IPR009017; GFP_like.
InterPro; IPR000786; Green_fl_protein.
Pfam; PF01353; GFP; 1.
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ProDom; PD013756; Green fl protein; 1.
Luminescence; 3D-structure.
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-i- BIOTECHNOLOGY: Has become a useful and ubiquitous tool for making chimeric proteins of GFP linked to other proteins where it functions as a fluorescent protein tags GFP colerates N-and C-terminal fusion to a broad variety of proteins. It has been expressed in bacteria, yeast, slime mold, plants, Drosophila, zebrafish, and in mammalian cells. As a noninvasive fluorescent marker in living cells, it allows for a wide range of applications where it may function as a cell lineage tracer, reporter of gene expression, or as a measure of protein-protein interactions.

NOTE_ISSUE (1) of June 2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                 K-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF MUTANT WITH YELLOW EMMISSION
                                                                                                                                                                       MEDLINE=98455509; PubMed=9782051;
Wachter R.M., Elsliger M.A., Kallio K., Hanson G.T., Remington S.J.;
"Structural basis of spectral shifts in the yellow-emission variants
of green fluorescent protein.";
Structure 6:1267-1277 (1998).
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                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
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104 DGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADK-QKNGI 162

181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238

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                                                                                                            202
365 DEEIDLTKQAFVEHGKLVNSDEFDGKNF--DGAFNG-------IADKLEKLGV 408
                                                                                                                                                                            Alvarenga R., Alvee L.O., Arruda P., Abreu F.A., Acencio M., Alvaelnuk-20365717; PubMed=10910347; Baia G.S., Baptista C.S., Alvaelnuk A. Alvee L.M.C., Arruda P., Abreu F.A., Acencio M., Alvaen L.M.C., Arruda P., Abreu F.A., Baiaco B. M.B.; Barros M.H., Bonacocrais E.D., Bordin S., Bove J.M., Briones M.R.S., Barros M.H., Colombo C., Costa M.C.R., Costa M.C.R., Costanco C.M., Colombo C., Costa M.C.R., Costance C.M., Couthol L.L., Cristofani M.Dias-Neco E. Docena C., El-Dorry H., Ra Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Goldman G.H., Goldman M.H.S., Gomes S.L., Ritajima J.P., Ra Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Ritajima J.P., Raieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., Ra Lemos B.C.M., Mardiac A.M.B.N., Madeira H.M.F., Marino C.L., Ra Lemos B.C.M., Martins E.A.L., Martins E.M.F., Martino C.L., Martins E.A.L., Martins E.M.F., Martino C.L., Martins E.C.M., Nacina A.M.B., Madeira H.M.F., Marino C.L., Nobreda M.A., Nascimento A.L.T.O., Netto L.E.S., Abaris A.M. R. Acolon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Abaris A.M. R. Acolon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Abaris A.M. R. Acolon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Abaris A.M. Acolon D.H., Nagai M.A., Nascimento A.M., Allada S.I.Va A.M. Acolon D.H., Nascimento A.B., Salva M.A., Acolon D.H., Nascimento A.B., Salva M.A., Martina G.A.G., Pereira H.A. Jr., Sawasaki H.E., Acolon D.H., Nascimento A.B., Silva M.A. Jr., Acolon D.H., Nascimento A.B., Salva M.A., Martina B.H., Van Sluya M.A., Variovski-Almeida S., Vettore A.L., Acago M.H., Rago M.B., Salva M.L., Sawasaki H.E., Ragoma Salva M.P., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva M.A., Salva 
                                                                                                            163 ---KVNFKIRH------NIEDGSVQLADHYQQNTPIGDGPVLLPDNHYL-
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-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
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                                                                                                                                                                                                                                                                                                                   203 STOSALSKDPN 213
                                                                                                                                                                                                                                                                                                                                                                                                                          462 GVKSPINADPN 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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lisk; hl03-/; -.
InterPro; IPR00184; Bac_surfAg_D15.
Pfam; PF01103; Bac_surface_Ag; I.
Antigen; Outer membrane; Sīgnal; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                            78;
                                                                                                                                                                                                                                                                                                                                     Local Similarity 21.9%; Pred. No. 11; es 48; Conservative 30; Mismatches
     removed.
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modified and this statement is not remorentities requires a license agreement (( or send an email to license@isb-sib.ch)
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STRAIN-Serotype B;
MEDLINE-95255676; PubMed=7737523;
                                                                                               EMBL; U32773; AAC22575.1; -. TIGR; HI0917; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAEIN
                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                    Query Match
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P46024;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.1 TNEQLEV-WVANFVLMAYGTGAVMAVFGHDQRDQEF--ANKYGLPIRQVIALKEPKNQDE 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----KTRAEVKFEGDTLVNRIBLKGIDFKEDGNILGHKLEYNYNSHNVYI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.54 MADKQKNG-IKVNFKIRHNIEDGSVQLADHYQQNTPI-------GDGPVLLPDN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 TIGKLPVPWPTLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNY--
                                                                                          Pfam; PF00133; tRNA-synt_1; 1.
PRINTS; PR00965; TRNASYNTHLEU.
TIGRPAMS; TIGR00396; leug. dect; 1.
PROSTIE; PS00178; AA TRNA_LIGASE I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        378 STWEPDVWRDWYADKTR---EFE---LINSAEFDGLDYQDAFEVLAERFE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;

Pleistchmann R.D., Addam M.D., White O., Clayton R.A., Kirkness E.F.,

Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidmen J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Wienerkeck T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine I.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SIMILARITY: Belongs to the surface antigen D15 family.
                                                                                                                                                                                                                                                                                                                                                                                                              68; Indels
                                                                                                                                                                                                                                                                                                                    9FDCCB992092919E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NVV-1995 (Rel. 32, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Protective surface antigen D15 precursor (80 kDa D15 (D-15-Ag) (Outer membrane protein D15).
                                                                                                                                                                                                                                                                    "KMSKS" REGION.
ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                            7.0%; Score 89.5; Di
22.2%; Pred. No. 10;
ve 29; Mismatches
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"KMSKS" REGIO
InterPro; IPR002302; Leu-tRNAsyntla.
InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_l.
InterPro; IPR009008; ValRs_lieRs_edit.
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                                                                                                                                                                                                                                                                                                                    99796 MW;
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641
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                                                                                                                                                                                                                                                                                        640 6
879 AA;
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                                                                                                                                                                                                                       Complete proteome.
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              543 RNLYIQSMKFKGNGIKTN-----DPDFSFGWNYNSLNRGYFPTKGVKASLG-GRVTI 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            427 IGYGTESGISYQASVKQDNFLGTGAAVSIAGTKNDYGTSVNLGYTEPYFTKDGVSLGGNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 FFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNI---LGH-----KLEYNYNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   487 FFENYDNSKSDTSSNYKRTTYGSNVTL-GFPVNENNSYYVGLGHTYNKISNFALEYN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63;
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Pasteurellaceae; Haemophilus.
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annocation update)
Protective surface antigen D15 precursor (80 kDa D15 antigen)
(D-15-Ag) (Outer membrane protein D15).
                                                                                                                                                                                                                                                                                                                                         1 19 POTENTIÁL.
20 795 PROTECTIVE SURFACE ANTIGEN D15.
795 AA; 87478 MW; B85691FC22E6ED44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.9%; Score 88.5; DB 1; Length 795;
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-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SIMILARITY: Belongs to the surface antigen D15 family.
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     entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pasteurellaceae; Haemophilus.
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Protective surface antigen D15 precursor (80 kDa D15 antigen)
(D-15-Ag) (Outer membrane protein D15).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 797;
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-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SIMILARITY: Belongs to the surface antigen D15 family.
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16-OCT-2001 (Rel. 40, Last annotation updat
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21.9%; Pred. No. 11
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                                                   or send an email to license@isb-sib.ch).
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                                                                                                                                     EMBL; U13961; AAA85645.1; -.
EMBL; U60832; AAB61974.1; -.
EMBL; U60833; AAB61976.1; -.
BIR; JC4078; JC4078.
InterPro; IPR000184; Bac_BurfAg_D15.
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InterPro; IPR00184; Bac sutfAg DIS.
Pfam; PF01103; Bac surface Ag; I.
Antigen; Outer membrane; Signal.
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MEDLINE=97427952; PubMed=9284140;
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Antigen; Outer membrane; Signal.
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Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21534947; PubMed=11677608; Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Parkhill J., Dougan G., James K.D., Holden M.T.G., Sebaihia M., Enker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,
                                                                                                                                                                                                                                             100 FFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNI---LGH-----KLEYNYNS
                                                                                                                                                                                                     427 IGYGTESGISYQTSIKQDNFLGTGAAVSIAGTKNDYGTSVNLGYTEPYFTKDGVSLGGNI
                                                                                                                                                                                                                                                                                   487 FFENYDNSKSDTSSNYKRTTYGSNVTL-GFPVNENNSYYVGLGHTYNKISNFALEYN---
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
LEUS OR STY0699 OR T2219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Próteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                DB 1; Length 793;
1 19 POTENTIAL.
20 793 PROTECTIVE SURFACE ANTIGEN D15.
793 AA; 87511 MW; 51BFDB2036801A14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Bacteriol. 185:2330-2337(2003)
-!- CATALYTIC ACTIVITY: ATP + L-Leucine + tRNA(Leu) = AMP diphosphate + L-LaucyJ-tRNA(Leu).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                 ----FKSAMPEGYVQE-
                                                                                                                      IndelB
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                                                                                                                                                                                                                                                                                                                                                                                                                                     79;
                                                                              6.9%; Score 87.5; D
22.4%; Pred. No. 13;
tive 28; Mismatches
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MEDLINE=22531367; PubMed=12644504;
                                                                                                                                                               65 LSYGVQCFSRYPDHMKQHDF----
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                                                                                                   Similarity 22.48 49; Conservative
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send an email to license@isb-sib.ch)
                                                              EMBL; AE008725; AAL19599.1; -.
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P19424;
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BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 TTGKLPVPWPTLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :: | | :: | | : | | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.0 | 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----NIEDGSVQLADHYQQNTPIGDGPVLLPDNHYL-STQSALSKDP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371 SEQALTEKGVLFNSGEFDGLAFEAAFNAIADKL-------AEKGVGERKVNYRLR 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    419 DWGVSRQRYWGAPIPWYTLEDGTV-----LPTPEDQLPVILPEDVWDGITSPIKADP 471
                                                                                                                                                                                                                                                                                          Pfam; PF00133; tRNA-synt 1; 1. PRINTS: PR0986; TRNA-SYNTHLEU.
TIGRPAM6; TIGR00396; leus best; 1. PROSTT3; PS00178; AA TRNA_LIGASE 1; 1. Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENTE FROM N.A.
STRAIN=LTZ / SGSC1412 / ATCC 700720;
MEDLINE=LTZ / SGSC1412 / DubMed=11677609;
MEDLINE=21534948; PubMed=11677609;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Mguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Watersicon R., Wilson R.K.,
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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-!- CACKALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP +
diphosphate + L-leucyl-tRNA(Leu).
-!- SUBJCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-6CT-2003 (Rel. 42, Created)
10-6CT-2003 (Rel. 42, Last sequence update)
10-6CT-2003 (Rel. 42, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS).
LEUS ON STWO648.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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2F95E480BBAB23C4 CRC64;
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6.9%; Score 87.5; D
Best Local Similarity 23.3%; Pred. No. 15;
Matches 42; Conservative 21; Mismatches
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email to license@isb-sib.ch)
                                                                                          EMBL, AE016841; AA069822.1; -.
HAMAP; MF 00049; -; 1.
InterPro; IPR002302; Leu-tRNAsyntla.
InterPro; IPR002300; TRNA-synt_la.
InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR001412; tRNA-synt_I.
Flam; PF00133; tRNA-synt_I.
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623 "KG
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96940 MW;
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                                                           EMBL; AL627267; CAD05125.1; -.
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SEQUEN'SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ::|| | ::|| | 314 TGEEIPV-WAANFVLMEYGTGAVMAVPGH-DQRD-YEFASKYGLTIKPVILAADGSEPDL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371 SEQALTEKGVLFNSGEFDGLAFEAAFNAIADKL------AEKGVGERKVNYRLR 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         419 DWGVSRQRYWGAPIPMVTLEDGTV-----LPTPEDQLPVILPEDVVMDGITSPIKADP 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 H-------NIEDGSVQLADHYQQNTPIGDGPVLLPDNHYL-STQSALSKDP
39; Gaps
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Ozaki K., Shikata S., Kawai S., Ito S., Okamoto K.;
Ozaki K., Shikata S., Kawai S., Ito S., Okamoto K.;
"Molecular cloning and nucleotide sequence of a gene for alkaline cellulase from Bacillus sp. KSM-635.";
J. Gen. Microbiol. 136:137-1337-1334(1990).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic linkages in cellulose, lichenin and cereal beta-D-glucosid:
-!- SIMILARITY: Belongs to cellulase family A (family 5 of glycosyl hydrolases).
-!- SIMILARITY: Contains 3 S-layer homology (SLH) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Endoglucanase precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)
(Alkaline cellulase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.9%; Score 87.5; DB 1; Length 860; Best Local Similarity 23.3%; Pred. No. 15; Matches 42; Conservative 21; Mismatches 78; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus sp. (strain KSM-635).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                              42 52 "HIGH" REGION.
619 623 "KMMSKS" REGION.
622 622 "ATP (BY SIMILARITY).
860 AA; 96985 MW; D5003584DFBCCAB6 CRC64;
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east 12:505-514(1996).
                                                                                                                                                                                                                                                                             REPLICATION
                                                                                                                                                                                                         cerevisiae.
                                                                                                                                             Sugino A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320 -----FEHDMYVIVDWH---VHAPGDPRADVYSGAYDFFEEIADHYKDH---- 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------EKRDHMVLI 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 ----PKNHYIIWELANEPSPNNNGGPGLTNDEKGWEAVKEYAEPIVEMLREKGDNMILV 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 PDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 NILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSV----QLADHYQQNTPIGD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 LVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLSYGVQCFSRY 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96310631; PubMed=8740425; Sen-Gupta M., Lyck R., Fleig U., Niedenthal R.K., Hegemann J.H.; Sen-Gupta M., Lyck R., Fleig U., Niedenthal R.K., Hegemann J.H.; The sequence of a 24,152 bp segment from the left arm of chromosome "I'the sequence Saccharomyces cerevisiae between the BNI1 and the POL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          272 -EIVNENAFVALSNDWGSNMIRLAMYIGENGYATNPEVK---DLVYEGIELA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
PDB; 1GOC; 31-DEC-02.

InterPro; IPR005086; CBM 17 28.

InterPro; IPR001597; Gal_bind like.

InterPro; IPR001597; Glyco_hydro_5.

InterPro; IPR00119; SLH.

Pfam; PF00424; CBM 17 28; 2.

Pfam; PF00450; cellulase; 1.

Pfam; PF00150; cellulase; CBM 17 28; 2.

PROSITE; PS001659; GLH; 3.

PROSITE; PS01072; SLH DOMAIN; 2.

Cellulose degradation; Hydrolase; Glycosidase; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
DNA polymerase epsilon, catalytic subunit A (EC 2.7.7.7) (DNA polymerase II subunit A).
POLZ OR DUNZ OR YNLZ62W OR NO825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.9%; Score 87.5; DB 1; Length 941;
20.3%; Pred. No. 16;
tive 33; Mismatches 62; Indels 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 1214-1221.
MEDLINE=90381771; PubMed=2169349;
Morrison A., Araki H., Clark A.B., Hamatake R.K., Sugino A.;
"A third essential DNA polymerase in S. cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                     373 373 PROTON DONOR (BY SIMILARITY) 485 485 NUCLEOPHILE (BY SIMILARITY) . 941 AA; 104628 MW; BEA2AC3B169BFADA CRC64;
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                                                                                                                                                                                                                                                                                     -i- CATALYTIC ACTIVITY: N deoxymucleoside triphosphate = N diphosphate + {DNA} (N).
                                                                                                                                                                                                                                                                                                                                                   54 LPVPWP-TLVTTLSYGVQCFSRXPDHM-----KQHDFFKSAMPEGYV----QERTI
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Best Local Similarity 28.2%; Pred. No. 46;
Matches 37; Conservative 14; Mismatches 49; Indels 31; Gaps
                                                                                                                  ^{\circ}\mathrm{DiA} polymerase II, the probable homolog of mammalian DNA polymerase spsilon, replicates chromosomal DNA in the yeast Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha, beta, gamma, delta, and epsilon which are responsible for different reactions of DNA synthesis.
-!- SIMILARITY: Belongs to the DNA polymerase type-B family.
                                                                                                                                                                                                           EMBO J. 11:733-740(1992).
-!- FUNCTION: DNA POLYMERASE II PARTICIPATES IN CHROMOSOMAL DNA
                              MEDLINE=92164663; PubMed=1537345;
Araki H., Ropp P.A., Johnson A.L., Johnston L.H., Morrison A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO, GO:0000731, P:DNA repair synthesis, IMP...
InterPro; IPR006172; DNA_DOl_B.
InterPro; IPR006134; DNA_DOl_B_dom.
InterPro; IPR006133; DNA_DOl_B_exo.
Pfam; PF00136; DNA_DOl_B; 1.
Pfam; PF01104; DNA_DOl_B_exo; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M60416; AAA88711.1; -... EMBL; X92494; CAA63235.1; -... EMBL; Z71538; CAA6169.1; -... PIR; A36028; A56028. GermOnline; 143268; -... SGD; S005206; POL2.
PEMPERATURE SENSITIVE MUTANTS.
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689 AA;
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XX MEDINELS2388257; PubMed=1247932,

XX Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Straubberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

X Alachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

X Richaris S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,

Rakesley R.W., Touchman J.W., Garcia A.M., Gibbs R.A.,

Rakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Generation and initial analysis of more than 15,000 full-length human
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MEDLINE=21638749; PubMed=11780052;
MEDLINE=21638749; PubMed=11780052;
MEDLINE=21638749; PubMed=11780052;
MEDLINE=21638749; PubMed=11780052;
MEDLINE=21638749; PubMed=11780052;
MEDLINE=21638749; MEDLER D. H., Babbage A. K., Bagguley C. L., A. Jones M., Stavrides G., Almeida J.P., Babbage A. K., Bagguley C. L., MEDLINE D. Barlow K.F., Batter D.M., Barlow K.F., Batter D.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R.D., Frankland J.A., Frankland P.D., Gwilliam R., Hall R.E., A. Blington A.G., Frankland J.A., Heath P.D., Ho. S., Holmen P.J., M. Blington A.G., Harley J.L., Heath P.D., Ho. S., Holmen P.J., M. Burkle E., Hunt A.R., Hunt S.E., Jekosech K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Lehvaeelalaho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConnachie L.J., McLay K., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Sudur B.J., Sycamore N.T., Scoderlund C., Steward C.A., Sulston J.E., Swan R.M., Sycamore N.T., Scoderlund C., Steward C.A., Sulston J.E., Swan R.M., Sycamore N., Tromans A.C., Vaudin M., Wallis J.M., Whitehead S.L., Whitteker P., Willey D.L., Williams L., Williams S.A., Willing J., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Walder J. L., Whitehead S.L., Willey P.W., Hubbard T., Durbin R.M., Bentley D.R., Bentley D.R., Beck S., Walder J. L., Waray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Waldin J. L., Willey D.M., Bentley D.R., Bentley D.R., Beck S., Waldin J. L., Willey D.R., Willey D.R., Bentley D.R., Bentley D.R., Bentley D.R., Wallis J. Walley D.R., Bentley D.R., Bentley D.R., Bentley D.R., Bentley D.R., Walley D.R., Walley D.R., Walley D.R., Walley D.R., Walley D.R., Walley D.R., Walley D.R., Walley D.R., Walley D.R., Walley D.R., Walle
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TISSUE-Placenta, and Tongue;
Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
Katsuta N., Sato K., Tanikawa M., Yamazaki M., Irie R., Sato H.,
                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                               OSUNDE1, 081V99; OSUN234; Q96JII; Q96JX6; Q9NU28; 10-OCT-2003 (Rel. 42, Created) 110-OCT-2003 (Rel. 42, Last sequence update) 110-OCT-2003 (Rel. 42, Last annotation update) Acetyl-coenzyme A synthetase 2-like, mitochondrial precursor (EC 6.2.1.1) (Acette--CoA ligase 2) (Acetyl-CoA synthetase ACAS2L OR KIAA1846.
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                                689 AA
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                                STANDARD;
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Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
Kikuchi H., Murakawa K., Takahashi-Fujih A., Oshina A., Sugiyama A.,
Kawakami B., Ota T., Hayashi K., Sugiyama T., Otsuki T., Ishibashi T.,
Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S.,
Kawai Y., Wakamatsu A., Kanehori K., Suzuki Y., Sugano S.,
Nagahari K., Masuho Y., Nagai K., Isogai T.;
"NEDO human cDNA sequencing project.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CAUTION: Ref.1 (CAB81884) sequence differs from that shown due to erroneous gene model prediction.
-!- CAUTION: Ref.3 sequence differs from that shown due to a frameshift in position 250 and numerous sequencing errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XX. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 8:85-95(2001).
-!-FUNCTION: Converts acetate to acetyl-CoA so that it can be used for oxidation through the tricarboxylic cycle to produce ATP and CO(2) (By similarity).
-!-CATALYTIC ACTIVITY: ATP + acetate + CoA = AMP + diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52; Gaps
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-!- SUBSCELLULAR LOCATION: Mitochondrial matrix (By similarity).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note=No experimental confirmation available;
-!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 6.8%; Score 87; DB 1; Length 689; Local Similarity 24.1%; Pred. No. 13; hes 33; Conservative 16; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH44588).
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V -> M (IN REF. 2; AAH39261)
V -> M (IN REF. 2; AAH44588)
GEB4E39302AD08B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=09NUB1-2; Sequence=VSP 007249;
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 336-689 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q9NUB1-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AK027817; BAB55390.1; ALT_INIT.
EMBL; AK092295; BAC03853.1; ALT_SEQ.
EMBL; AB058749; BAB47455.1; -.
EGENW; HGNC:16091; ACAS2D.
InterPro; IPR000873; AMP-bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL080312; CAB81884.1; ALT_SEQ.
BC039261; AAH39261.1; -.
BC044588; AAH44588.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21245130; PubMed=11347906;
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Q87C65;
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Matches
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473 FFGIVPVLMDEKGSV------VEGSNVSGALCIS------QAWPGMARTI--- 510
                                                                                        69 VQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRA---EVKFEGDTLVNRIE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Geber A., Hitchcock C.A., Swartz J.E., Pullen F.S., Marsden K.E., Kwon-Chung K.J., Bennett J.E.,
"Delection of the Candida glabrata ERG3 and ERG11 genes: effect on cell viability, cell growth, sterol composition, and antifungal susceptibility.";
                                                                                                                                                | | | : | : | | | | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Rapid detection and identification of Candida albicans and Torulopsis (Candida) glabrata in clinical specimens by species-specific nested PCR amplification of a cytochrome P-450 lanosterol-alpha-demethylase (IIA1) gene fragment.";
J. Clin. Microbiol. 32:1902-1907(1994).
-!- FUNCTION: Catalyzes CI4-demethylation of lanosterol which is critical for ergosterol hissynthesis. It transforms lanosterol into 4,4'-dimethyl cholesta-8,14,24-triene-3-beta-ol (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001128; Cytochrome_P450.
Pfam, PF00067; p450; 1.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME P450; 1.
Electron transport; Oxidoreductase; Monooxygenase; Membrane; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CP51_CANGA STANDARD, PRT, 533 AA.
P50859; Q02312;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cytochrome P450 51 (EC 1.14.13.70) (CYPLI) (Sterol 14-
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MEDLINE=95081364; PubMed=7989540;
Burgener-Kairuz P., Zuber J.P., Jaunin P., Buchman T.G., Bille J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha-demethylase) (Lanosterol 14-alpha demethylase) (P450-14DM)
ERG11 OR CYP51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NADP(+) + 3 H(2)0.
-!- PATHWAY: Ergosterol biosynthesis.
-!- SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrob. Agents Chemother. 39:2708-2717(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Candida glabrata (Yeast) (Torulopsis glabrata).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96161286; PubMed=8593007;
                                                                                                                                                                                                                                                                         126 LKGIDFKEDGNILGHKL 142
                                                                                                                                                                                                                                                                                                                                                             554 -----NISGHRL 560
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SEQUENCE OF 60-473 FROM N.A.
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ID _CP51_CANGA

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REQUENCE FROM N.A.

RA VAN Sluye M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,

A VAN Sluye M.A., de Oliveira M.C., da Silva A.C.R., Moon D.H.,

RA Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,

RA Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,

RA Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M.,

RA Garrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,

RA Carrer H., Carraro D.R., Abreu I.L., Alves L.M.C., do Amaral A.M.,

RA Marino C.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,

Raid G.S., Blanco S.R., Ritto M.S., Canavana F.S., Celestino A.V.,

RA da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,

RA Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sassaki F.T., Sena J.A.D.,

RA de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G.,

Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,

RA Kitajima J.P.;

RA Comparative analyses of the complete genome sequences of Pierce's

RT disease and citrus variegated chlorosis strains of Xylella
                                                                                                                                                                                                                                                                                                                                                                                                                        109 GHEFIFNAKLADVSAEAAYSHL-------TTPVFGKGVIYDCPNHRLM 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 KOHDFPKSAM-PEGYV-----OERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDF 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 KEDGNILCHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGD 191
                                                                                                                                                                                                                                                                                                                                       25 GHKFSVS---GEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLSYGVQCFSRYPDH--M 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 TASRSLLGKEMRDKLDTDFAYLYSDLDKGFTPINF-VFPNLPLEHYRKRDHAQQAIS---
                                                                                                                                                                                                                                                         Gaps
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-!- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP +
diphosphate + L-leucyl-tRNA(Leu).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
                                                                                                                                                                                                                                            49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xylella fastidiosa (strain Temecula1 / ATCC 700964).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
NCBI_TaxID=183190;
                                                                                                                                                          6.8%; Score 86.5; DB 1; Length 533; 21.4%; Pred. No. 10; tive 32; Mismatches 81; Indels 49
64 I -> M (IN REF. 2).
173 I -> T (IN REF. 2).
61305 MW; A0506C17507E6EF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         879 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 GPVLLPDNHYLSTQSALSKDPNEKRD 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 -----GTYMSLIKERREKND 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE012557; AA029080.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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10-OCT-2003 (Rel. 42, Last seq
                                                                                                                                                                                                                                                     44; Conservative
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64
473
533 AA;
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183 18
275 27
1603 AA;
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TRMA_CAMJE
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MEDLINE=82269643; PubMed-4022780;

A Spieth J., Denison K., Kirtland S., Cane J., Blumenthal T.;

Spieth J., Denison K., Kirtland S., Cane J., Blumenthal T.;

The C. elegans vitellogenin genes: short sequence repeats in the promoter regions and homology to the vertebrate genes.";

Inucleic Acids Res. 13:5283-5295(1985).

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Inucleic Acids Res. 13:5283-5295(1985).

Inucleic Acids Res. 13:5283-5295(1985).

Inuclei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 TTGKLPVPWPTLVTTLSYGVQCFSRYPDHMKQHDFPKSAMPEGYVQERTIFFKDDGNY-- 107
                                                                                                                                                                                                                                                                                                                                                                                          321 TNEQLPV-WVANFVLMAYGTGAVMAVPGHDQRDQEF--ANKYGLPIRQVIALKEPKNQDE 377
                                                                                                                                                                                                                                                                                                                                                                                                                            108 -------KTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                 378 STWEPDVWRDWYADKTR---BFE---LINSAEFDGLDYQGAFEVLABRFE------
                                                                       Pfam; PF00133; tRNA-synt_1; 1.
PRINNS; PR00985; TRNASYNTHLEU.
TIGRPAMS; TIGR00396; leuS_bact; 1.
PROSITE; PS00178; AA TRNA_LIGASE I: 1.
Aminoacy1-tRNA synthētase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                   57;
                                                                                                                                                                                                                                                                            DB 1; Length 879;
                                                                                                                                                                                                                                                                                                                   69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-282 FROM N.A.
Blumenthal T., Spieth J., Zucker E.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                     "KMSKS" REGION.
ATP (BY SIMILARITY).
4C2EE01B8FDC497E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CABEL DIAM. CABEL PIBBA7; Q9BPP3; 01-NOV-1990 (Rel. 15, Last sequence update) 10-OCT-2003 (Rel. 42, Last senocation update) CAT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                              ch 6.8%; Score 86.5; Di
1 Similarity 22.2%; Pred. No. 18;
44; Conservative 28; Mismatches
                                                                                                                                                                                      "HIGH" REGION
InterPro; IPR002302; Leu-tRNAsyntla.
InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR0019008; ValRS_ILERS_edit.
Pfam; PF00133; tRNA-synt 1; 1.
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                                                                                                                                                                                                                                            99823 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-OCT-2003 (Rel. 42, Las Vitellogenin 4 precursor. VIT-4 OR F59D8.2. Caenorhabditis elegans.
                                                                                                                                                                                    55
641
640
                                                                                                                                                                                                                                            879 AA;
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                       Complete proteome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 LNVNGQEVVKSETRAKVTFVEESKINR-EIK------KVSGPKEELVYSMENEKLIEQ 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 -----NYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMAD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 MESDKDSLFFNVHEKTMEGDCEV---AYTIVQEG-GKTIYTKSVNFDKCITR-----PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEG-YVQERTIF---FKDDG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campylobacter jejuni.
Bacteria, Froteobacteria, Epsilonproteobacteria, Campylobacterales;
Campylobacteraceae, Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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SETAAIN=NCTC 11168;
MEDLINE=2015.0912; PubMed=10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (tRNA (M-5-U54)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 1603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'S T -> S (IN REF. 2).
186307 MW; E303170325BC99BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y -> V (IN REF. 3).
L -> V (IN REF. 2).
EVAYT -> RSRLH (IN REF. 2).
T -> S (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 KOKNG-----IKVNFKIRHNIEDGSVQLADHYQQNTP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 FYKOGDKAEVNPFKAIEIEQKV-EQLEEIFROIQEH-EQNTP
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ERNA (Uracil-5-)-methyltransferase (EC 2.1.1.35)
methyltransferase) (RUMT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Storage protein; Multigene family; Signal.
SIGNAL 1 15 POTENTIAL.
CHAIN 16 1603 VITELLOGENIN 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.8%; Score 86.5; D
23.4%; Pred. No. 38;
ive 32; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VWFD.
                                                                                                                                                                                                                                                                                                                                    Wormbep; F59D8.2; CE26817.
InterPro; IPR001747; Lipid_transpx
InterPro; IPR001846; WWF D.
Ema; PF001847; Vitellogenin_N; 1.
SMART; SM00638; LPD N; 1.
SMART; SM00616; VWD; 1.
                                                                                                                                                                                                                                    EMBL; AC024137; AAK09074.1; -.
                                                                                                                                                                                                                                                              EMBL; M11498; AAA28163.1; -. EMBL; X02754; CAA26531.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 23.4 es 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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187
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us-09-887-784-222i.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R EMBL; AL139076; ...

R PRIS; G81355, G81355.

DR PIR; G91355, G81355.

DR InterPro; IPR000051; SAM bind.

DR PROSITE; PS01230; TRNA 1; 1.

DR PROSITE; PS01231; TRNA 2; FALSE NEG.

RW Transferase; Methyltransferase; LRNA processing; Complete proteome.

SISSIMILARITY.

SISSIMILARITY.

135 BY SIMILARITY.

" 1; Length 357;
                                                reveals hypervariable sequences.";

Nature 403:65-668(2000).
-!- FUNCTION: Catalyzes the formation of 5-methyl-uridine at position 54 (M-5-U54) in all tRNA (By similarity).
-!- CATALYTY: S-adenosyl-Lumethionine + tRNA = S-adenosyl-Lumethionine + tRNA = S-adenosyl-Lumocysteine + tRNA containing thymine.
-!- SIMILARITY: Belongs to the RNA M5U methyltransferase family. TrmA
genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                        subfamily
STTTT BEAUTY OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE
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Search completed: June 21, 2004, 15:55:23 Job time : 7.55556 secs

80 KQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKF--EGDTLV------NRIELKG 128

34; Gaps

14 EKHSPIKKYFKEFYTKDFKLFASKDKHYRTRAELSFYHENDTLFYAMFDPKSKKKYIIEY 73

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129 IDFKED------GNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIE 173 

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093125 aequorea vi

08ghe4 azomonas ag

08ghe3 azomonas ag

017105 aequorea vi

08wpc6 aequorea ma

08wpc6 aequorea ma

08wc6 aequorea ma

08wc6 aequorea ma

08wc6 aequorea ma

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09bu67 aequorea ma

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1 MVSKGEELFTGVVPILVELD......VLiGFVTAAGITLGMDELYK
                                                                                                                                                                                                          1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                         - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Q963F5	QBT6U0	6M0Z40	Q816J8	Q9U6Y3	Q720W4	Q8MU48	QSTSF1	Q7Z0W6	Q720W7	Q8MMA1	Q8MMA2	Q8T5F2	Q8MU47	9Y9U6Q	Q962P9	Q7Z0W8	Q9GPI5	Q9BLY9	Q86LV7	Q95P04	086LV8	Q95VT0	Q9U6Y8	Q9GZ28	Q7Z168	Q8T6T9	Q9U6Y7	Q8T5F0
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#### ALIGNMENTS

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PRT; 238 AA.	Created) Last sequence update) Last annotation update)			Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Azotobacter.				"Occurrence of green fluorescence protein in diazotrophic bacteria		Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.		/B; IEA.	cotein.			ein; 1. F84840F1F9064018 CRC64;	Score 1241; DB 2; Length 238;	Pred. No. 3.6e-96; 3; Mismatches 3; Indels 0; Gaps		VSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTIGKLFVFWFTL	MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL	VITLSYGVOCFSRYDDHMKQHDFFKSAMPBGYVQBRTIFFKDDGNYKTRABVKFEGDTLV
ď				Gammaj ter.			X	escen		e EMB		athway	ike.	1	ENT.	Drot.	SGC	n			Locovi	МКОНD
PRELIMINARY;	(TrEMBLrel. 23, (TrEMBLrel. 23, (TrEMBLrel. 25,		vinelandii.	Bacteria, Proteobacteria, Gam Pseudomonadaceae, Azotobacter	54;	M N.A.	Berenyi M Bu	of green fluor	Azomonas and Azotobacter.";	IOV-2000) to th	EMBL; AF324408; AAN86140.1;	191; P:energy p	InterPro; IPR009017; GFP_11Ke. InterPro: IPR000786: Green fl protein.	3; GFP; 1.	.229; GFLUORESC	ProDom; PD013756; Green fl_protein; 1. SEQUENCE 238 AA; 26914 MW; F84840F	97.48;	larity 97.5%; Conservative		GEELFTGVVPILVE	GEELFTGWPILVE	TLSYGVOCFSRYPDH
LT 1 E2 Q8GHE2	01-MAR-2003 01-MAR-2003 01-OCT-2003	Green fluore	Azotobacter vinelandii.	Bacteria, Pr Pseudomonada	NCBI_TaxID=354;	SEQUENCE FROM N.A.	Koranyi D Ber	"Occurrence	Azomonas and	Submitted (N	EMBL; AF3244	GO; GO: 00060	InterPro; IP	Pfam; PF0135	PRINTS; PR01	ProDom; PD01 SEQUENCE 2	Query Match	Simi 2:		2 VSK :	1 MSK	62 VTT 
RESULT Q8GHE2 ID Q0	444	E N	so	88	ŏ ≅	RP	ם אַכ	Z Z	RT	RL	DR	ä	<u> </u>	DR	DR	S OR	8	M B	!	ò	q	ò

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96.9%; Score 1235;
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NCBI_TaxID=354;
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01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25, Green fluorescence protein.
                                                                    Bacteria, Proteobacteria; Gi
Pseudomonadaceae, Azomonas.
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                                                                                            NCBI_TaxID=116849;
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                                                    Azomonas agilis.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
    61 VTTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                              NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
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                                                                                              VSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
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EMBL; U73901; AAB18957.1; -.
                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96305137; PubMed=8707053;
Cormack B.P., Valdivia R.H., Falkow S.;
"FACS-optimized mutants of the green fluorescent protein (GFP).";
                                                                                                                                                                                                                                                                 Aequorea victoria (Jellyfish).
Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=6100;
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Brown A.J.P.;
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PRODON; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 26840 WW; A28622809A9DEA60 CRC64;
                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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Pred. No. 6.5e-96;
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InterFro; IPR009017; GFP_like.
InterFro; IPR000786; Green_fl_protein.
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01-MAR-2003 (TrEMBLrel. 23, Created)
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                                                                                                                                                                                                                                               Green fluorescent protein mutant 3.
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97.1%;
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01-FEE-1997 (TrEMBLrel. 02,
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Best Local Similarity 97.1
Matches 231; Conservative
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Q8GHE4
                                                                                                                                                     RESULT 2
Q93125
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62 VTTLSYGVOCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
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                                                                                                                                                                                                                       Koranyi P., Berenyi M., Burg K.; "Occurrence of green fluorescence protein in diazotrophic bacteria Azomonas and Azotobacter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                          Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                               Azomonas and Azotobacter.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
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ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 26902 MW; 15FE9B9C5B4F6B89 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tch al Similarity 97.0%; Score 1236; DB 2; al Similarity 97.1%; Pred. No. 9.6e-96; 231; Conservative 3; Mismatches 4;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                           Aequorea victoria (Jellyfish).
Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=6100;
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A SEQUENCE FROM N.A.

A Warkins J.N., Campbell A.K.;

Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.

E SHBL; X83959; CASS8789.1; -.

R PIR; JG0692; JGJ514.

R SSP; P42212; IGFL.

R GO; GO:0006031; P:energy pathways; IEA.

InterPro; IPR00917; GFP_like.

R InterPro; IPR009786; Green_fl_protein.

Pfam; PF01333; GFP; 1.

PRINTS; PR01229; GFLUORESCENT.

PRODOM; PD013756; Green_fl_protein; 1.
NON TER 238 238 - SEQÜENCE 238 AA; 26950 MW; 26E2BE450E748E44 CRC64;
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Q17105;
01-NOV-1996 (TrEMBLrel. 01,
                            Matches 231; Conservative
              Best Local Similarity
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238 AA

PRT;

PRELIMINARY;

017106

9 RESULT Q17106 ID Q1

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61 VITFSYGVQCFSRYPDHMKQHDFLKSAMPEGYVQERIFYKDDGNYKTRAEVKFEGDTLV 120
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Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedueae;
Aeguoreidae; Aeguorea.
NCBI_TaxID=6100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Watking J.N. Campbell A.K.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; X83960; CAA58790.1; -.
PIR, J80692; JQ1814.
HSSP; P42212; LBFP.
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR00796; Gren_fl_protein.
Pfam; PF0135; GRP; 1.
PRINTS; PR01229; GFLUORESCENT.
Probom; PD013756; Gren_fl_protein; 1.
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Submitred (OCT-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; AF491541; AAL33916.1; -.
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR000786; Green_fl_protein.
Fign; PF0153; GFP; I.
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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                                                                                                                                 Green fluorescent protein (Fragment)
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                                                                                                                                                                                                                         Aequorea victoria (Jellyfish)
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STRAIN=GFPXm, and GFPdnaxm;

Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Qin Y.X., Pang S.Q.,
Lus J., Xia N.S.;

Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AY01824; AAK02062.1; -.

EMBL, AY01821; AAK02069.1; -.

EMBL, AY01821; ARC0505.1; -.

InterPro; IPR009017; GFP_like.

InterPro; IPR00086; Green_fl_protein.
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                                                                                                                     Gaps
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Eukaryota, Metazoa; Cnidaria, Hydrozoa, Hydroida, Leptomedusae,
Aequoreidae, Aequorea.
NCBI_TaxID=147615;
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                                                                            Length 238;
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                                                                      Query Match

Best Local Similarity 81.9%; Pred. No. 6.6e-83;
Matches 195; Conservative 21; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINT; PR01229; GFLUORESCENT.
Probon; P0013756; Green fl protein; 1.
SEQUENCE 238 AA; 27049 MW; 8185D0E55529012B CRC64;
                     ProDom; PD013756; Green_fl_protein; 1.
SEQUENCE 238 AA; 27015 MW; 6B8FD75E88926903 CRC64;
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Last sequence update)
Last annotation update)
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Best Local Similarity 81.5%; Pred. No. 1.4e-82;
Matches 194; Conservative 21; Mismatches 23;
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PR01229; GFLUORESCENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Green fluorescent protein.
GFPXM.
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PRINTS;
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62 VITLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
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Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
macrodactyla.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                      STRAIN=ShG24;
Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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                                                                                                                                                             Aequorea macrodactyla.
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
84.4%; Score 1075; DB 5; Length 2
Best Local Similarity 82.4%; Pred. No. 3.1e-82;
Matches 196; Conservative 18; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 macrodactyla.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
BMB.; AF4554333. AAL33918.1;
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR000901; GFP-like.
InterPro; IPR000786; Green_fl_protein.
PRINTS; PR01259; GFLUORESCENT.
PRODM; P0013756; Green fl_protein; 1.
SEQUENCE 238 AA; 26956 WW; 75521EAF0CEBA73A CRC64;
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Last sequence update)
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Last annotation update)
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PRT;
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                                             01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25, Green fluorescent protein.
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122 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
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                                                                                                                                                                                                                                                                            RESULT 12
QBWTC9
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C08WTC7
AC Q08WTC7
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DT 01-MA
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BE Green
GN GRP.
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Eukaryota; Metazoa; Chidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q.,
Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
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   (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                             Pfam; PF01353; GFP; 1.
PRINTS, PR01229; GFLUORESCENT.
SEQUENCE 238 AA, 26997 WW; 5F80A192173CB84D CRC64;
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SEQUENCE 238 AA; 27047 MW; 5F80A18FA1E7C84D CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                  Score 1073; DB 5;
Pred. No. 4.5e-82;
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81.1%; Pred. No. 5.5e-82;
iive 21; Mismatches 24
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81.1%; Pred. No. 4...
11. Mismatches
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                      EMBL, AF435427, AAL33912.1; -...GO, GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IPR000786; Green_fl_protein.
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GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR0001017; GFP_like.
InterPro; IPR000786; Green_fl_protein.
Pfam; PF01353; GFP; 1.
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                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 81.19
Matches 193; Conservative
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Matches 193; Conservative
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61 VITLGYGIQCFARYPEHMKANDFPKSAMPEGYIQERIFFRQDDGKYKTRGEVKFEGDILV 120
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                                                                                    182 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLIGFVTAAGITLGMDELYK 239
                                                                                                                    181 HYOTNVPLGDGPVLIPINHYLSYOTAISKDRNETRDHMVFLEFFSACGHTHGMDELYK 238
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Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
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EMBL, AF435428; AAL33913.1; -...
EMBL, AF435428; AAL33913.1; -...
EMBL, AF435428; AAL33913.1; -...
EMBL, AF435428; AAL39913.1; -...
InterPro; IPR00901; GFP interPro; IPR0090186; Green fl_protein.
PRINTS; PR01229; GFLUORESCENT.
PRODOM; PR013756; Green fl_protein; 1.
SEQUENCE 238 AA, 27031 WW; 5F80A19C19DC584D CRC64;
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81.1%; Pred. No. 5.5e-82;
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                                                                                                    Chen M.,
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Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M. Li S.G., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
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LO W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q.,
Li S.J., Xia N.S.,
Li S.J., Xia N.S.,
"Colorful mutants of green fluorescent protein from Aequorea
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP435432; AAL33917.1; -.
EMBL, GA900901; P:energy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR000786; Green_fl_protein.
                                                                                                                                                                                                      macrodactyla.";
Submitted (OCT-2013) to the EMBL/GenBank/DDBJ databases.
EMBL; AF435430; AAL3315.1; -.
GO; GC:0006091; P:energy pathways; IEA.
InterFro; IPR009017; GFP like.
InterFro; IPR00786; Green_fl_protein.
Pfan; PF01353; GFP; I.
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PRODON; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 27018 WW; 75521EA5534E573A CRC64;
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ProDon; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 27002 MW; BD5BA2982264C018 CRC64;
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Last annotation update)
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81.1%; Pred. No. 8.1e-82;
iive 21; Mismatches 24;
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Matches 193; Conservative
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1 MSKGEELFTGVVPILVELDGDVHGHKFSVRGEGEGDADYGKLEIKFICTTGKLPVPWPTL
                                                                                                                                                                               62 VITLSYGVOCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cyan fluorescent protein (Fragment).
Montastraea cavernosa (great star coral).
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia; Favilida; Favilida;
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Montastraea cavernosa fluorescent protein.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AYOS4660; AALI7905.1;
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IPR009086; Green_fl_protein.
Pf01353; GFP; I.
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PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl_protein; 1.
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Job time: 31.7778 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

June 21, 2004, 15:41:49; Search time 47.1111 Seconds (without alignments) 1433.395 Million cell updates/sec Run on:

US-09-887-784-222L 1274 Title: Perfect score:

1 MVSKGEELFTGVVPILVELD......VLlGFVTAAGITLGMDELYK 239 BLOSUM62 Gapop 10.0 , Gapext 0.5 Sequence:

Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2003s:*
6: geneseqp2003bs:*
7: geneseqp2003bs:*
8: geneseqp2003bs:* genesch1980s: *
genesch21990s: *
genesch2000s: *
genesch2001s: *
genesch2002s: *
genesch2003s: *
genesch2003bs: *
genesch2003bs: * Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	Aae17518 Enhanced	Abr40352 Human ami	Aag65781 Amino aci	Aag65782 Amino aci	Aael7517 Enhanced	Aab22882 Enhanced	Aay54349 Amino aci		Aab50804 Jellyfish	Aab85900 A. victor	Aab31171 Amino aci	Aag66198 A. victor	Abg94444 Protease	Aae14599 Aeguorea		Aag79829 Green flu	Abr83616 Green flu	Ada38074 Aequorea		Adc18358 EGFP (enh	Abw00914 Aequorea	Ade28570 Enhanced	Abm79011 Enhanced	Aag68319 Jellyfish	Aau99804 Biomembra
ΩΙ	AAE17518	ABR40352	AAG65781	AAG65782	AAE17517	AAB22882	AAY54349	AAY79584	AAB50804	AAB85900	AAB31171	AAG66198	ABG94444	AAE14599	AAE34958	AAG79829	ABR83616	ADA38074	ABU63204	ADC18358	ABW00914	ADE28570	ABM79011	AAG68319	AAU99804
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Length	239	363	893	1132	239	239	239	239	239	239	239	239	239	239	239	239	239	239	239	239	239	239	246	248	259
% Query Match	100.0	100.0	100.0	100.0	99.4	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1
Score	1274	1274	1274	1274	1266	1263	1263	1263	1263	1263	1263	1263	1263	1263	1263	1263	1263	1263	1263	1263	1263	1263	1263	1263	1263
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Wild-type Biomembra Biomembra Biomembra Biomembra	Green flu EGFP-MODC EGFP-MODC	EGFP/ hum EGFP/ hum EGFP/ hum GPP-DEVD-	Caspase-3 Recombina EGFP/DRM HUB1-GFP GFP mutan RUB1-GFP
Aaw97451 Aau99803 Aau99802 Aau99800 Aau99801	Aay50142 Aay50142 Aau10888	Ade28564 Ade28568 Ade28568 Ade28566 Ade28566	Aay/9638 Abg94422 Aay42181 Abr83620 Aay54359 Abr83621
AAW97451 AAU99803 AAU99802 AAU99801 AAU99801	AAY50142 AAB24252 AAU10888	ADE28564 ADE28568 ADE28566 AAB22860	AAY79638 ABG94422 AAY42181 ABR83620 AAY54359 ABR83621
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# ALIGNMENTS

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/note= "Wild type Glu substituted with Gly; This corresponds to position 222 in the wild type protein"
                                                                                                                                                                                 /note= "Wild type Phe substituted with Leu; This
corresponds to position 64 in the wild type protein"
Misc-difference 223
                                                                                                        Jellyfish; green fluorescent protein, GPP; protein redistribution; cellular function; genetic reporter; mutant; Stoke's shift; mutein.
                                                                                    Enhanced F64L-E222G jellyfish green fluorescent protein mutant.
                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                     Thastrup 0;
                     Ą.
                     AAE17518 standard; protein; 239
                                                                                                                                                                                                                                                                                                                          19-JUN-2000; 2000DK-00000953.
20-JUN-2000; 2000US-021268IP.
10-MAY-2001; 2001DK-00000739.
10-MAY-2001; 2001US-0290170P.
                                                                                                                                                                                                                                                                                                      18-JUN-2001; 2001WO-EP006848
                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                     Bjorn SP, Pagliaro L,
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-098224/13.
N-PSDB; AAD28163.
                                                                                                                                                                                                                                                                                                                                                                                (BIOI -) BIOIMAGE AS.
                                                                                                                                                                         Key
Misc-difference 65
                                                                                                                                         Aequorea victoria.
                                                                                                                                                                                                                                                            WO200198338-A2
                                                              22-APR-2002
                                                                                                                                                                                                                                                                                  27-DEC-2001.
                                                                                                                                                    Synthetic.
                                          AAE17518;
RESULT 1
AAE17518
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Novel fluorescent protein in in vitro assay for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution, has a green fluorescent protein with F64L and E222G mutation.

Claim 9; Page 37; 41pp; English.

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The invention relates to a fluorescent protein derived from green fluorescent protein (GFP) or its analogue. The GFP containing mutations fluorescent protein (GFP) or its analogue. The GFP containing mutations can reful and E323C has a bigger compared to other GFP's making it very suitable for high throughput screening due to better resolution. The fluorescent protein is useful in studying protein redistribution. The fluorescent protein is useful in studying collular functions in living cells, separable tags, secretion marker and genetic reporter. The fluorescent protein is also useful as a cell or organelle integrity marker, a marker for changes in cell morphology, as transfection marker. The fluorescent protein is also useful as a cell or organelle integrity marker to be used in combination with fluorescence activated cell sorting (FACS). The novel proteins can also be used as reporters to monitor live or dead biomass of organisms, such as fungi. The fluorescent protein as markers in transcriptional and translational transposons encoding the fluorescent protein are for bacterial detection. Transposons encoding the fluorescent protein are constant for screening promoters and for tagging plasmids and chromosomes. The fluorescent protein engineered into the genome of a phage is useful for designing diagnostic tool. The present sequence is a DNA encoding channed F6AL-E22CG jellyfish green fluorescent protein (GFP) mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; heterologous conjugate; intracellular protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human amino acid sequence SEQ ID NO: 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABR40352 standard; protein; 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCF-2001; 2001DK-00001433.
11-OCF-2001; 2001US-0328896P.
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Best Local Similarity 100.
Matches 239; Conservative
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Terry BR, Nielsen SJ; (BIOL-) BIOLMAGE AS

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The invention relates to a novel cell, comprising three heterologous conjugates (HC), a first HC (HC1) comprising an anchor protein that specifically binds to an internal structure within the cell conjugated to an interactor protein (IP) of type A, a second HC (HC2) comprising IP of type B conjugated to a first protein of interest, and a third HC (HC3) comprising a second protein of interest conjugated to detectable group. The cell is useful for detecting if a compound disrupts or induces the interaction between two intracellular proteins. The cell is also useful for screening compounds that modulate the interaction between two intracellular proteins. The present sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel cell for identifying modulators of protein interaction, contains a first conjugate comprising anchor protein, second conjugate having type B interactor protein and third conjugate with detectable group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
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                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDB4; central nervous system; antiinflammatory; cytostatic; nootro
autoimmune; ischemic; osteopathic; GFP; green fluorescent protein;
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                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1274; DB 6; Length 363; 100.0%; Pred. No. 8.8e-123; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of HSPDE4A1-E222G fusion protein.
                                                                                                                      Disclosure, Page 112-113; 118pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG65781 standard; protein; 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-APR-2000; 2000DK-0000651.
29-MAY-2000; 2000DK-0000849.
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Matches 239; Conservative
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           WPI; 2003-430211/40.
N-PSDB; ACC72604.
                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                     Sequence 363 AA;
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25-OCT-2001.

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The invention relates to determining, if a compound, is a dislocator of PDB4. The method comprises testing if the compound removes PDB4 spots, which may optionally be induced by a Rolipram-like reference compound, and testing if inhibits the catalytic activity of the PDB4, where the compound is a dislocator of PDB4, if it removes PDE spots and if it does not inhibit the catalytic activity of PDB4. The method is useful for identifying compounds useful for the treatment of diseases of the central nervous system such as joint inflammation, Crohn's diseases of inflammatory disease, respiratory diseases, chronic obstructive pulmonary disease (COPD), including asthma, chronic bronchitis, pulmonary emphysema, postiabis, bone resorption diseases, repertusion injury, cancer and HIV infection. The use of a reagent that can mimic or reverse the effect of the compound with affinity for the catalytic site on intracellular distribution of the PDB for the preparation of a medicament. The present distribution of the PDB for the preparation of a HSPDE4A1-E22G fusion
                                                                                                          Determining if a compound is a dislocator of PDE4 for identifying compounds for treating CNS and inflammatory disease comprises identifying compounds which remove PDE4 spots.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MVSKGEBLFTGVVPILVBLDGDVNGHKFSVSGBGBGDATYGKLTLKFICTTGKLPVDWPT 60
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Bjorn SP, Thastrup O, Almholt DC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of HSPDE4A4-E222G fusion protein.
                                                                                                                                                                                      Example 1; Page 156-160; 160pp; English.
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Scudder KM,
                                                       WPI; 2001-611727/70
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                                                                          N-PSDB; AAI66852
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                   Praestegaard M;
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The invention relates to determining, if a compound, is a dislocator of PDB4. The method comprises testing if the compound removes PDB4 spots, which may optionally be induced by a Nollpram-like reference compound, and testing if it inhibits the catalytic activity of the PDB4, where the compound is a dislocator of PDB4, if it removes PDE spots and if it does not inhibit the catalytic activity of PDB4. The method is useful for compound is a dislocator of PDB4, if it removes PDE spots and if it does not inhibit the catalytic activity of PDB4. The method is useful for disease such as joint inflammation, Crohn's disease, inflammatory bowel disease, respiratory diseases, chronic obstructive pulmonary disease. (COPD), including asthma, chronic obstructive pulmonary disease. COPD), including asthma, chronic bronchitis, pulmonary emphysema, psoriasis, bone resorption diseases, reperfusion injury, cancer and HIV confection. The use of a reagent that can mimic or reverse the effect of the compound with affinity for the catalytic site on intracellular distribution of the PDE for the capparation of a medicament. The present sequence represents the amino acid sequence of a HSPDE4A4-E222G fusion
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                                                                                                                                                                                Thastrup O, Almholt DC;
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                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 162-167; 160pp; English.
                                                                                                                                                                                Bjorn SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE17517 standard; protein; 239
                                      11-APR-2001; 2001WO-DK000264.
                                                                              17-APR-2000; 2000DK-0000651.
29-MAY-2000; 2000DK-00000849.
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                                                                                                                                                                                  Scudder KM,
                                                                                                                                                                                                                                          WPI; 2001-611727/70.
N-PSDB; AAI66853.
                                                                                                                                        (BIOI-) BIOIMAGE AS
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AAE17517
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DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK

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Jellyfish, green fluorescent protein, GFP, protein redistribution, cellular function, genetic reporter; mutant; Stoke's shift, mutein.
                                                                                                                                                                                                                            Example 1; Page 35; 41pp; English.
                                                                                                              19-JUN-2000; 2000DK-00000953.
20-JUN-2000; 2000US-02126BIP.
10-MAY-2001; 2001DK-00000739.
10-MAY-2001; 2001US-0290170P.
                                                                                                  18-JUN-2001; 2001WO-EP006848
                                                                                                                                                           Bjorn SP, Pagliaro L,
                                                                                                                                                                         2002-098224/13.
                                                                                                                                                (BIOI-) BIOIMAGE AS
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                              Misc-difference 65
                    Aequorea victoria.
                                                                                                                                                                                N-PSDB; AAD28162
                                                                                                                                                                                                                                                                                                                                                                                      Sequerice 239 AA;
                                                                         WO200198338-A2
                                                                                      27-DEC-2001
                           Synthetic
                                                                                                                                                                                                                mutation.
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238;

Matches

61

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screening or detection of compounds which affect particular biological functions. The methods of the invention utilise fluorescent biodetector functions. The methods of the invention utilise fluorescent biodetector molecules which, when acted on by a compound of interest, cause an alteration in the cellular distribution of at least the fluorescent conjecty. In one embodiment, the biosensors comprise heat shock proteins (HSPS) fused to a fluorescent protein (e.g., jellyfish green fluorescent the cytoplasm, but on stress activation translocate to the nucleus. In the cytoplasm, but on stress activation translocate to the nucleus. In another embodiment biodetector proteins can be used to detect protease cativity. Such protease biodetector fusion proteins comprise one or more cativity. Such protease biodetector fusion proteins comprise one or more cativity. Such protease biodetector fusion proteins comprise one or more components may be components of a single protein which is cleaved by the protease, or may be from heterologous sources. Due to the components may be from heterologous sources. Due to the components may be from heterologous sources. Due to the components of a single protein is localised to a particular cregion of the cell. Once acted on by the protease of interest, the fluorescent protein is cleaved from the localisation sequence, and is second localisation signal attached from the localisation sequence. The fluorescent protein to be directed to a different cellular compartment after cleaved of the protease recognition sequence. The magning methods with a high degree of spatial resolution. The methods and imaging methods with a high degree of spatial resolution. The methods and
                                                                                                                                                                                                                                                                                                                                                                             Biodetector protein; fusion protein; recognition site; cellular targetting sequence; cellular localisation; fluorescent protein; protease activity detection; toxin detection; cellular stress detection;
181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to systems, methods and reagents for cell-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Automated cell-based characterization of toxin by contacting cells containing luminescent reporter molecules with test substance and analyzing optically.
                                                                                                                                                                                                                                                                                                                            Enhanced green fluorescent protein (EGFP), SEQ ID NO:46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       drug discovery; cell based screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 11; Fig 29A; 336pp; English
                                                                                                                                                                    AAB22882 standard; protein; 239 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0122152P.
99US-0123399P.
99US-00352171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-FEB-2000; 2000WO-US004794.
                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CELL-) CELLOMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aequorea victoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAA93373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                             AAB22882;
                                                                                                                                                  AAB2288
                                                                                                                                                                                                      d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a fluorescent protein derived from green
fluorescent protein (GFP) or its analogue. The GFP containing mutations
at F64L and E225G has a bigger compared to other GFP's making it very
suitable for high throughput screening due to better resolution. The
fluorescent protein is useful in invitro assays for measuring protein
kinase activity or dephosphorylation activity, or for measuring protein
containing in living cells as protein ts useful in studying cellular
functions in living cells as protein tags in transgenic animals, living
and fixed cells, organelle tags, secretion marker and genetic reporter.
Che fluorescent protein is also useful as a cell or organelle integrity
marker, a marker to be used in combination with fluorescence activated
call sorting (FACS). The novel proteins can also be used as reporters to
connict live or dead blomass of organisms, such as fungi. The fluorescent
protein is also useful as markers in transcriptional and translational
fusions for performing transposon vector mutagenesis and as a reporter
con because in detection. Transposons encoding the fluorescent protein are
cuseful for screening prometers and for tagging plasmids and chromosomes.
The fluorescent protein engineered into the genome of a phage is useful
is allowed an invited the present sequence is enhanced F64L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel fluorescent protein in in vitro assay for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution, has a green fluorescent protein with F64L and E222G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTKFICTTGKLPVPWPT
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                                                                                                                      /note= "Wild type Phe substituted with Leu; This corresponds to position 64 in the wild type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1266; DB 5;
Pred. No. 3.2e-122;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        jellyfish green fluorescent protein (GFP) mutant
                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thastrup 0;
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cellular activities and to screen compounds which modulate these activities. Biosensors containing a recognition site for caspase, for example, may be used for the screening of compounds which modulate apoptosis, while biosensors containing other protease recognition sites may be used for the detection of proteolytic toxins (such as anthrax lethal factor). The method provides improved target validation and candidate compound optimisation by combining many cell screening formats with fluorescence-based molecular reagents and computer-based feature extraction, data analysis and automation, resulting in increased quantity and speed of data collection and faster evaluation of drug candidates. Sequences AAB22881-B22885 represent fluorescent proteins which may used as components of biosensor fusion proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                        61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                           61 LVITLIYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKIRAEVKFEGDIL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biosensors of the invention can be used to investigate a wide range of
                                                                                                                                                                                                                                                                                                                                      1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fluorescent protein; green fluorescent protein, emission intensity; fluorescence, pH detection; pH sensor; EGFP.
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                                                                                                                                                                                                                                                                     Length 239;
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                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                   Score 1263; DB 3;
Pred. No. 6.6e-122;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.2%;
Matches 237; Conservative
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                                                                                                                                                                                                                                      Sequence 239 AA;
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The present sequence represents a functional engineered fluorescent protein based on the Aequorea green fluorescent protein (GFP). The emission intensity changes as pH varies between 5 and 10 of the present protein are novel. The functional engineered fluorescent proteins show reversible changes in fluorescence over physiological pH ranges. They can be used for determining the pH of samples and cells. The polynucleotides can also be used to produce transgenic animals. The fluorescent protein pH sensors can be delivered to cells in the form of polynucleotides encoding the protein sensor fused to a targeting signal. The targeting signal directs the expression of the protein sensors to restricted cell locations. This makes it possible to measure the pH of a precisely defined cellular region or organelle
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                                                                        New functional engineered green fluorescent proteins, used for measuring the pH in biological samples and cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                       Length 239;
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                                                                                                                                                                                                                                                                                                                                                                                     99.1%; Score 1263; DB 3; 99.2%; Pred. No. 6.6e-122;
                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
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                                                                                                                        Disclosure; Page 9; 89pp; English
Wachter RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY79584 standard; peptide; 239
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99US-0136078P.
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Matches 237; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CETT-) CETTOWICS INC
Tsien RY, Llopis J,
                            WPI; 2000-116540/10.
N-PSDB; AAZ45642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGFP signal domain.
                                                                                                                                                                                                                                                                                                                                                        Sequence 239 AA;
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99US-00316919. 99US-00316920.

21-MAY-1999;

21-MAY-1999;

(REGC ) UNIV CALIFORNIA. Baird GA;

WPI; 2001-032017/04.

Tsien RY,

N-PSDB; AAC90488.

17-MAY-2000; 2000WO-US013684.

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Aequorea victoria; jellyfish; fluorescent protein indicator; green fluorescent protein; GFP; linker moiety; sensor; calmodulin-binding domain; mutant; mutein.
                                                                                                                                                                                                                                                                               AAB50804 standard; protein; 239
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                                                                                                                                                                                                                                                                                                             Jellyfish GFP mutant EGFP.
                                                                                                                                                                 Local Similarity 99.2
    WPI; 2000-365644/31
                                                                                                                                                                                                                                                                                                                                          Aequorea victoria
                                                                                                                                                    Sequer.ce 239 AA;
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The present sequence is that of the EGFP signal domain, which can be included in novel recombinant protease biosensors (PBS) of the invention. The PBS (see AAY79538-54) comprise: a first domain (see AAY79579-87) comprising at least 1 detectable polypeptide signal such as the present sequence; a second domain (see AAY79588-622) comprising at least 1 comprising at least 1 least and a third domain (see AAY79531) comprising at least 1 reactant target sequence. A recombinant nucleic comprising at least 1 reactant target sequence. A recombinant nucleic acid (see AAA27627-43) encoding the PB, an expression vector, and a contacting a host cell are also claimed. A claimed method for identifying compounds that modify protease activity in a cell involves contacting a host cell that possesses the recombinant PB with a test compound, and determining the PB distribution in the host cell, where compounds that modify protease activity in a host cell include the compounds that modify protease activity in a host cell include the compounds that modify protease activity in a host cell include the compounds that modify protease activity in a host cell include the compounds coll, or the recombinant PB, or the vector, or the vector, or the vector, or the vector, or the vector, or the vector, or the vector, or the vector or the vector, or the vector or the vector or the vector. Or the vector or activation of example of a known recognition motiff identify specific activity based or colleavage of a known recognition motif LVTTLSYGVOCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120 61 LVTILIYGVQCFSRYPDHWKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDIL 120 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180 9 9 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239 1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT 1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTKFICTTGKLPVPMFT Gaps Recombinant nucleic acid encoding a protease biosensor useful for fluorescence based cell and molecular biochemical assays for drug discovery comprising three operably linked nucleic acid sequences. ; 0 Length 239; 1; Indels 99.1%; Score 1263; DB 3; 99.2%; Pred. No. 6.6e-122; tive 1; Mismatches 1; Claim 14; Fig 29A; 218pp; English.

The present sequence is a fluorescnet protein used in the construction of a fluorescent protein indicator. The indicator comprises a sensor polypeptide that is responsive to a chemical, biological, electrical or physiological parameter, and a fluorescence protein functional group. The sensor polypeptide is operatively inserted into the fluorescent moiety. The fluorescent indicator is useful for detecting the presence of a response inducing member in a sample. The method involves contacting the sample with the indicator and detecting a change in fluorescence, in which a change is indicative of the effect of the parameter on the sensor polypeptide. The novel fluorescent proteins are advantageous due to their reduced size as compared to the FRET (fluorescence resonance energy transfer)-based sensors

Novel fluorescent proteins comprising a sensor protein inserted into them, useful for measuring the response of a sensor biological, chemical, electrical or physiological parameter in vivo or in vitro.

Disclosure; Page 24; 94pp; English.

120 VNRIBLKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWVLGFVTAAGITLGMDELYK 239 9 9 61 LVTTLSYGVOCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 1 MVSKGEBLFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT Melanin concentrating hormone receptor; MCHR; MCH; chimeric; fusion; fluorescent polypeptide; orexigenic; anabolic; food intake; GFP; green fluorescent protein. A. victoria green fluorescent protein (GFP) and linker sequence. Score 1263; DB 4; Length 239; Pred. No. 6.6e-122; 1; Mismatches 1; Indels C AAB85900 standard; protein; 239 Query Match 99.1%; Best Local Similarity 99.2%; Matches 237; Conservative (first entry) Sequence 239 AA; 30-NOV-2001 181 181 AAB85900; 121 RESULT 10 AAB85900 g ò g ò d

Aequorea victoria

Synthetic

WO200168706-A1.

us-09-887-784-2221.rag

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The specification describes a method for assessing the growth rate and death rate of a micro-organism within a predetermined time period in a desired environment. The method comprises introducing at least two reporter genes encoding luminescent and/or fluorescent products into the micro-organisms, incubating the micro-organism within the desired environment, and detecting luminescence and/or fluorescence after a predetermined time period. Use of two different markers within a micro-organism enables the differentiation between growth and death rates. The method is used to assess the growth rate and death rate of a micro-organism within a predetermined time period in a desired environment. The present sequence represents a green fluorescent protein (GFP), and is encoded by a plasmid which encodes luminescent and fluorescent proteins, and is used in the method of the invention
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                                                                                                                                                                                                                                              Assessing growth and death rates of a micro-organism in a desired environment, by introducing 2 reporter genes encoding luminescent and fluorescent products and detecting luminescent fluorescence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 239;
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Best Local Similarity 99.29
Matches 237; Conservative
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                                                                                                                                 Lilius E, Virta M;
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                                                                   (LILI/) LILIUS E.
                                                                                        VIRTA M.
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                                                                                                                                                                                                                                                                                                                                                                                                                   The invention provides melanin concentrating hormone (MCH) receptor (MCHR) chimeric and fusion proteins. The MCHR chimeric proteins comprise MCHR polypeptide regions from different species. The MCHR fusion protein comprise MCHR polypeptide region and a fluorescent polypeptide region protein joined directly, or via a linker, to the carboxy side of the MCHR polypeptide region. The MCHR fusion proteins can be expressed by standard recombinant methodology. MCH action promotes feeding (orexigenic) and up regulation of MCH activity stimulates food intake. The present sequence represents a A. victoria green fluorescent protein (GFP) and a linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                                                                                                                                                                                        Fusion proteins comprising melanin concentrating hormone receptor peptides and fluorescent proteins, useful for identifying appetite
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99.2%; Pred. No. 6.6e-122;
iive 1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 14; 71pp; English
                                       14-MAR-2001; 2001WO-US008071
                                                                                     15-MAR-2000; 2000US-0189698P
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Matches 237; Conservative
                                                                                                                             (MERI ) MERCK & CO INC
                                                                                                                                                                                                                       WPI; 2001-565791/63
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17-SEP-1999;
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                                        KAPU/)
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                                                                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                      The invention relates to a gene encoding proteins having cyan-green fluorescence characteristic and having a function of showing stable fluorescence characteristic in acid region. A method for the preparation of a cyan-green fluorescent protein is provided which involves a transformed by a recombinant vector comprising the gene, where the transforment is cultured and the protein is collected from the culture. The present sequence represents the A. victoria green fluorescent protein (EGFP)
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                                                                                                                                                                                                                                                                                                                                                           Detection; classification; identification; toxin detection; protease; ADP-ribosylating toxin; cytotoxic phospholipase; exfoliative toxin; toxic threat agent.
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                                                                                                                                                                                                         Length 239;
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                                                                                                                                                                                                         Score 1263; DB 5;
Pred. No. 6.6e-122;
                                                                              A gene encoding cyan-green fluorescent protein
                                                                                                                                                                                                                          1; Mismatches
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                                                                                               Example; Page 14; 20pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-00810983.
98US-00031271.
99US-012152P.
99US-0123399P.
99US-00352171.
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99.2%;
    04-AUG-2000; 2000JP-00237165
                     04-AUG-2000; 2000JP-00237165
                                    (RIKA ) RIKAGAKU KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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Best Local Similarity 99.2
Matches 237; Conservative
                                                      WPI; 2002-299190/34.
                                                                N-PSDE; ABL40628
                                                                                                                                                                                           Sequence 239 AA;
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27-FEB-1998;
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The invention describes methods of automated detection, classification and identification comprising treating cells containing luminescent reporter molecules (I) in array of locations with a test substance, where (I) are detectors, classifiers or identifiers, imaging cells in each contain to obtain luminescent signals and converting optical information location to obtain luminescent signals and converting optical information into digital data to interpret presence of toxins into the test substance. The method are useful for detection of toxins chosen from proteases, ADP-cribosylating toxins, cytotoxic phospholipases, and exfoliative toxins. Three classes of cell-based luminescent reporter molecules such as detectors, classifiers and identifiers are described and serve as choracterisation ensure a rapid readout of toxin class without characterisation ensure a rapid readout of toxin class without several complex mixtures of known toxins. This is the amino acid sequence several complex mixtures of known toxins. This is the amino acid sequence of a protease biosensor related signal sequence used in the cell-based
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                                                                                                                                                                                                                                                                                                                                                Automated cell-based toxin detection, classification, and/or identification by treating cells involves use of three classes of luminescent reporter molecules such as detectors, classifiers or identifiers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.1%; Score 1263; DB 5; 99.2%; Pred. No. 6.6e-122; ive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 10; Fig 29A; 214pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE14599 standard; protein; 239
99US-00398965.
99US-00430656.
99US-0168408P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 237; Conservative
                                                                                                                                                                                                                                 Kapur R;
                                                                                                                                                                                                                                                                                            WPI: 2002-634730/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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Synthetic.
                                                                                                                                  GIULIANO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               screening system
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Aequorea victoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          operative linkage.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 239 AA;
                                                                                                                                                                                                                                                                                                WO200295058-A2.
                                                                                                                                                                    28-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                             Tsien RY,
             181
                                                                                                                                         AAE34958;
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                                                                                 RESULT 15
                                                                                                AAE34958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or more primers that have a nucleotide sequence containing at least one mutation and a phosphorylated 5'-terminus are annealed to a template DNA and then subjected to an elongation reaction using a thermostable bNA and then subjected to an elongation reaction using a thermostable bNA and then subjected to an elongation reaction using a thermostable bNA lightide it is a closured by means of a thermostable bNA lightide it is step of DNA synthesis a circular DNA containing the primers, a digestion in which the step of DNA synthesis are digested into several times to amplify the DNA containing the primers and then, at least DNAs other than the amplified circular DNA synthesis in which, with the several fragments obtained in the step of DNA synthesised above, followed by an elongation reaction performed using the thermostable high-fidelity DNA polymerase. The method is useful for mutagenesis, particularly for introducing certain mutations at certain sites of the nucleotide sequence. The present method is simple, speedy, economical and widely applicable. The present method is simple, speedy, economical and widely applicable. The present method is simple, by altering the green fluorescent protein (GFP) sequence of Aequorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 VNRIELKGIDPKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                                                                                                                                                                                                       Method for mutagenesis, e.g. for introducing certain or random mutations at certain sites of the nucleotide sequence, comprises synthesizing a mutated strand and a complementary strand by use of megaprimers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for mutagenesis that comprises synthesising a mutated strand and a complementary strand by use of megaprimers. The method basically comprises a DNA synthesis in which one
                            . .3
note= "Wild-type GFP Met-Ser are replaced with Met-Val-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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                                                                               "GFP Phe64 is replaced by Leu"
                                                                                                            /note= "GFP Ser65 is replaced by Thr"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 13-14; 31pp; English.
             Location/Qualifiers
                                                                                                                                                                                                                           2000JP-00237166.
                                                                                                                                                                                                03-AUG-2001; 2001EP-00306650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237; Conservative
                                                                                  'note=
                                                                                                                                                                                                                                                                                   Miyawaki A, Sawano A;
                                                                                                                                                                                                                                                                                                             WPI; 2002-208112/27.
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                                                                                                                                                                                                                                                     (RIKE ) RIKEN KK.
                                                                                                                                                                                                                                                                                                                            N-PSDB; AAD27910.
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                          Misc-difference
                                                                  Misc-difference
                                                                                              Misc-difference
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                                                                                                                                                                    06-FEB-2002
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Matches
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comprising a phosphorylation polypeptide and a fluorescent procein or in poperative linkage, a donor molecule, a phosphorylatable domain, a phosphominoacid binding domain (PAABD) and an acceptor molecule. The phosphorylation indicators of the invention are useful for detecting kinases or phosphatases in a biological sample. They are also useful in high throughput analysis e.g. for detecting a kinase inhibitor. The present sequence is Aequorea victoria enhanced green fluorescent protein (EGPP) used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 DHYQQNTFIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phosphorylation indicator; fluorescent protein; detection; phosphatase; kinase; enhanced green fluorescent protein; EGFP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to chimeric phosphorylation indicators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel chimeric phosphorylation indicators, useful for detecting kinase/phosphatase in samples, has donor molecule, phosphorylatable domain, phosphoaminoacid binding domain, and acceptor molecule, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                               Aequorea victoria enhanced green fluorescent protein (EGFP).
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Pred. No. 6.6e-122;
1; Mismatches 1;
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                                                                                                                                                                                             AAE34958 standard; protein; 239
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99.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAY-2001; 2001US-00865291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang
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Best Local Similarity 99.2
Matches 237; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA.
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181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 239

Search completed: June 21, 2004, 15:54:11 Job time : 48.1111 secs

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Sequence 4, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 21, Appl
Sequence 6, Appli
Sequence 129, Appli
Sequence 129, Appli
Sequence 127, Appli
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Sequence 127, Appli
Sequence 127, Appli
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647, Appl
63, Appl
39, Appl
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125, Appl
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41, Appl
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                                                          June 21, 2004, 15:46:55 ; Search time 12.7778 Seconds (without alignments) 965.630 Million cell updates/sec
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Sequence 125, A
Sequence 2, Apj
Sequence 6, Apj
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Sequence
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Sequence
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-513-783A-46

US-09-502-641-3

US-09-920-922-2

US-09-920-922-2

US-09-921-921-2

US-09-172-063-1

US-09-172-063-21

US-09-172-063-21

US-09-172-063-21

US-09-177-1029

US-09-177-197-129

US-09-177-197-113

US-09-177-197-113

US-09-177-197-113

US-09-177-197-113

US-09-177-197-65

US-09-417-197-65

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                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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US-08-818-253-2
US-08-818-253-6
                                                                                                                                                                                389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                         protein search, using sw model
                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
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Match Length
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Maximum DB &
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Sequence 61, Ag
Sequence 43, Ag
Sequence 117, A
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; Sequence 3, Application US/09172063
; Patent No. 6150176
; GENERAL INFORMATION:
; APPLICANT: Hydwaki, Atsushi
; APPLICANT: Hopis, Juan
; APPLICANT: Hopis, Juan
; APPLICANT: Remington, S. James
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/071001
; CURRENT APPLICATION NUMBER: US/09/172,063
; CURRENT FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 09/094,359
; BARLIER FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1.4e-127;
1; Mismatches 1;
                                    US-08-818-253-4

US-09-417-197-51

US-09-417-197-51

US-09-417-197-71

US-09-417-197-71

US-09-513-783A-176

US-09-417-197-141

US-09-417-197-143

US-09-417-197-61

US-09-417-197-61

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                  -08-818-252-6
-08-818-253-4
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ORGANISM: Aequorea victoria
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Best Local Similarity 99.2
Matches 237; Conservative
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OTHER INFORMATION: EGFP
NAME/KEY: VARIANT
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DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239

181 1

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121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVOLA 180
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Best Local Similarity 99.2%;
Matches 237; Conservative
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ORGANISM: Aequorea victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: EGFP US-09-602-641-3
                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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US-09-920-922-2
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  RESULT 2
US-09-513-783A-46

US-09-513-783A-46

Sequence 46, Application US/09513783A

Patent No. 641659

GENERAL INFORMATION:
APPLICANT: Giuliano, Kenneth A.
TITLE OF INVENTION: A System for Cell Based Screening
TITLE OF INVENTION: A System for Cell Based Screening
CURRENT APPLICANION NUMBER: US/09/513,783A

CURRENT FILING DATE: 2000-02-25

NUMBER OF SEQ ID NOS: 180

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 46
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; APPLICANT: Taien, Roger Y.
; APPLICANT: Taien, Roger Y.
; TITLE OF INVENTION: ELUORESCENT PROTEIN INDICATORS;
; FILE REFERENCE: 07257/073001
; CURRENT APPLICATION NUMBER: US/09/316,919
; CURRENT FILING DATE: 1999-05-21
; NUMBER CF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                              Score 1263; DB 4;
Pred. No. 1.4e-127;
1; Mismatches 1;
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Pred. No. 1.4e-127;
1; Mismatches 1;
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Patent Nc. 6469154
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99.2%;
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Best Local Similarity 99.2%;
Matches 237; Conservative
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ORGANISM: Artificial Sequence
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ORGANISM: Aequorea victoria
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Best Local Similarity 99.2
Matches 237; Conservative
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US-09-316-919-4
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                                                                                                    1 MVSKGBELFTGVVPILVBLDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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APPLICANT: Miyawaki, Atsushi
APPLICANT: Miyawaki, Atsushi
APPLICANT: Miyawaki, Atsushi
APPLICANT: More, Juan
APPLICANT: Macher, Rebekka M.
APPLICANT: Wachter, Rebekka M.
APPLICANT: Wachter, S. Jame
TITLE OF INVENTION: FUURESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 0725/071001
CURRENT APPLICATION NUMBER: US/09/602,641
CURRENT APPLICATION NUMBER: US/09/612,641
PRIOR APPLICATION NUMBER: 09/172,063
PRIOR APPLICATION NUMBER: 09/172,063
PRIOR PILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 239
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Pred. No. 1.4e-127;
1; Mismatches 1;
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TITLE OF INVENTION: METHOD FOR MUTAGENESIS
FILE REFERENCE: 11283-012001
CURRENT APPLICATION NUMBER: US/09/920,922
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: JP 2000-237166
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                Sequence 3, Application US/09602641 Patent No. 6608189
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Partent No. 66/3610
GENERAL INFORMATION:
APPLICANT: Miyawaki, Atsushi
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Sequence 1, Application US/09364946
Patent No. 6306600
GENERAL INFORMATION:
APPLICANT: Kain, Steve
APPLICANT: Li, Xianqiang
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US-09-513-783A-2
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Patent No. 6130313
GENERAL INFORMATION:
APPLICANT: Kain, Steve
APPLICANT: Li, Xiangiang
TITLE OF INVENTION: Rapidly Degrading GFP-Fusion Proteins and Methods
TITLE OF INVENTION: of Use
FILE REFERENCE: D6100
CURRENT APPLICATION NUMBER: US/09/062,102
CURRENT APPLICATION NUMBER: US 60/060,855
EARLIER PILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 3
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Pred. No. 1.8e-127;
1; Mismatches 1;
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2
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                                                                                             ORGANISM: Aequorea victoria
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Best Local Similarity 99.2
Matches 237; Conservative
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US-09-062-102-1
                                                  LENGTH: 239
TYPE: PRT
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US-09-062-102-1
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TITLE OF INVENTION: Rapidly Degrading GFP-Fusion Proteins and Methods TITLE OF INVENTION: of Use FILE REFERENCE: D6100CIP/D2 CURRENT APPLICATION NUMBER: US/09/364,946 CURRENT FILING DATE: 1999-07-30 EARLIER APPLICATION NUMBER: US 09/191,233 EARLIER FILING DATE: 1998-11-13 NUMBER OF SEQ ID NOS: 14 LENGTH: 281
                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Sequence of the EGFP-MODC422-461 fusion protein.
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Patent No. 6416959
GENERAL INFORMATION:
APPLICANT: Giuliano, Kenneth A.
APPLICANT: Giuliano, Kenneth A.
TITLE OF INVENTION: A System for Cell Based Screening
TITLE OF INVENTION: A System for Cell Based Screening
CURRENT APPLICATION WHERE: US/09/513,783A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 180
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 294
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: GFP-DEVD-Annexin II construct
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Best Local Similarity 99.2%; Pred. No. 1.8e-127;
Matches 237; Conservative 1; Mismatches 1;
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                                                                 61 LVTTLTYGVQCFSRXPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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; Sequence 21, Application US/09172063
; Patent Nc. 6150176
; GENERAL INFORMATION:
    APPLICANT: Hiyawaki, Atsushi
    APPLICANT: Hiyawaki, Atsushi
    APPLICANT: Hopis, Juan
    APPLICANT: Remington, S. James
    TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
    TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
    PLIE REFERENCE: 07257/071001
    CURRENT APPLICATION NUMBER: US/09/172,063
    CURRENT FILING DATE: 1998-10-13
    EARLIER APPLICATION NUMBER: 09/094,359
    BARLIER FILING DATE: 1998-06-09
    NUMBER OF SEQ ID NOS: 38
    SOFTWARE: FastSEQ for Windows Version 4.0
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OTHER INFORMATION: GT-EGFP
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Matches 237; Conservative
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US-09-172-063-21
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US-09-602-641-21
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LENGTH: 323
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Sequence 21, Application US/09602641; Patent No. 6608189; GENERAL INFORMATION:

APPLICANT: Tsien, Roger Y. APPLICANT: Miyawaki, Atsushi, APPLICANT: Llopis, Juan

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Sequence 6, Application US/09085305

Sequence 6, Application US/09085305

Patent No. 6191269

GENERAL INFORMATION:

APPLICANT: Pollock, Allan

APPLICANT: Turck, Johanna

TITLE OF INVENTION: Selective Induction of Apoptosis in

TITLE OF INVENTION: Malignant Cancer Cells by Delivery of N-Terminal

TITLE OF INVENTION: Interleukin-1-Alpha Pro-Piece Polypeptide

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bozicevic & Reed, LLP

STREET: 285 Hamilton Ave, Suite 200

CITY: Palo Alto
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               APPLICANT: Reminger, S. James
TITLE OF INVENTION: FUUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 0.7557/071001
CURRENT APPLICATION NUMBER: US/09/602,641
CURRENT FILING DATE: 2000-06-22
PRIOR PILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 323
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Best Local Similarity 99.2%; Pred. No. 2.3e-127;
Matches 237; Conservative 1; Mismatches 1;
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29-MAY-1998
Wachter, Rebekka M
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Aequorea victoria
FEATURE:
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (0)...(0)
; OTHER INFORMATION: GT-EGFP
US-09-602-641-21
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APPLICATION NUMBER:
FILING DATE:
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RESULT 14
US-09-417-197-127
US-09-417-197-127
Sequence 127, Application US/09417197
Sequence 127, Application US/09417197
Sequence 127, Application US/09417197
Sequence 127, Application US/09417197
GENERAL INFORMATION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patentin version 3.0
SEQ ID NO 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LVTTLSYGVQCFSRYPDHMKQHDFPKSAMPEGYVQERTIFPKDDGNYKTRAEVKFEGDTL 120
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                       181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
                                                 321 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 379
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Pred. No. 3.5e-127;
1; Mismatches 1;
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                                                                                                                                                                           Sequence 48, Application US/09800170 Patent No. 6481667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT;
CORGANISM: Synechocystis PCC6803
US-09-800-170-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 99.1%;
Best Local Similarity 99.2%;
Matches 237; Conservative
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ORGANISM: Artificial Sequence
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APPLICANT: Ole THASTRUP, et al.
TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An TITLE OF INVENTION: On A Cellular Response
FILE REFERENCE: 3759-0110P
CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                                                                                                                                                                                                                                                                Length 364;
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Pred. No. 2.7e-127;
1; Mismatches 1;
                                                                 6510/102US1
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Patent No. 6518021
                     NAME: Francis, Carol L
REGISTRATION NUMBER: 36,513
REFERENCE/DOCKET NUMBER: 6510
TELECOMMUNICATION INFORMATION:
TELERHONE: 650-327-3400
TELEFAX: 650-327-3231
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.2%;
Matches 237; Conservative
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Matches 237; Conservative
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US-09-085-305-6
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US-09-417-197-129
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LENGTH: 379
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                                                                                                                                              LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                            VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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US-09-513-783A-170
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99.1%; Score 1263; DB 4; Length 459;
Best Local Similarity 99.2%; Pred. No. 3.8e-127;
Matches 237; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                US-09-512-7837-1701

Sequence 170, Application US/09513783A

Fatent Nc. 6416959

GENERAL INFORMATION: Kenneth A.

APPLICANT: Gapur, Ravi

TITE OF INVENTION: A System for Cell Based Screening;

FILE REFERENCE: 97-022-11

CURRENT FILING DATE: 2000-02-25

NUMBER CF SEQ ID NOS: 180

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                      RESULT 15
US-09-513-783A-170
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SEQ ID NO 170
LENGTH: 459
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Search completed: June 21, 2004, 16:04:03 Job time : 13.7778 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compuger Ltd.
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OM protein - protein search, using sw model

June 21, 2004, 15:54:20 ; Search time 34.7778 Seconds (without alignments) 1940:117 Million cell updates/sec Run on:

US-09-887-784-222L Perfect score: Title:

1274 1 MVSKGEELFTGVVPILVELD......VLIGFVTAAGITLGMDELYK 239 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

,1163542 segs, 282313646 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processir, Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

/ptodata/1/pubpaa/PCT Published_

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prodata/1/pubpaa/US09B_PUBCOMB.pep:*
prodata/1/pubpaa/US09C_PUBCOMB.pep:
prodata/1/pubpaa/US09_NEW_PUB.pep:*
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prodata/1/pubpaa/US10A_PUBCOMB.pep:* 6/ptodata/1/pubpaa/US10C_PUBCOMB.pep 6/ptodata/1/pubpaa/US10 NEW PUB.pep: 6/ptodata/1/pubpaa/US60 NEW B.pep: 6/ptodata/1/pubpaa/US60_PUBCOMB.pep: /prodata///pubpaa/US06 NEW PUB.pep: /ptodata///pubpaa/US06 PUBCOMB.pep: /ptodata///pubpaa/US07 NEW PUB.pep: /ptodata///pubpaa/PCTUS PUBCOMB.pep: /ptodata///pubpaa/US08 NEW PUB.pep: /ptodata///pubpaa/US08 NEW PUB.pep: /ptodata///pubpaa/US08 NEW PUB.pep: bpaa/US07_PUBCOMB.pep cgn2/

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Sequence 4, Appli	Sequence 4, Appli		Sequence 30, Appl	Sequence 32, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 4, Appli	_	<u>.</u>	Sequence 4, Appli	Sequence 3, Appli	Sequence 13, Appl	
ID	US-09-887-784-4	US-10-296-953-4	US-10-270-223-6	US-10-257-909A-30	US-10-257-909A-32	US-09-887-784-2	US-10-296-953-2	US-09-920-922-2	US-09-999-745-4	US-09-866-538-4	US-09-797-496B-2	US-09-794-308-4	US-09-865-291-4	US-10-457-982-3	US-10-121-258-13	
DB	6	12	14	14	14	σ	12	σ	σ	10	10	10	10	12	14	
% Query Match Length DB	239	239	363	893	1132	239	239	239	239	239	239	239	239	239	239	
A Query Match	100.0	100.0	100.0	100.0	100.0	99.4	99.4	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	
Score	1274	1274	1274	1274	1274	1266	1266	1263	1263	1263	1263	1263	1263	1263	1263	
Result No.	-	8	m	•	ហ	9	7	89	o,	10	11	12	13	14	15	

Sequence 7, Appli sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 11, Appli Sequence 11, Appli Sequence 2, Appli Sequence 31, Appli Sequence 31, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli	Sequence 3, Applia Sequence 9, Applia Sequence 9, Applia Sequence 33, Applia Sequence 33, Applia
US-10-221-461-7 US-10-100-957A-46 US-10-110-957A-46 US-10-138-411-3 US-10-389-640-3 US-10-389-640-3 US-10-314-861-11 US-09-931-23-1 US-10-314-861-37 US-10-314-861-37 US-10-314-861-39 US-10-314-861-39 US-10-314-861-39 US-10-314-861-39 US-10-314-861-39 US-10-314-861-39 US-10-318-411-11 US-10-338-411-13 US-10-338-411-13 US-10-338-411-13 US-10-389-640-11 US-10-389-640-11 US-10-389-640-11 US-10-389-640-11 US-10-389-640-11 US-10-389-640-11 US-10-389-640-11 US-10-389-640-11 US-10-389-640-11	10-338-411 10-389-640 10-388-411 10-389-640 10-033-717
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## ALIGNMENTS

RESULT 1  RESULT 1  Sequence 4, Application US/09887784  Patent No. US20020177189A1  GENERAL INFORMATION: APPLICANT: BJORN, Sara et al TILE OF INVENTION: MOVEL FLUORESCENT PROTEINS FILE REFERENCE: 3759-0115P  CURRENT FILING DATE: 2001-06-19  NUMBER OF SEQ ID NOS: 24  SOFTWARE: Patentin version 3.0  SEQ ID NO 4  LENGTH: 239  TENGTH: 239  TENGTH: 239  TENGTH: 239  TORGANISM: Aequoria Victoria
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		ö	09	09	120	120
		0; Gaps	PVPWPT	PVPWPT	FEGDIL	FEGDTL
239;		°,	CTTGKL	CTTGKL	TRAEVK	TRAEVK
Length		Indels	KLTLKFI	KLTLKFI	KDDGNYK	KODGNYK
DB 9;	-124;	0,	SEGDATYC	SEGDATYC	OERTIFE	OERTIFE
1274;	No. 2e-	natches	(FSVSGE	(FSVSGE	SAMPEGY	SAMPEGY
Score	Pred.	), Misn	GDVNGH	GDVNGH	COHDFFKS	KOHDFFKS
100.0%; Score 1274; DB 9; Length 239;	100.08;	ive (	VPILVEL	VPILVELI	SRYPDHME	SRYPDHM
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ch	1 Simil	239; C	1 MVSK	1 MVSK	61 LVTT	61 LVTT
Query Match	Best Local Similarity 100.0%; Pred. No. 2e-124;	Matches 239; Conservative 0; Mismatches 0; Indels	ò	ā	ž.	۵
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	VNR I	DHAC	HYC DHYC
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-10-296-953-4

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APPLICANT: Bernard R. TERRY et al.
TITLE OF INVENTION: Live cell procedures to identify compounds modulating intracelluli.
TITLE OF INVENTION: Live cell procedures to identify compounds modulating intracelluli.
FILE OF INVENTION: distribution of phosphodiesterase (PDE) enzymes
FILE REFERENCE: 3759-0125P
CURRENY APPLICATION NUMBER: US/10/257,909A
CURRENY FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 36
SEQ ID NOS: 36
SEQ ID NO 30
SEQ ID NO 30
LENGTH: 893
                                                                                                                                                                                       121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNYYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                           LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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100.0%; Score 1274; DB 14; Length 893;
Best Local Similarity 100.0%; Pred. No. 1.3e-123;
Matches 239; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Fusion between Aequorea victoria and human US-10-257-909A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 30, Application US/10257909A Publication No. US20030187056A1 GENERAL INFORMATION:
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Publication No. US2003014363471

GENERAL INFORMATION:

APPLICANT: Bioimage A/S

TITLE OF INVENTION: ANI IMPROVED WETHOD TO DETECT INTERACTIONS BETWEEN CELLULAR COMPON TITLE OF INVENTION: INTERACTIONS EFFECT OF EXTRACT QUANTITATIVE INFORMATION INTERACTIONS BY FLUORESCENCE REDISTRIBUTION.

FILE REFERENCE: 3759-0126P

CURRENT APPLICATION UNDERS: US/10/270,233

CURRENT FILING DATE: 2002-10-11
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Pred. No. 2e-124;
; Mismatches 0; 1
                         Sequence 4, Application US/10296953
Publication No. US20040072995A1
GENERAL INFORMATION:
APPLICANT: BJORN, SARA P.
APPLICANT: PAGLIARO, LEN
APPLICANT: THASTRUP, OLE
TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS
                                                                                                                                                                                  THILE DEFINITION INVEST. US/10/296,953
CURRENT APPLICATION NUMBER: US/10/296,953
CURRENT FILING DATE: 2002-11-26
PRIOR PILING DATE: 2000-10-619
PRIOR FILING DATE: 2000-06-19
PRIOR PLING DATE: 2000-06-19
PRIOR PLING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 60/212,681
PRIOR PLING DATE: 2001-05-10
PRIOR PLING DATE: 2001-05-10
PRIOR FILING DATE: 2001-05-10
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver: 2.1
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100.0%; Sc
Best Local Similarity 100.0%; Pr
Matches 239; Conservative 0;
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SEQ ID NO 6
LENGTH: 363
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- ORGANISM: Aequorea victoria
18-10-296-953-4
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procedures to identify compounds modulating intracellule:
TITLE OF INVENTION: Live cell procedures to i TITLE OF INVENTION: Live cell procedures to i TITLE OF INVENTION: Live cell procedures to i TITLE OF INVENTION: distribution of phosphod FILE REFERENCE: 3759-0125P
CURRENT APPLICATION NUMBER: US/10/257,909A
CURRENT FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 3.0
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Gaps

363;

Obery Match
Best Local Similarity 100.0%; Score 1274; DB 14; Length
Best Local Similarity 100.0%; Pred. No. 3.7e-124;
Matches 239; Conservative 0; Mismatches 0; Indels

TYPE: PRT

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RESULT 8
US-09-920-922-2
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Best Local Similarity 100.0%; Pred. No. 1.9e-123;
Matches 239; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                 ; OTHER INFORMATION: Fusion between Aequorea victoria and human US-10-257-909A-32
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TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS
FILE REFERENCE: 3759-0115P
CURRENT APPLICATION NUMBER: US/09/887,784
CURRENT FILING DATE: 2001-06-19
NUMBER OF EQ ID NOS: 24
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09887784 Patent No. US20020177189A1 GENERAL INFORMATION:
                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-887-784-2
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LENGTH: 239
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SEQ ID NO 32
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                                                                                                                        FEATURE:
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61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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Best Local Similarity 99.6%; Pred. No. 1.4e-123;
Matches 238; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                APPLICANT: BJORN, SARA P.
APPLICANT: THASTRUP, OLE
TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS
FILE REFERENCE: PLO095
CURRENT APPLICATION NUMBER: US/10/296,953
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: PA 2000 00953
PRIOR APPLICATION NUMBER: 60/212,681
PRIOR FILING DATE: 2000-06-19
PRIOR FILING DATE: 2001-05-10
PRIOR FILING DATE: 2001-05-10
PRIOR FILING DATE: 2001-05-10
PRIOR FILING DATE: 2001-05-10
PRIOR PRIOR SEQ ID NOS: 24
SOFTWARE: PAREIT NUMBER: PA 2001 00739
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PAREITING DATE: 2011-05-10
ILENGTH: 239
Sequence 2, Application US/09920922
Patent No. US20020083488A1
GENERAL INFORMATION:
APPLICANT: Miyawaki, Atsushi
APPLICANT: Sawano, Asako
TITLE OF INVENTION: METHOD FOR MUTAGENESIS
FILE REFERENCE: 11283-012001
CURRENT APPLICATION NUMBER: US/09/920,922
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: JP 2000-237166
PRIOR REPLICATION NUMBER: JP 2000-237166
PRIOR REPLICATION NUMBER: JP 2000-237166
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: '9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 239
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US-09-920-922-2
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; ORGANISM: Aequorea victoria
US-10-296-953-2
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Sequence 2, Application US/10296953 Publication No. US20040072995A1 GENERAL INFORMATION:

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                  61 LVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                          VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVOLA 180
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Sequence 4, Application US/0999745;
Patent Nc. US20020157120A1;
GENERAL INFORMATION:
APPLICANT: THE REGENES OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: Taien, Geoffrey
TITLE OF INVERTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS;
FILE REFERENCE: REGEN1470-1;
CURRENT APPLICATION NUMBER: US/09/999,745
CURRENT FILING DATE: 1999-05-21
PRIOR AFPLICATION NUMBER: 09/316,920
PRIOR AFPLICATION NUMBER: 09/316,920
PRIOR PLING DATE: 1999-05-21
NUMBER CF SEQ ID NOS: 67
SOUTHWARE: PATENTIN VERSION 3.0
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LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL
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Sequence 4, Application US/09866538

Publication No. US20030032088A1

GENERAL INFORMATION:

APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA

APPLICANT: Campbell, Robert

APPLICANT: Campbell, Robert

TITLE 0: INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS

FILE REFERENCE: REGENTS:00-2

CURRENT APPLICATION NUMBER: US/09/866,538

CURRENT FILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 29

SOFTWARS: Patentin version 3.0

SEQ ID NO 4
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Pred. No. 2.8e-123;
1; Mismatches 1; Indels
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99.2%;
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ORGANISM: Aequorea victoria
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Best Local Similarity 99.2
Matches 237; Conservative
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LENGTH: 239
TYPE: PRT
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LENGTH: 239
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US-09-999-745-4
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Aequorea victoria green fluorescent protein modified as described
OTHER INFORMATION: in specification
US-09-797-496B-2
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CURRENT APPLICATION NUMBER: US/09/797,496B
CURRENT FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 99.1%; Score 1263; DB 10; Best Local Similarity 99.2%; Pred. No. 2.8e-123; Matches 237; Conservative 1; Mismatches 1;
                                                   Score 1263; DB 10;
Pred. No. 2.8e-123;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09797496B Publication No US20030049597A1 GREENATION:
APPLICANT: Simon, Sanford M. APPLICANT: Chen, Yu
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; Sequence 4, Application US/09794308
; Publication No. US20030170911A1
; PUBLICATION:
; APPLICANT: REGENTS OF THE UNIVERS!
                                                     Query Match 99.1%;
Best Local Similarity 99.2%;
Matches 237; Conservative
; ORGANISM: Aequorea victoria
US-09-866-538-4
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Sequence 3, Application US/10457982
Publication No. US20030212265A1
GENERAL INFORMATION:
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ORGANISM: Aequorea victoria
FEATURE:
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Matches 237; Conservative
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LOCATION: (0)...(0)
OTHER INFORMATION: EGFP
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TING, Alice
APPLICANT: ZHANG, Jin
TILLE OF INVENTION EMISSION RATIOMETRIC INDICATORS OF PHOSPHORYLATION
FILE REFERENCE: REGENTS 09/09/865,291
CURRENT FILING DATE: 201-05-24
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PATCHIN VERSION 3.0
SEQ ID NO 4.5
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APPLICANT: ZACHARIAS, David
APPLICANT: BAIRD, Geoffrey
TITLE OF INVENTION: NON-ÓLIGOMERIZING FLUORESCENT PROTEINS
FILE REFERENCE: REGENIS30
CURRENT APPLICATION NUMBER: US/09/794,308
CURRENT FILING DATE: 2001-02-26
                                                                                                                                                                                                                                                                                                                                 1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICT
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Best Local Similarity 99.2%; Pred. No. 2.8e-123;
Matches 237; Conservative 1; Mismatches 1;
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                                                                                                                             PatentIn version 3.0
                                                                                                                                                                                  ; TYPE, PRT; ORGANISM: Aequorea victoria
US-09-794-308-4
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Matches 237; Conservative
                                                                                                        NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin vo
SEQ ID NO 4
LENGTH: 239
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181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
                              1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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; Publication No. US20030059835A1
; GENERAL INFORMATION.
; APPLICANT: Tsien, Roger
APPLICANT: Tsien, Roger
; TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
; TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME
; TITLE OF INVENTION: PROTEIN VALIANTS AND METHODS FOR MAKING SAME
; TITLE OF INVENTION: PROTEIN VALIANTS AND METHODS FOR MAKING SAME
; CURRENT APPLICATION NUMBER: 02/10/121,258
; CURRENT FILING DATE: 2001-02-04-10
; PRIOR APPLICATION NUMBER: 09/794,308
; PRIOR FILING DATE: 2001-02-26
; PRIOR FILING DATE: 2001-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                      GENERAL INCOMMENTATION:
APPLICANT: Taien, Roger Y.
APPLICANT: Miyawaki, Atsushi
APPLICANT: Miyawaki, Atsushi
APPLICANT: Llopis, Juan
APPLICANT: Llopis, Juan
APPLICANT: Wachter, Rebekka M.
APPLICANT: Wachter, Rebekka M.
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
TILE REFERENCE: 7025/071001
CURRENT APPLICATION NUMBER: US/10/457,982
CURRENT FILING DATE: 2003-06-09
PRIOR PLING DATE: 2000-06-22
PRIOR PLING DATE: 1996-10-13
PRIOR PLING DATE: 1998-10-13
PRIOR PLING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 239;
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99.2%; Pred. No. 2.8e-123;
iive 1; Mismatches 1;
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0
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                                                                                                                                                                                                                                                                                                                                                          181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                   1 MVSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                        0; Gaps
                                                                                                                                                       Query Match 99.1%; Score 1263; DB 14; Length 239; Best Local Similarity 99.2%; Pred. No. 2.8e-123; Matches 237; Conservative 1; Mismatches 1; Indels 0
) NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ IDN 0.13
; LENGTH: 2.39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Enhanced Green Fluorescent Protein (EGFP)
US-10-121-258-13
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Search completed: June 21, 2004, 16:09:28 Job time : 35.7778. sećs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 21, 2004, 15:46:00; Search time 10.3333 Seconds (without alignments) 2224.817 Million cell updates/sec

1 MVSKGEELFTGVVPILVELD.........VLIGFVTAAGITLGMDELYK 239 US-09-887-784-222L 1274 score: Title: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

283366 segs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Датараве :

PIR 78:*
1: Dir1:*
2: Dir2:*
3: Dir3:*
4: Dir4:* . . . . .

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	green-fluorescent			DNA-binding protei	leucyl-tRNA synthe	100		leucyl-tRNA synthe	DNA-directed DNA p	hypothetical prote	ipoa	S-layer protein pr	protective surface	protective surface	tRNA (uracil-5-)-m	DNA-directed DNA p	a-t	cellulase (EC 3.2.			hypothetical prote	u	imidazoleglycerol-	DNA-directed DNA p	IgA Fc receptor pr		photosystem II chl	hypothetical prote	alpha-amylase homo
		JQ1514	H72228	H64102	T06586	E82590	D83917	E70390	AC0582	A36028	D71614	140794	JC4930	JC4078	F64102	G81355	JDVLHH	JC5576	S29043	AD2052	JH0414	C97354	A99552	E84941	JDVLD	A60234	FCSOAG	T06936	T27856	T39539
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ۇ ئۇ	Match	97.4	8.2	7.2	7.1	7.0	6.9	6.9	6.9	6.9	6.9	6.9		6.8	•	6.8	6.7	6.7	6.7	6.7	6.7	9.9	9.9	٠	•	9.9	9.9	6.5	6.5	6.5
	COL	1241	0	91.5	90	89.5	88.5	87.5	۲.	87.5	7	87	87	86.5	86.5	98		85.5	85.5	82	85		84.5	84		83.5		83	83	83
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nitrogenase (EC 1.	neuraminidase, pro	hypothetical prote	hypothetical prote	carboxy-terminal p	proprotein convert	lipoxygenase (EC 1	water-stress-induc	synergohymenotropi	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	coatomer complex a	conserved hypothet
NICLMA	G95153	D90946	H85794	A41798	KXRTC1	T11852	S53488	S68225	G86643	C64468	S76940	T13674	T13673	ERHUAH	C64613
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534	740	682	682	682	752	865	263	310	1983	336	355	734	743	1224	393
6.5	6.5	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.3
82.5	82.5	82	82	82	82	82	81.5	81.5	81.5	81	81	81	81	81	80.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1	
JQ1514	

Green-fluorescent protein [validated] - hydromedusa (Aequorea victoria)
C;Species: Aequorea victoria
C;Date: 03-Dec-1999 #sequence revision 03-Dec-1999 #text change 23-Mar-2001
C;Accession: J80692; JQ1514; FQ0335; S48693; S51330; S51331
C;Accession: J80692; JQ1514; FQ0335; S48693; S51330; S51331
R;Prasher, D.C.; Eckenrode, V.K.; Ward, W.W.; Prendergast, F.G.; Cormier, M.J.
Gene 111, 229-233, 1992
A;Ritle: Primary structure of the Aequorea victoria green-fluorescent protein.
A;Reference number: JQ1514; MUID:92175527; PMID:1347277
A;Accession: JS0692
A;Molecule type: DNA
A;Residues: 1-107, S', 109-238 <PRA1>
A;Accession: JQ1514
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A,Accession: S1330
A,Molecule type: mRNA
A,Residues: 1-13, 'v',15-4,'Q',26-44,'N',46-153,'G',155-156,'P',158-171,'K',173-227,'R',;
A,Cross-references: EMBL:X8359; NID:g634008; PIDN:CAA58789.1; PID:g634009
A,Experimental source: clone gfp1
A,Accession: S5131
A,Molecule type: mRNA
A,Residues: 1-24,'Q',26-29,'R',31-83,'L',85-153,'G',155-156,'P',158-171,'K',173-208,'Q',;
A,Cross-references: EMBL:X83860; NID:g634010; PIDN:CAA58790.1; PID:g634011
A,Residues: 1-24,'Q',26-29,'R',31-83,'L',85-153,'G',155-156,'P',158-171,'K',173-208,'Q',;
A,Cross-references: EMBL:X83860; NID:g634010; PIDN:CAA58790.1; PID:g634011
A,Experimental source: clone gfp2
A,Experimental source: clone gfp2
A,Experimental source: clone gfg2
A,Experimental source: clone gfg2
A,Experimental source: A65692; PDB:10FL
A,Experiments: annotation; X-ray crystallography, 1.9 angstroms, residues 'A',2-79,'R',81-96
A,Note: engineered sequence based on JQ1514, cloned and expressed in Escherichia coli
B,Yang, F; Moss, LG.; Phillips Jr., G.N.
A,Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 'A',2-79,'R',81-96
A,Note: engineered sequence based on JQ1514, cloned and expressed in Escherichia coli
A,Note: Diotechnol. 14, 1246-1251, 1996
A,Title: The molecular structure of green fluorescent protein.
A,Reference number: A58953; MUID:98294543; PMID:9631087

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C,Accession: T06586
R;Sato, N.; Kazuno, A.A.; Ohta, N.; Ohshima, K.
submitted to the EMBL Data Library, June 1996
A,Description: Identification of a novel family of DNA-binding proteins with A;Reference number: Z15774
A,Accession: T06586
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-binding protein PD2 - garden pea
C;Species: Pisum sativum (garden pea)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-632 <SAT>
A;Cross-references: EMBL:X98740; NID:e995229; PIDN:CAA67292.1; PID:e275185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 LVBLDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLSYGVQCFSRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.1%; Score 90; DB 23.3%; Pred. No. 12; :ive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 PDHMKQHDFFKSAMPEGYV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: cv. Alaska
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ses 49; Conserv
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A,Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A,Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A,Reference number: A72200; MUD: 99287316; PMID: 10360571
A,Reference number: DNA
A,Molecule type: DNA
A,Redidues: 1-785 <ARN>
A,Redidues: 1-785 <ARN>
A,Redidues: 1-785 <ARN>
A,Redidues: 1-785 <ARN>
A,Cross-references: GB: AE001806; GB: AE000512; NID: 94982196; PIDN: AAD36691.1; PID: 9498219
A,Gene: TM1624
A, Contents: annotation, X-ray crystallography, 1.9 angstroms
C; Comment: This protein is excited by the photoprotein aequorin (see PIR:AQJFNV) emittin C; Comment: The chromophore of this protein is formed by modification of Ser-dehydro-Tyr-C; Genetics:
A, Genetics:
A, Genetics:
A, Introns: 69/3; 167/3
A, Introns: 69/3; 167/3
C; Superfamily: green-fluorescent protein
C; Keywords: chromoprotein; luminescence
F; 65-67/Cross-link: 5-imidazolinone (Ser-Gly) #status experimental
F; 66/Modified site: dehydrotyrosine (Tyr) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
H7228
hypothetical protein TM1624 - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
R;Nelson, K.B.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TILSYGVOCFSRYPDHMKQHDFFKSAMPEGYVOERTIFFKDDGNYKTRAEVKFEGDTLVN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 RIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADH 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VTTFSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFYKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                  VITLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTLV 121
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                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLV
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                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                           Query Match 97.4%; Score 1241; DB 1; Best Local Similarity 97.1%; Pred. No. 1.2e-96; Matches 231; Conservative 4; Mismatches 3;
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Best Local S
Matches 46
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DB 2; Length 632; 12;

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Rightenson H64102
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Rightenson R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A. Godyne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Science 269, 496-512, 1995
Rightenson 269, 496-512, 1995
A,Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, C.A.; Reference number: A64000, MUID:95350630; PMID:7542800
A,Reference number: A64000, MUID:95350630; PMID:7542800
A,Accession: H64102
A,Accession: H64102
A,Accession: H64102
A,Accession: H64102
A,Accession: GB:U32774; GB:L42023; NID:g1573942; PIDN:AAC22581.1; PID:g1573943; T:
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      leucine-tRNA ligase (BC 6.1.1.4) - Haemophilus influenzae (strain Rd KW20)
NyAlternate names: leucyl-tRNA synthetase
C;Species: Haemophilus influenzae
C;Species: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       409 GKRQVNYRLRDWGVSRQRYWGAPIPMLTLENGDVVPA------PMEDLPIILPEDVVWD
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C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
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Best Local Similarity 24.1%; Pred. No. 13;
Matches 46; Conservative 26; Mismatches
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0y 126 LKGIDFKENDLINGTRELENGWARTSGEREGEBELKUSGNSERDTKKELEDGGKNG-E 467  0y 126 LKGIDFKENDLINGTKELENGWARTKEINSPRINGTRINGYTVARKKKN 160  468 LKGIZFYNSTRILDEKERALGAKILKEINSPRINGVENDRAKKKN 160  161 GIKVNFKIRNIEDGSVOLAMHY 184  162 GIKVNFKIRNIEDGSVOLAMHY 184  163 GIKVNFKIRNIEDGSVOLAMHY 184  164 GIKVNFKIRNIEDGSVOLAMHY 184  165 S28 OSGVEDVAKKNIQDDSKPEBESLHKADKYR 557  RESEUTS 5  165 GIKVNFKIRNIEDGSVOLAMHY 184  167 GIKVNFKIRNIEDGSVOLAMHY 184  168 GIKVNFKIRNIEDGSVOLAMHY 184  168 GIKVNFKIRNIEDGSVOLAMHY 1857  168 GIKVNFKIRNIEDGSVOLAMHY 1857  169 GIKVNFKIRNIEDGSVOLAMHY 1857  169 GIKVNFKIRNIEDGSVOLAMHY 1857  169 GIKVNFKIRNIEDGSVOLAMHY 1857  169 GIKVNFKIRNIEDGSVOLAMHY 1857  160 GIKVNFKIRNIEDGSVOLAMHY 1857  160 GIKVNFKIRNIEDGSVOLAMHY 1857  160 GIKVNFKIRNIEDGSVOLAMHY 1857  160 GIKVNFKIRNIEDGSVOLAMHY 1857  160 GIKVNFKIRNIEDGSVOLAMHY 1857  160 GIKVNFKIRNIEDGSVOLAMHY 1857  160 GIKVNFKIRNIEDGSVOLAMHY 1857  160 GIKVNFKIRNIEDGSVOLAMHY 1857  160 GIKVNFKIRNIEDGSVOLAMHY 1857  160 GIKVNFKIRNIEDG	Nuclear Acids Res 28, 411-431, 2000  Afficiac Acids Res 28, 411-431, 2000  Afficiac Acids Res 28, 411-431, 2000  Afficiac Acids Res 28, 411-431, 2000  Afficiac Acids Res 28, 411-431, 2000  Afficiac Res 28, 411-431, 2000  Afficiac Res 28, 411-431, 2000  Afficiac Res 28, 411-431, 2000  Afficiac Res 28, 411-431, 2000  Afficiac Res 28, 411-431, 2000  Afficiac Res 28, 411-431, 2000  Afficiac Res 28, 411-431, 2000  Afficiac Res 28, 411-431, 2000  Afficiac Res 28, 411-431, 2000  Afficiac Res 28, 411-431, 2000  C. Superfamily DNA topoicomerae (ATP-hydrolyzing) chain B  Query Match  Best Local Similarity 21.94; Pred. No. 17;  Afficiac Res 20, 411-431, 2000  C. Superfamily DNA topoicomerae (ATP-hydrolyzing) chain B  Query Match  Best Local Similarity 21.94; Pred. No. 17;  Afficiac Res 20, 411-41, 2000  C. Superfamily DNA topoicomerae (ATP-hydrolyzing) chain B  Query Match  Best Local Similarity 21.94; Pred. No. 17;  Afficiac Res 20, 2000  C. Superfamily DNA topoicomerae (ATP-hydrolyzing) chain B  C. Superfamily DNA topoicomerae (ATP-hydrolyzing)  C. Superfamily DNA topoicomerae (ATP-hydrolyzing)  C. Superfamily DNA topoicomerae (ATP-hydrolyzing)  C. Superfamily DNA topoicomerae (ATP-hydrolyzing)  C. Superfamily DNA topoicomerae (ATP-hydrolyzing)  C. Superfamily DNA topoicomerae (ATP-hydrolyzing)  C. Superfamily DNA topoicomerae (ATP-hydrolyzing)  C. Superfamily DNA topoicomerae (ATP-hydrolyzing)  C. Superfamily DNA topoicomerae (ATP-hydrolyzing)  C. Superfamily DNA topoicomerae (ATP-hydrolyzing)  C. Superfamily DNA topoicomerae (ATP-hydrolyzing)  C. Superfamily DNA topoicomerae (ATP-hydrolyzing)  Afficiac BNA topoicomerae (ATP-hydrolyzing)  Afficiac BNA topoicomerae (ATP-hydrolyzing)  Afficiac BNA topoicomerae (ATP-hydrolyzing)  Afficiac BNA topoicomerae (ATP-hydrolyzing)  Afficiac BNA topoicomerae (ATP-hydrolyzing)  Afficiac BNA topoicomerae (ATP-hydrolyzing)  Afficiac BNA topoicomerae (ATP-hydrolyzing)  Afficiac BNA topoicomerae (ATP-hydrolyzing)  Afficiac BNA topoicomerae (ATP-hydrolyzing)  Afficiac BNA topoicomerae (
200 -HYLSTQSALSKDPNEKR 216	A.Combermily: nitrogen fixation protein nifS C.Superfamily: nitrogen fixation protein nifS C.Keywords: phosphoprotein; pyridoxal phosphate; sulfurtransferase F.195/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted F.318/Active site: Cys (cysteine persulfide intermediate) #status predicted
Db 483 VAFSGTGSPIKTDPEWRK 500 RESULT 6 D83917 DNA topoisomerase IV subunit B BH2140 [imported] - Bacillus halodurans (strain C-125) C;Species: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C;Accession: D83917	Query Match Best Local Similarity 25.4%; Pred. No. 9.7; Best Local Similarity 25.4%; Pred. No. 9.7; Matches 49; Conservative 30; Mismatches 91; Indels 23; Gaps 8;  Qy

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94 VQERTIFFKD--DGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYN--YNSH 149
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DNA-directed DNA polymerase (EC 2.7.7.7) II catalytic chain - yeast (Gaccharomyces cerev DNA-directed DNA polymerase II chain A; protein N0825; protein YNL262 C; Species: Saccharomyces cerevisiae
C; Species: Saccharomyces cerevisiae
C; Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 21-Jul-2000
C; Accession: A36028; B36028; 5560319; S63235; S65121
R; Morrison, A.; Araki, H.; Clark, A.B.; Hamatake, R.K.; Sugino, A.
Ccell 62, 1143-1151, 1990
A; Title: A third essential DNA polymerase in Saccharomyces cerevisiae.
A; Reference number: A36028
A; Molecule type: DNA
A; Residues: 1-222 < MOR>
A; Accession: A36028
A; Molecule type: DNA
A; Residues: 1-222 < MOR>
A; Accession: B36028
A; Molecule type: protein
A; Residues: 1214-1216, 'X', 1218-1221 < MO2>
A; Residues: 1214-1216, 'X', 1218-1221 < MO2>
A; Residues: 1214-1216, 'X', 1218-1221 < MO2>
A; Residues: 1214-1216, 'X', 1218-1221 < MO2>
A; Residues: 1214-1216, 'X', 1218-1221 < MO2>
A; Residues: 1214-1216, 'X', Date Inbrary, October 1995
A; Description: The sequence of a 24152 by segment from the left arm of chromosome XIV fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cybecies: Salmonella enterica subsp. enterica subsp. enterica serovar Typhi (s Cybecies: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi (cybecies: Davecies has also been called Salmonella typhi (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybecession: ACOS82 (cybe
224 NGKRSGTENVVGILSLAKALEIIVSNFSRYQBQLKKLRDLFENLLLEA-LPDAQIVGKDA 282
                                                                                                                                                                                                ERSPSISSVIMPKFFGAEIVNKLSEKGIYCSTGSACLSGEYEPNKHMLKMGFSQEKALRM 342
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23.3%; Pred. No. 29;
tive 21; Mismatches
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                                                                                                                                                                                                                                                                                                                     162 IKVNFKIRHNIED 174
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343 VRFSFGLLNKEEE 355
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Matches 42; Conservative
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A;Reference number: S63235
A;Accession: S63235
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-222 <SEW>
A;Cross-references: RBB1.Z1538; NID:g1302316; PIDN:CAA96169.1; PID:g1302317; GSPDB:GN000,
A;Experimental source: strain S288C
R;Sen-Gupta, M.; Lyck, R.; Fleig, U.; Niedenthal, R.K.; Hegemann, J.H.
Yeast 12, S05-514, 1996
A;Title: The sequence of a 24 152 bp segment from the left arm of chromosome XIV from Sac
A;Reference number: S65111; MUID:96310631; PMID:8740425
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A,Residues: 1-2573 <GAR>
A,Cross-references: GB:AE001396; GB:AE001362; NID:g3845188; PIDN:AAC71881.1; PID:g384519()
A,Experimental source: clone 3D7
C,Genetics:
A,Gene: PFB0460c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: D71614
R;Gardner, M.J; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.
P;Gardner, M.J; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A1600; MUID:99021743; PMID:9804551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Status: nucleic acid sequence not shown, translation not shown
A;Nateus: nucleic acid sequence not shown, translation not shown
A;Nalecule type: DNA
A;Cross-references: EMBL:X92494, NID:g1045236, PIDN:CAA63235.1; PID:g1045247
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
C;Genetics:
A;Gene: SGD:POL2; MIPS:YNL262w
A;Cross-references: SGD:S0005206; MIPS:YNL262w
A;Gene: SGD:POL2; DUN2; MIPS:YNL262w
A;Gene: SGD:POL2; DUN2; MIPS:YNL262w
A;Cross-references: SGD:S0005206; MIPS:YNL262w
C;Nexefamily: DNA-directed DNA polymerase II
C;Keywords: DNA binding; nucleotidyltransferase; nucleus; zinc finger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               943 FFEVDGPYKAMILPSSKEEGKGIKKRYAVFNEDGSLAELKGFELKRKGEL---QLIKNFQ 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-2221 <SEN>
A,Cross-terences: EMBL:X92494; NID:g1045236; PIDN:CAA63235.1; PID:g1045247
R,Sen-Gupta, M.; Lyck, R.; Niedenthal, R.K.; Fleig, U.N.; Hegemann, J.H.
submitted to the Protein Sequence Database, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein PFB0460c - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 LPVPWP-TLVTTLSYGVQCFSRYPDHM-----KQHDFFKSAMPEGYV----QERTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       883 LPKSFPETYFFTLENGKKLYLSYPCSMLNYRVHQKFTNHQYQELKDPLNYIYETHSENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.9%; Score 87.5; DB 1; Length 2222; 28.2%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.9%; Score 87.5; Dl
Best Local Similarity 28.2%; Pred. No. 1e+0'
Matches 37; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 FFKDDGNYKTR--AEVKFEGDTLVNR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1000 SDIFKVFLEGD 1010
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Indels 13;

53;

14;

668

97

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surface antigen of Haemophilus influ
                                     A;Cross-references: GB:U38842; NID:g1055336; PIDN:AAC44405.1; PID:g1055337
A;Experimental source: strain NM105
C;Comment: This protein is a glycoprotein. It functions as protective coats, molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :|:| |||| :|
551 KEVPPQTGVVKVLDVTTTNEGSIGTSSIKVKGENVĞAGTIHFQNPNASGEGYĞSLHVEVT 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 TIFFKDDGNYKTRAEVKFEGDTLVNRIELKGID---FKEDGNILGHKLEYNYNSHNVYIM 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----NGIKVNFKIRHN---IEDGSVQLADH 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 FFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNI---LGH-----KLEYNYNS 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       669 RV-----GNDKI-ASAKIEGKTLKVTGKTAGVTDVILTKDGATAGH-ATITVTQENIQIT 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       722 SVKFKDVEVEQFENRKVNIDRVLDVVKSDKDDVLNGIKLNISTEHKVRIVDEGTEG---- 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 HNVYIMADKQK-NGIKVNFKIRHNIEDGSVQLADHYQQ------NTPIGDGPVLL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Variety: type b
C;Date: 30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 29-Sep-1999
C;Accession: JG4078
R;Flack, F.S.; Loosmore, S.; Chong, P.; Thomas, W.R.
Gene 156, 97-99, 1995
A;Title: The sequencing of the 80-kDa D15 protective surface antigen of Haer
A;Reference number: JG4078, MUID:95255676, PMID:7737523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 CTTGKLPVPWPTLV-----TTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           611 KSNIGHEAPRLELVSKAGQKGEAADTTLGAGNTVAYQLSNYTTEGVYADAADLAGY--EF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 LSYGVQCFSRYPDHMKQHDF-------RTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A/Accession: JC4078
A/Molecule type: DNA
A/Molecule type: DNA
A/Molecule type: DNA
A/Molecule type: DNA
A/Molecule type: DNA
A/Molecule type: DNA
A/Experimental source: type b
A/Experimental source: type b
C/Superfamily: protective surface antigen D-15
C/Superfamily: protective surface antigen
F/1-19/Domain: signal sequence #status predicted <SIG>
F/1-19/Pomain: signal sequence #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - Haemophilus influenzae (type
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11.9%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                          Length 874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 YQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTA
                                                                                                                                            C)Generics:
A;Gene: olpA
S;Superfamily: S-layer repeat homology
F;1-29/Domain: signal sequence #status predicted <SIG>F;30-874/Product: S-layer protein #status predicted <MAT>F;157-209/Domain: S-layer repeat homology <SLR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 BELF--TGVVPIL---VELDGDVNGHKFSVSGEGEGDAT
                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                      Match 6.8%; Score 87; DB Cocal Similarity 22.8%; Pred. No. 33; les 65; Conservative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.9%; Pred. No. 32;
tive 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protective surface antigen D-15 precursor
C;Species: Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 ADKQK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 21.9
hes 48; Conservative
       A;Residues: 1-874 <ZHU>
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Best Local S:
Matches 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    5-layer protein precursor - Bacillus licheniformis
C;Species: Bacillus licheniformis
C;Date: 22-Oct-1996 #sequence_revision 01-Nov-1996 #text_change 15-Oct-1999
C;Accession: JC4930
B;Zhu, X.; McVeigh, R.R.; Malathi, P.; Ghosh, B.K.
Gene 173, 189-194, 1996
A;Title: The complete nucleotide sequence of the Bacillus licheniformis NM105 S-layer-en
A,Reference number: JC4930; MUD:97082965; PMID:8964497
A,Accession: JC49310
A,Accession: JC49310
A,Accession: JC49310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Pathway: acetoin dehydrogenase enzyme system
C; Superfamily: Alcaligenes dihydrolipoamide dehydrogenase; dihydrolipoamide dehydrogenase
C; Superfamily: Alcaligenes dihydrolipoamide dehydrogenase; dihydrolipoamide
C; Superfamily: Alcaligenes dihydrolipoamide; NAD; oxidoreductase; redox-active disulfide
F; S-77/Domain: lipoyl/biotin-binding homology cLPB>
F; 119-56/LDomain: dihydrolipoamide dehydrogenase homology cLDb>
F; 287-315/Region: beta-alpha-beta NAD nucleotide-binding fold
F; 287-315/Region: beta-alpha-beta NAD nucleotide-binding fold
F; 153-158/Disulfide bonds: redox-active #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Description: catalyzes the oxidation of dihydrolipoamide to lipoamide using NAD A; Pathway: acetoin dehydrogenase enzyme system
                                                                               209
                                                                                                                     :|:: ; | : |
126 LKKETILCKDIKSGSNDPMDEISLFKDDMVDDKELK--DFEKSSLKIKNKEVYNFIYNKM 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 TLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNR 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         347 CKVTRIEQGEDGLKVSFIGDKGEESIDVEKVLIAVGRRSNIEGLDVE-KIGVKTEGGSII 405
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                                                                           NVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALS
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C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52;
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dihydrolipoamide dehydrogenase (BC 1.8.1.4) [validated]
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237 TYLKRERDYM 246
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A; Residues: 1-578 < KRU>
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Search completed: June 21, 2004, 16:01:57 Job time: 10.3333 secs
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: G8135.
C;Accession: G8135.
R;Parkhili, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 655-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENA (uracil-5-)-methyltransferase (EC 2.1.1.35) Cj0831c [imported] - Campylobacter jeju
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A;Molecule type: DNA
A;Residues: 1-37× cPAR>
A;Cross-references: GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB73096.1; PID:g696827
A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                          protective surface antigen D-15 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 18-Sep-1998
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 18-Sep-1998
C;Coccession: F64102
R;Plaischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, i. Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Killey, J.M.; Weidman, i. D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Glodek, A.; Kelley, J.M.; Weidman, Science 269, 496-512, 1995
A;Authors: Ghehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Accession: F64102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 PFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNI---LGH------KLEYNYNS 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FFENYDNSKSDISSNYKRITYGSNVTL-GFPVNENNSYYVGLGHTYNKISNFALEYN--- 555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           556 RNLYIQSMKFKGNGIKTN-----DFDFSFGWNYNSLNRGYFPTKGVKASLG-GRVTI 606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-808 <TIGR>. A;Residues: 1-808 <TIGR>. A;Cross-references: GB:L42023; TIGR:HI0917 C;Superfamily: protective surface antigen D-15 C;Keywords: surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 808;
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12;
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197 P--DNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLG 233
                                  594 PGSDNKYYKLSADVQGFYPLDRDHLWVVSAKASAGYANG 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 HNVYIMADKQK-NGIKVNFKIRHNIEDGSVQLADHYQQ--
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C;Keywords: methyltransferase; S-adenosylmethionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
6.8%; Score 86.5; D
Best Local Similarity 21.9%; Pred. No. 33;
Matches 48; Conservative 30; Mismatches
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Best Local Similarity
Matches 30; Conserva
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--GNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIE 173
14 EKHSFIKKYFKEFYTKDFKLFASKDKHYRTRABLSFYHENDTLFYAMFDPKSKKKYIIEY 73
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

June 21, 2004, 15:42:24; Search time 6.44444 Seconds (without alignments) 1931.085 Million cell updates/sec

US-09-887-784-222L 1274 1 MVSKGEELFTGVVPILVELD......VLlGFVTAAGITLGMDELYK 239 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P42212 aequorea vi				Q8zqz6 salmonella	P21951 saccharomyc		bacillu	-	haemoph:			P18947 caenorhabdi						P24506 discopyge o		Q98qp0 mycoplasma	Q8ehp4 shewanella		Q8wts6 homo sapien		O88900 rattus norv	O00116 homo sapien		-		_	386	P28840 rattus norv
SUMMARIES	ID	GFP AEQVI	SYL_HAEIN		SYL_SALTI	SYL_SALTY	DPOE_YEAST		SLAP_BACLI	CP51_CANGA	D152 HAEIN	D151_HAEIN	SYL XYLFT	VIT4 CAEEL	TRMA CAMJE	DPOL_HPBHE	D153 HAEIN	ITH3_MESAU	GUN_BACS6	SY62 DISOM	AMPA_WIGBR	PEPF_MYCPU	SYL SHEON	HIS7_BUCAI	SET7_HUMAN	YC03 KLEPN	GRBE RAT	ADAS_HUMAN				NIFD_CLOPA		NECI_RAT
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Q7vnf0 haemophilus Q58743 methanococc	Q99nbl mus musculu P53621 homo sapien	O25443 helicobacte	P97275 cavia porce	Q8xbn8 escherichia	Q8fjy9 escherichia	P07813 escherichia	Q08684 chlamydomon	P91679 drosophila	Q9pkt7 chlamydia m
SYD_HAEDU YD48_METJA	AC2L_MOUSE COPA_HUMAN	TRMB_HELPY	ADAS_CAVPO	SYL_ECO57	SYL_ECOL6	SYL ECOLI	PSBC CHLEU	OPT1 DROME	TRXB_CHLMU
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589 336	682 1224	393	658	860	860	860	461	737	312
6.4	6.4 4.4	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.2
81.5 81	81 81	80.5	80.5	80.5	80.5	80.5	80	80	79.5
34 35	36 37	38	39	40	41	42	43	44	45

### ALIGNMENTS

RESULT 1

X-RAY

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Query Match
Best Local Similarity 98.3
Matches 234; Conservative
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238 AA,
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ZEMN;
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-i- BIOTECHNOLOGY: Has become a useful and ubiquitous tool for making chimeric proteins of GFP linked to other proteins where it functions as a fluorescent protein tag. GFP tolerates N-and C-terminal fusion to a broad variety of proteins. It has been expressed in bacteria, yeast, slime mold, plants, Drosophila, zebrafish, and in mammalian cells. As a noninvasive fluorescent marker in living cells, it allows for a wide range of applications where it may function as a cell lineage tracer, reporter of gene expression, or as a measure of protein-protein interactions.

NOTE-ISBUE 10 d'une 2001, WWW-"http://www.expasy.org/spotlight/articles/sptl1011.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-aib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

MEDLINE-99238003; PubMed=10220315;

MEDLINE-99238003; PubMed=10220315;

A Elsiger M.A., Wachter R.M., Hanson G.T., Kallio K., Remington S.J.;

Structural and spectral response of green fluorescent protein

variants to changes in pH.";

L Biochemistry 38:2296-3301(1999).

- |- FUNCTION: Energy-transfer acceptor. Its role is to transduce the blue chemiluminescence of the protein aequorin into green fluorescent light by energy transfer. Fluorescess in vivo upon receiving energy from the Ca(2+)-activated photoprotein aequorin. Absorbs light maximally at 395 nm and exhibits a smaller absorbance peak at 470 nm. The fluorescence emission spectrum peaks at 509 nm with a shoulder at 540 nm.

- I SUBUNIT: Monomer.

- TISSUE SPECIFICITY: Photocytes.
              CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF MUTANT WITH YELLOW EMMISSION
                          MEDLINE-98455509; PubMed-9782051; Wachter R.M., Elsliger M.A., Kallio K., Hanson G.T., Remington S.J.; Wachter R.M., Elsliger M.A., Kallio K., Hanson G.T., Remington S.J.; "Structural basis of spectral shifts in the yellow-emission variants of green fluorescent protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M62654; AAA27722.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M62653; AAA27721.1; -. EMBL; L29345; AAA58246.1; -. EMBL; X96418; CAA65278.1; -.
                                                                       of green fluorescent protei
Structure 6:1267-1277(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189C; 17-NOV-00.
18FP; 07-JUL-97.
1C4F; 14-JUN-00.
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1EME;
1EMF;
1EMG;
1EMK;
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07-JAN-03. 28-AUG-02. 10-APR-02.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVQLAD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWVLLGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VITLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                  5-imidazolinone (Ser-Gly)
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                                                                                                                                                   2,3-DIDEHYDROTYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3,
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98.3%; Pred. No. 4.7e-96;
iive 1; Mismatches 3;
                                                                                                                                                                   PDB; ZEMO; 20-AUG-97.
InterPro; IPR009017; GFP_like.
InterPro; IPR000786; Green_fl_protein.
Pfam; PF01353; GFP; 1.
                                                                          PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl protein; 1.
Luminescence; 3D-structure.
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181 HYQQNTFIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | | | | : | : | : | | | | | | | | 314 TGDKLPI-WANFVLMHYGTGAVMAVPAH-DQRDF-----EFAQKYSLPIKQVIAPLA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TICRFAMS; TICR00396; leuS bact; 1.
PROSITE; PS00178; AA TRNA_LIGASE I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diphosphate + L-leucyl-tRNA(Leu).
-!- SUBUNT: Monomer (By similarity).
-!- SUBCELLULA LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-95350630; PubMed=7542800; Recommender Krazo, Kirkness E.F., Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Rarlavage A.R., Bult C.J., Tomb., F.F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom B., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                            01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59;
                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
NCBL_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.2%; Score 91.5; DB 1; Length 861;
24.1%; Pred. No. 6.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60; Indels
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ATP (BY SIMILARITY)
                                 861 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP, MF_00049; -; 1.
InterPro; IPR002302; Leu-tRNASyntla.
InterPro; IPR001300; tRNA-synt la.
InterPro; IPR001412; tRNA-synt l.
InterPro; IPR001412; tRNA-synt l.
InterPro; IPR00131; tRNA-synt l.
InterPro; IPR003008; ValRS_ILERS_edit.
Pfam; PF00133; tRNA-synt l.; 1.
PRINTS; PR00985; TRNASYNTHEU.
                                                                                                 01-NOV-1995 (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U32774; AAC22581.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 269:496-512(1995)
                                 STANDARD;
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623
622
                                                                                                                                                                                                                                                                Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; H64102; H64102.
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                                                                                                                                                                                                                                     OR HI0921.
                                                                                                                                01-NOV-1995
28-FEB-2003
                                 SYL HAEIN
P43827;
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SEQUENCE
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SYL HAEIN

1D SYB H

1D SYB H

1D O1-NO

DT O1-NO

DT O1-NO

DT O1-NO

DT O1-NO

OS Bacteo

OC Baste

OC Bacteo

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                                                                                                     202
104 DGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADK-QKNGI 162
                                                                                                                                      SIGNATURE-20365717; PubMed=10910347;
Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
Simpson A.J.G., Reinach F.C., Arruda P.B., Baia G.S., Baptista C.S.,
Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
Barros M.H., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
Colauto M.R.P., Canargo L.E.A., Carraro D.M., Carrer H.,
Colauto M.B., Colombo C., Costa F.F., Costa M.C.R., Costa Neto C.,
R. Colombo C., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
R. Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
R. Faranca S.C., Franco M.C., Frohme M., Furlan L.R.,
R. Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
R. Chemos M.D., Junqueira M.L., Kemper B.L., Kitajima J.P.,
R. Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
R. Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
R. Macques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
Marques M.V., Martins E.C., Miyaki C.Y., Montetoriar O.L.,
Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
Moon D.H., Nobrege F.G., Nunes L.R., Oliveira M.R.,
A de Soliveira M.C., de Sluva M.B.L.Z., Squeira W.J., Reavaski H.E.,
A da Silva A.C.R., da Silva M.M., da Silva F.R., Silva M.A., Tsuhako M.H.,
A da Silveira U.F., Silvestri M.L.Z., Squeira W.J., Tsuhako M.H.,
A da Silveira W.P., Terenzi M.F., Truffi D., Tsai S.N., Tsuhako M.H.,
A da Silveira W.S., Sattla M.A., Satz M., Maidanis J., Setubal J.C.,
A dago M.A., Zatz M., Maidanis J., Setubal J.C.,
A dayanty M. A., Zatz M., Maidanis J., Setubal J.C.,
A dayanty M. L. L. Shueira W.J., Band M. H.,
A dayanty M. L. L. Solveira M.A., Janda M. H.,
A dayanty M. L. L. Solveira M.A., Jatz M., Maidanis J., Setubal J.C.,
A zago M.A., Zatz M., Maidanis J., Setubal J.C.,
A zago M.A., Zatz M., Maidanis J., Setubal J.C.,
A langal W. M. L. L. Langer M. M. L. L. Langer M. M. L. L. Langer M. M. L. L. Langer M. M. L. L. Langer M. M. L. L. Langer M. M. L. L. Langer M. 
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-----IADKLEKLGV
                                                                                                     ---NIEDGSVQLADHYQQNTPIGDGPVLLPDNHYL-
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-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
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                                                365 DEEIDLTKQAFVEHGKLVNSDEFDGKNF--DGAFNG
                                                                                                                                                                                                                                                                                                                                                                                          879 AA.
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                                                                                                        163 ---KVNFKIRH-------
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                                                                                                                                                                                                                                                         462 GVKSPINADPN 472
                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                         203 STQSALSKDPN
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CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.9%; Score 87.5; 23.3%; Pred. No. 14
                                diphosphate + L-leucyl-tRNA(Leu).
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Best Local Similarity 23.3.
Best Local Similarity 23.3.
Local Similarity 23.3.
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623
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Q8ZQZ6;
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SYL_SALTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 MADKQKNG-IKVNFKIRHNIEDGSVQLADHYQQNTPI-------GDGPVLLPDN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321 TNEQLPV-WVANFVLMAYGTGAVMAVPGHDQRDQEF--ANKYGLPIRQVIALKEPKNQDE 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------KTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :| | :||:::| | :||::|| | .: | | .: | | .: | | .: | | .: | | .: | | .: | | .: | | .: | | .: | | .: | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .
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STRAIR=TY2 / ATCC 700931;
STRAIR=22531367; PubWed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.,
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18";
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                                                                                                                         Pfam; PF00133; tRNA-synt_i; 1. PRINTS; RR00965; TRNASYNTHLEU.
TIGRPAMS; TIGR00396; leuS_bect; 1. PROSTITE; PS00178; AA TRNA_LIGASE I; 1. Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
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MEDLINE-21534947; PubMed=11677608;
MEDLINE=21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J Parkhill J., Dougan G., James K.D., Holden M.T.G., Sebahhia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18";
Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeurS)
LEUS OR STY0699 OR T2219.
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Enterobacteriaceae, Salmonella
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; Pred. No. 9.8;
29; Mismatches 68; Indels 57
                                                                                                                                                                                                                                                                                                                                                                                                                      9FDCCB992092919E CRC64;
                                                                                                                                                                                                                                                                                                                   "HIGH" REGION.
"KMSKS" REGION.
ATP (BY SIMILARITY)
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InterPro; IPR002302; Leu-tRNAsyntla.
InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR009008; ValRS_IDES_edit.
Pfam: PF00133; tRNA-synt 1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                      99796 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44; Conservative
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640
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640 64
879 AA;
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Best Local Similarity
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SERAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCC1elland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AL627267; CAD05125.1; -.
EMBL; AR016841; AAO69822.1; -.
HAMAP; MF_00049; -; 1.
InterPro; IPR002300; Leu. TRNAsyntla.
InterPro; IPR002300; TRNA-synt_la.
InterPro; IPR00412; FRNA-synt_la.
InterPro; IPR0040412; TRNA-synt_la.
InterPro; IPR009008; ValRS; IPRS_edit.
Pfam; PF00133; TRNA-Synt_lileS_edit.
PRINTS; PR00985; TRNASYNTHLEU.
PRINTS; PR00985; TRNASYNTHLEU.
PROSITE; PS00178; AA TRNA_LIGASE i.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 TGEELPV-WAANFVLMEYGTGAVMAVPGH-DORD-YEFASKYGLTIKPVILAADGSEPDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39; Gaps
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
LEUS OR STW0648.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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622 622 ATP (BY SIMILARITY).
860 AA; 96940 MW; 2P95E480BBABA33C4 CRC64;
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cerevisiae.
                                                                                                   Sugino A.;
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                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 TTGKLPVPWPTLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 TGEEIPV-WAANFVLMEYGTGAVMAVPGH-DQRD-YEFASKYGLTIKPVILAADGSEPDL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 RAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 H-------NIEDGSVQLADHYQQNTPIGDGPVLLPDNHYL-STQSALSKDP 212
                                                                                                                                                                                 Suygener, 307; fr; ruce.

InterPro; IPR002302; Leu-tRNAsyntla.

InterPro; IPR002302; Leu-tRNAsyntla.

InterPro; IPR003001; tRNA-synt_la.

InterPro; IPR0004013; tRNA-synt_la.

Pfam; PF00133; tRNA-synt_l; 1.

PRINTS; PR00135; TRNASNTHLE.

PROBITS; PS00178; AA TRNA_LIGASE 1; 1.

PROSITE; PS00178; AA TRNA_LIGASE 1; 1.

Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
           diphosphate + L-leucyl-tRNA(Leu).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                    39; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=S288c / FY1679;
MEDLINE=96310631; PubMed=8740425;
Sen-Gupta M., Lyck R., Fleig U., Niedenthal R.K., Hegemann J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
DNA polymerase epsilon, catalytic subunit A (EC 2.7.7.7) (DNA polymerase II subunit A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 1214-1221.
MEDLINE=90381771; PubMed=2169349;
MORTHSON A., Araki H., Clark A.B., Hamatake R.K., Sugino A.;
"A third essential DNA polymerase in S. cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                            Length 860;
CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP
                                                                                                                                                                                                                                                                                                                                                                                                                    78; Indels
                                                                                                                                                                                                                                                                                                                            "HIGH" REGION.
"KMSKS" REGION.
ATP (BY SIMILARITY).
; D5003584DFBCCAB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 2222 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                   21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 6 9%; Score 87.5; I
Best Local Similarity 23.3%; Pred. No. 14;
Matches 42; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                             EMBL; AE008725; AAL19599.1; -.
                                                                                                                                                                                                                                                                                                                                                                   96985 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-2221 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                           StyGene; SG????; leuS.
                                                                                                                                                                                                                                                                                                                               52
623
622
                                                                                                                                                                                                                                                                                                                               42
619
622
660 AA;
                                                                                                                                                                                                                                                                                                                   Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPOE YEAST
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                      BINDING
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      943 FFEVDGPYKAMILPSSKEEGKGIKKRYAVFNEDGSLAELKGFELKRRGEL---QLIKNFQ 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPLICATION.
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate + {DNA}(N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- TUBNIT CONSISTS OF FIVE SUBUNITS (200 kDa, 80 kDa, 34 kDa, 30 kDa, AND 29 kDa).
-1- SUBUNIT CONSISTS OF FIVE SUBUNITS (200 kDa, 80 kDa, 31 kDa, AND 29 kDa).
-1- SUBLELLULAR LOCATION: Nuclear.
-1- DOMAIN: THE DNA POLYMERASE ACTIVITY DOMAIN RESIDES IN THE N-TERMINAL HALF OF THE PROTEIN, WHILE THE C-TERMINUS IS NECESSARY FOR COMPLEXING SUBUNITS B AND C.
-1- MISCELLANGOUS: In eukaryotes there are five DNA polymerases: alpha, beta, gamma, delta, and epsilon which are responsible for different reactions of DNA synthesis.
-1- SIMILARITY: Belongs to the DNA polymerase type-B family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 LPVPWP-TLVTTLSYGVQCFSRYPDHM-----KQHDFFKSAMPEGYV----QERTI
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"The sequence of a 24,152 bp segment from the left arm of chromosome XIV from Saccharomyces cerevisiae between the BNI1 and the POL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBO J. 11:733-740(1992).
-!- FUNCTION: DNA POLYMERASE II PARTICIPATES IN CHROMOSOMAL DNA
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92164663; PubMed=1537345;
Araki H., Ropp P.A., Johnson A.L., Johnston L.H., Morrison A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R EMBL; M60416; AAA88711.1; -.
R EMBL; x92494; CAA6325.1; -.
R EMBL; z715.38; CAA6169.1; -.
R EMBL; z715.38; CAA6169.1; -.
R Germonline; 143268; -.
SGD5206; POL2.
R GGCO10000731; P.10NA repair synthesis; IMP.
R InterPro; IPR006134; DNA_pol_B .
R InterPro; IPR006134; DNA_pol_B .
R InterPro; IPR006134; DNA_pol_B .
R InterPro; IPR006134; DNA_pol_B .
R Ffam; PF00104; DNA_pol_B . 1.
R Pfam; PF00104; DNA_pol_B . 1.
R SWARY; SW00486; POLES; 1.
R SWARY; SW00486; POLES; 1.
R PROSITE; PS00116; DNA_POLYMERASE B; FALSE NEG.
W TRAINGERASE, DNA_directed DNA_pol_werase; DNA_replication; T ZN_FING . 2100 £ Annow the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of th
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710 710 P -> S (IN POL2-18 TS MUTANT).
2222 AA; 255669 MW; CBCDDE2AB147D65B CRC64;
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EMBL;
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RECUINGE-238825; PubMed=1247932;

RELINE-238825; PubMed=1247932;

RIGALINE-238825; PubMed=1247932;

RIGALINE-238825; PubMed=1247932;

RIGALINE-238825; PubMed=1247932;

RIGALINE-238825; PubMed=1247932;

RIGALINE-RD., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zebebrg B. B., Buetow K.H., Schaefer C.F., Bhata N.K.,

RA Altschul S.F., Zebebrg B. B., Buetow K.H., Schaefer C.F., Bhata N.K.,

RA Altschul S.F., Zebebrg B. B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.U., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rakesley R.W., Touchman J.W., Schmutz J., Myers R.W.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

Rahe mutacrfield Y.S.N., Krzywinski M.I., Skalaka W.R.;

Reneration and initial analysis of more than 15,000 full-length human metalysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21638749; PubMed=11780052;

MEDLINE-21638749; PubMed=11780052;

RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggaley C.L.,

RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,

Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,

Balley J., Bard C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Beasley O.P., Blurler A.B., Carder C., Carter N.P.,

Clark S.V., Clark S.V., Clark S.V., Clee C.M.,

RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C.M.,

RA Chapman A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Grafham D.V., Griffiths R.E., Connor R.E., Corby N.R.,

Blington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Howden P.J.,

RA Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

RA MAN, M.M., Kimberley A.M., King A., Klights A., Laird G.K., Lavlor S.,

Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,

Milne S.A., Mistry D., Mocore M.J.F., Mullikin J.C., Nickerson T.,

A Nille S.A., Mistry D., Mocore M.J.F., Mullikin J.C., Nickerson T.,

Rann R.L., Spramore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,

Swann R.M., Sycamore N., Taylor R., Thomas D.W., Thorpe A.,

Race C.M., Sycamore N., Taylor R., Thomas D.W., Thorpe A.,

Race C.M., Sycamore N., Taylor R., Thomas D.W., Thorpe A.,

Race C.M., Sycamore N., Willey D.L., Williams L., Williams S.A.,

Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,

Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,

Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams L.,

Wanner R. D., Waray P.W., Hubbard T., Durbin R.W., Bentley D.R., Beck S.,

Recent R. D. Santh R. W., Belling R. W., Bentley D.R., Beck S.,

Recent R. Waray P.W., Whitehead S.L., Whittehead S.L., Whittehead S.L.,

Whitehead S.L., Whittehead S.L., Whittehead S.L., Whither R., Beck S.,

Recent R. Walley R. W., Ramsay R. W., Ramsay R. W., Recent R.,

Whitehead S.L., Whittehead S.L., Whithey W., Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                            AC2L HUMAN STANDARD; PRT; 689 AA.
QONUBL; QBLY99; QBN234; Q96JII; Q96JX6; Q9NU28;
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, List annotation update)
10-0CT-2003 (Rel. 42, List annotation update)
10-0CT-2003 (Rel. 42, List annotation update)
10-0CT-2003 (Rel. 42, List annotation update)
10-0CT-2003 (Rel. 42, List annotation update)
11-0CT-2003 (Rel. 42, List annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fissus=Placenta, and Tongue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 414:865-871(2001)
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                  ACAS2L OR KIAA1846.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Irie R., Sato H., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Marsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawatami B., Ota T., Hayashi K., Sugiyama T., Otsuki T., Ishibashi T., Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y., Wakamatsu A., Kanehori K., Suzuki Y., Sugano S., Ishii S., Nagai K., Isogai T.;
"NEDO human cDNA sequencing project.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDILYRE-21245130; PubMed=11347906;
Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
Nagase T. Nakayama M., Nakajima D., Kikuno R., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XX.
"The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA RSS. 8185-595(2001).
-i. FUNCTION: Converts acetate to acetyl-CoA so that it can be used for oxidation through the tricarboxylic cycle to produce ATP and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 t peptide, Alternative splicing.
MITOCHONDRION (POTENTIAL).
ACETYL-COENZYME A SYNTHETASE 2-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CO(2) (By similarity).

CATALYTIC ACTIVITY: ATP + acetate + CoA = AMP + diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isold-Q9NUB1-2; Sequence=VSP 007249;
Note=No experimental confirmation available;
-!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTIG=VSP 007249.
V -> M (IN REF. 2; AAH39261)
V -> M (IN REF. 2; AAH44588)
; 66E84E39302AD08B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-ALA.
Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing, Named isoforms=2;
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                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 336-689 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q9NUB1-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AKO27817, BAB55390.1; ALT_INIT.
EMBL, AKO92295; BACO3853.1; ALT_SEQ.
EMBL, ABO58749; BAB47476.1; -..
Genew, HGNC:16091; ACAS2L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL080312; CAB81884.1; ALT_SEQ.
BC039261; AAH39261.1; -.
BC044588; AAH44588.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LICETPRO; IPRO00873; AMP-bind.
Pfam; PF00501; AMP-binding; 1.
PROSITE; PS00455; AMP_BINDING; 1.
Ligase; Mitochondrion; Transit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL035661; CAB75500.1; -.
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689
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nes 33; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acetyl-CoA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=2
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------NGIKVNFKIRHN---IEDGSVQLADH 182
                                                             -----GKV-----YLDRNDNATFDGND-----VALGYVTA 802
                                           183 YQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                    Antimicrob. Agents Chemother. 39:2708-2717(1995)
                                                                                                                     533 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- PATHWAY: Ergosterol biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -! - CATALYTIC ACTIVITY: Obtusifoliol
                                                                                                                                                                                                                                                                                     MEDLINE=96161286; PubMed=8593007;
                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE OF 60-473 FROM N.A.
STRAIN=ATCC 2001;
                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          NCBI_TaxID=5478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
 155 ADKOK-
                                                                                                                                                                                               ERG11 OR CYP51.
                                                                                                                                                                                                                                                                           STRAIN=2001-L5;
                                                                                                                                                                                                                                                                                                                                                                                                                       Rossier M.;
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CANGA
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                                         69 VQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRA----EVKFEGDTLVNRIE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           611 KSNIGHEAPRLELVSKAGQKGEAADTTLGAGNTVAYQLSNYTTEGVYADAADLAGY--EF 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 TIFFKDDGNYKTRAEVKFEGDTLVNRIELKGID---FKEDGNILGHKLEYNYNSHNVYIM 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLSYG 68
                                                      ---QAWPGMARTI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 CTTGKLPVPWPTLV-----TTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQER
                                                                                                                                                                                                                                                                                              MEDLINE-97082965; Pubmed-8964497;
Zhu X., McVeigh R.R., Malathi P., Ghosh B.K.;
"The complete nucleotide sequence of the Bacillus licheniformis NM105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                             96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96; Indels
                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EFADCA4FF27D32AF CRC64;
                    FFGIVPVLMDEKGSV-----VEGSNVSGALCIS----
                                                                                                                                                                                                                   S-layer protein precursor (Surface layer protein). Bacillus licheniformis.
                                                                                                                                                                                  (Rel. 33, Created)
(Rel. 33, Last sequence update)
(Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S-LAYER PROTEIN.
                                                                                                                                                              874 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28; Mismatches
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SLH 2.
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155 SI
217 SI
92734 MW;
                                                                                   126 LKGIDFKEDGNILGHKL 142
                                                                                                         ------NISGHRL 560
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Signal; Cell wall; S-layer; sIGNAL
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Matches 65; Conservative
                                                                                                                                                              STANDARD;
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94
156
874 AA;
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   NCBI_TaxID=1402;
                                                                                                                                                                                                                                                                                      STRAIN=NM 105;
                                                                                                                                                                                   01-FEB-1996
                                                                                                                                                                                                          01-NOV-1997
                                                                                                                                                                                               01-FEB-1996
                                                                                                                                                              BACLI
                                                             511
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                                                                                                                                                              SLAP B
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between the Swiss Institute of Bioinformatics and the EMBL outstation—
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
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722 SVKFKDVEVEQFENRKVNIDRVLDVVKSDKDDVLNGIKLNISTEHKVRIVDEGTEQ---- 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Geber A., Hitchcock C.A., Swartz J.E., Pullen F.S., Marsden K.E.,
Kwon-Chung K.J., Bennett J.E.;
"Deletion of the Candida glabrata ERG3 and ERG11 genes: effect on cell
viability, cell growth, sterol composition, and antifungal
susceptibility.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
I -> M (IN REF. 2).
I -> T (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       methyl.5-alpha-ergosta-8,14,24(28)-trien-3-beta-ol + formate + 3 MADP(+) + 3 H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L40389; AAB02329.1; -.
EMBL; S75389; AAB32679.1; -.
InterPro; IPR00128; Cytochrome_P450.
Pfam; PF00067; p450; I.
PRINTS; PR00385; P450.
PRINTS; P800086; CYTOCHROME_P450; 1.
Electron transport; Cytidoreductase; Monooxygenase; Membrane; Heme; Sterol biosynthesis; NADP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95081364; PubMed=7989540;
Burgener-Kairuz P., Zuber J.P., Jaunin P., Buchman T.G., Bille J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lanosterol
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-!-FUNCTION: Caralyzes C14-demethylation of lanosterol which is critical for ergosterol biosynthesis. It transforms lanostero into 4.4'-dimethyl cholesta-8,14,24-triene-3-beta-ol (By
                                                                                                                                                                                                                                                                                                                                                                                                                                 P50859; Q02312;
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2003 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Cytochrome P450 51 (EC 1.14.13.70) (CXPLI) (P450-LIA1) (Sterol 1.alpha-demethylase) (Lanosterol 14-alpha demethylase) (P450-14DM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Candida glabrata (Yeast) (Torulopsis glabrata).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, mitosporic Saccharomycetales, Candida.
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Length 795;

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Query Match
Best Local Similarity 21.93
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nvasive disease."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klein M.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                           HAEIN
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                                                                                                                                                                                                                 109 GHEFIFNAKLADVSAEAAYSHL-------TTPVFGKGVIYDCPNHRLM 149
                                                                                                                                                                                            KOHDFFKSAM-PEGYV-----OERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDF 131
                                                                                                                                                                                                                                                                     132 KEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGD 191
                                                                                                                                                                                                                                                                                                         208 TASRSLLGKEMRDKLDTDFAYLYSDLDKGFTPINF-VFPNLPLEHYRKRDHAQQAIS--- 263
                                                                                                                  79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                  25 GHKFSVS---GEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLSYGVQCFSRYPDH--M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=Rd / RWZ0 / ATCC 51907;
STRAIN=Rd / KWZ0 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
File L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehn C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                               49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protective surface antigen D15 precursor (80 kDa D15 antigen)
(D-15-Ag) (Outer membrane protein D15).
                                         Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTECTIVE SURFACE ANTIGEN D15.
B85691FC22E6ED44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SIMILARITY: Belongs to the surface antigen D15 family.
                                                                               Indels
   61305 MW; A0506C17507E6EF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro, IPR000184; Bac_surfag_D15.
Pfam; PP01103; Bac_surface_Ag; 1.
Antigen; Outer membrane; Signal; Complete proteome.
SIGNAL 1 19 POTENTIAL.
                                     6.8%; Score 86.5; DB 1;
llarity 21.4%; Pred. No. 9.5;
Conservative 32; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 795 AA
                                                                                                                                                                                                                                                                                                                                              192 GPVLLPDNHYLSTQSALSKDPNEKRD 217
                                                                                                                                                                                                                                                                                                                                                                                    -----GTYMSLIKERREKND 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             795 P. 87478 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               795 AA;
     533 AA;
                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995
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                                                                               44;
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   SEQUENCE
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                                         Query Match
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                                      11;
                                                                                                                                                 148
                                                                                                            486
                                                                                                                                                                                                                      149 HNVYIMADKQK-NGIKVNFKIRHNIEDGSVQLADHYQQ------NTPIGDGPVLL 196
                                                                                                      427 IGYĞTESGISYQASVKQDNFLGTGAAVSIAGTKNDYGTSVNLGYTEPYFTKDGVSLGGNV
                                                                                                                                                 --KLEYNYNS
                                                                                                                                                                        543 RNLYIQSMKFKGNGIKTN-----DFDFSFGWNYNSLNRGYFPTKGVKASLG-GRVTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Outer membrane protein D15 is conserved among Haemophilus influenzae species and may represent a universal protective antigen against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Flack F.S., Loosmore S., Chong P., Thomas W.R.; "The sequencing of the 80-kDa D15 protective surface antigen of Haemophilus influenzae."; Gene 156:97-99(1995)
                                    63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gammaproteobacteria; Pasteurellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       precursor (80 kDa D15 antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
PROTECTIVE SURFACE ANTIGEN D15.
, 2P93DE538696AFIB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Infect. Immun. 65:3701-3707(1997).
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SIMILARITY: Belongs to the surface antigen D15 family.
                                                                         65 LSYGVQCFSRYPDHMKQHDF------FKSAMPEGYVQE-
                                      Indels
                                                                                                                                                 100 FFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNI---LGH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Minna / Serotype B, and Eagan / Serotype B; MEDLINE=97427952; PubMed=9284140;
                                    78;
6.8%; Score 86.5; DB 1;
1.9%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                  197 P--DNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLG
                                                                                                                                                                                                                                                                                                                                     594 PGSDNKYYKLSADVQGFYPLDRDHLWVVSAKASAGYANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Ą.
                                    30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  797
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EMBL; U60832; AAB61974.1; -.
EMBL; U60833; AAB61976.1; -.
PIR; JC4078; UC4078.
InterPror; IPRO00184; Bac surfag D15.
Pfam; PF01103; Bac surface Ag; I.
Antigen; Outer membrane; Sīgnal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protective surface antigen D15 precurs (D-15-Ag) (Outer membrane protein D15) Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-Serotype B;
MEDLINE-95255676; PubMed=7737523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87675 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gam
Pasteurellaceae; Haemophilus.
                   21.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                797
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797 AA;
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Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,

Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Sllva A.C.R., Moon D.H.,

Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Sllva F.R.,

Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M.,

Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M.,

Coutinho L.L., Kimura B.T., Perro E.S., Harakava R., Kuramae E.E.,

Marino C.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,

Baia G.S., Blanco S.R., Blito M.S., Cannavan F.S., Celestino A.V.,

Ad Cunha A.F., Fenille R.C., Ferro J.A., Formighieri B.F., Kishi L.T.,

Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sassaki F.T., Sena J.A.D.,

A Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,

Kitajima J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                   HNVYIMADKQK-NGIKVNFKIRHNIEDGSVQLADHYQQ------NTPIGDGPVLL 196
                                                                                                                                                                        127 IGYGTESGISYQASVKÓDNFLGTGAAVSIAGTKNDYGTSVNLGÝTEPYFTKDGVSLGGNV 486
                                                                                                                                                                                                                             100 FFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNI---LGH------KLEYNYNS 148
                                                                                                                                                                                                                                                                                487 FFENYDNSKSDTSSNYKRTTYGSNVTL-GFPVNENNSYYVGLGHTYNKISNFALEYN--- 542
                                                                                                                                                                                                                                                                                                                                                                                   543 RNLYIQSMKFKGNGIKTN-----DFDFSFGWNYNSLNRGYFPTKGVKASLG-GRVTI 593
                                                                                                                          -----RTI 99
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Bacteriol. 185:1018-1026(2003).
-!- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP + diphosphate + L-leucyl-tRNA(Leu).
-! SUBCELLULAR LOCATION: Cytoplasmic.
-! SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Comparative analyses of the complete genome sequences of Pierce's disease and citrus variegated chlorosis strains of Xylella
                                                                        63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Xylella.
                        Length 797;
                                                                                                                          --FKSAMPEGYVQE-
                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      594 PGSDNKYYKLSADVQGFYPLDRDHLWVVSAKASAGYANG 632
                                                                                                                                                                                                                                                                                                                                                                                                                                      197 P--DNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITLG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEUS OR PD1230.
Xylella fastidiosa (strain Temeculal / ATCC 700964).
                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    879 AA
                                                                     30; Mismatches
                     6.8%; Score 86.5; I 21.9%; Pred. No. 15;
                                                                                                                          65 LSYGVQCFSRYPDHMKQHDF-------
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InterPro; IPR002302; Leu-tRNAsyntla.
InterPro; IPR002300; tRNA-8ynt_la.
InterPro; IPR001412; tRNA-6ynt_l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 42, Created)
(Rel. 42, Last seq
(Rel. 42, Last anno
                                                                        48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=183190;
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Q87C65;
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                          Query Match
                                                Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 -------KTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 MADKQKNG-IKVNFKIRHNIEDGSVQLADHYQQNTPI-------GDGPVLLPDN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           422 ---RÖGRĞQRRVNYRLR----DWGVSRQRYWGCPIPVIYCPTCGAVPVPENQLPVILPEN 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 TIGKLPVPWPTLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||| :|| || || || 378 STWEPDVWRDWYADKTR---ERE---LINSAEFDGLDYQGAFEVLAERFE-----
                         Pfam; PF00133; tRNA-synt 1; 1. PRIALSYNTHLEU.
TIGRPAMB; TIGR00396; leuS_bact. 1. PROSITE; PS00178; AA TRNA_LIGASE 1; 1. Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spieth J., Denison K., Kirtland S., Cane J., Blumenthal T.;
"The C. elegans vitellogenin genes: short sequence repeats in the promoter regions and homology to the vertebrate genes.";

Nucleic Acids Res. 13:5283-5255(1985).
-!- FUNCTION: Precursor of the egg-yolk proteins that are sources of nutrients during embryonic development (Potential).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Synthesized in Caenorhabditis only by 32 cell building the intestine of adult hermaphroditic individuals; they are cotranslationally secreted into the body cavity and subsequently taken up by the gonad.
-!- SIMILARITY: Contains 1 VWFD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                 57; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 879;
                                                                                                                                                                                                                                                                                                                                                                                                                                    69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blümenthal T., Spieth J., Zucker E.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                         4C2EE01B8FDC497E CRC64;
                                                                                                                                                                                                                                            "KMSKS" REGION.
ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1990 (Rel. 16, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.8%; Score 86.5; DB Best Local Similarity 22.2%; Pred. No. 17; Matches 44; Conservative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1603 AA
                                                                                                                                                                                                               "HIGH" REGION
InterPro; IPR009008; ValRS IleRS edit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 -HYLSTOSALSKDPNEKR 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      475 VAFSGTGSPIKTDPEWRK 492
                                                                                                                                                                                                                                                                                                            99823 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-282 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-71 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vitellogenin 4 precursor.
VIT-4 OR F59D8.2.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                               55
641
640
                                                                                                                                                                                                                                                                                                         879 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Bristol N2;
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                                                                                                                                                                                                                                                                               BINDING
SEQUENCE
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ACT_SITE
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DPOL HPBHE
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                 212 TAYGLRFGSEC------KECEKEGQFVQPQTVYTYTFKNEKLQESEVNSIYT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----NYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMAD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258 LNVNGQEVVKSETRAKVTFVEESKINR-EIK-----KVSGPKEEIVYSMENEKLIEQ 308
                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                         61 LVTTLSYGVOCFSRYPDHMKQHDFFKSAMPEG-YVQERTIF---FKDDG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PERAIN-NCTC 11168;
MEDLINE-20150912; PubMed=10688204;
MEDLINE-20150912; PubMed=10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
White genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervariable sequences.";
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campylobacter jejuni.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
tRNA (Uracil-5-)-methyltransferase (EC 2.1.1.35) (tRNA(M-5-U54)
                                                                                                                                                                                                                                                                                                                                      69;
                                                                                                                                                                                                                                                                                                             Score 86.5; DB 1; Length 1603;
Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                      69; Indels
                                                                                                                                                                                                                                                                                        MW; E303170325BC99BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309 FYKQGDKAEVNPFKAIEIEQKV-EQLEEIFRQIQEH-EQNTP 348
                                                                                                                                                                                                                                                               EVAYT -> RSRLH (IN REF. 2)
T -> S (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KQKNG-----IKVNFKIRHNIEDGSVQLADHYQQNTP 188
                                                                                                                                                                                                                                        Y -> V (IN REF. 3)
L -> V (IN REF. 2)
                                                                                                                                                                                       Storace protein; Multigene family; Signal.
SIGNAL 1 15 POTENTIAL.
CHAIN 16 1603 VITELLOGENIN 4.
                                                                                                                                                                                                                                                                                                       6.8%; Sco. 23.4%; Pred. No. 50,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        357
                                                                                 EMBL; M1498; AAA28163.1; EMBL; X02754; CAA26531.1; -
EMBL; X02754; CAA26531.1; -
FIR, A43084; A43084.
Wormbep; F59D8.2; CE26817.
InterPro; IPR001747; Lipid transprt_N.
InterPro; IPR001846; WWF D.
Ffam; PF01347; Vitellogenin_N; 1.
SMART; SM00638; LPD N; 1.
                                                                                                                                                                                                                               VWFD.
                                                                          EMBL; AC024137; AAK09074.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                       1603 AA; 186307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         methyltransferase) (RUMT).
TRMA OR CJ0831C.
                                                                                                                                                                                                                                                                                                                                       52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 403:665-668(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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1603
1455
                                                                                                                                                                                                                                                                                                                            Local Similarity
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Q9PP92;
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                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|| :: || :: || || 74 LDFADEKICAFMPRLLEYLRQDNKLKEKL-----FGVEFLTTKQE--LSITLLYHKNIE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 KQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKF--EGDTLV-----NRIELKG 128
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-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
-!- FUNCTION: Catalyzes the formation of 5-methyl-uridine at position 54 (M-5-D54) in all tRNA (By similarity).
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-homocysteine + tRNA containing thymine.
-!- SIMILARITY: Belongs to the RNA MSU methyltransferase family. TrmA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 EKHSFIKKYFKEFYTKOFKLFASKDKHYRTRAELSFYHENDTLFYAMFDPKSKKKYIIEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 IDFKED------GNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIE
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16-007-2001 (Rel. 40, Last annotation update)
P protein [Includes: DNA-directed DNA polymerase (EC 2.7.7.7); RNA-directed DNA polymerase (EC 2.7.7.9); RNA-directed DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sprengel R., Kaleta B.F., Will H.; "Isolation and characterization of a hepatitis B virus endemic in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.8%; Score 86; DB 1; Length 357; 24.8%; Pred. No. 6.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CEC5328347CEE497 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   788 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
BY SIMILARITY.
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MEDLINE=88333160; PubMed=3418788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR, G81355, G81355.
HAMAP; MF 01011; -; IL
HACPP: JPR000051; SAM bind.
InterPro; IPR001566; TrmA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42276 MW;
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Best Local Similarity 24.8
Matches 30; Conservative
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                                                                                                                                                                  subfamily.
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P13846;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 WPTLVTTLSYGVQCFSRYPDHMKQH----DFFKSAMPEGYVQERT----IFFKDDGNYK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 T------RAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIM 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 ADKQKNGIKVNFKIRHNIEDGSVQLADHYQ-----QNTPIGDGPVLL-PDNHYL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246 ----NGRKISY---HSTRDGSHRLSGRTSDPTSRGALAGGDSTPIGPGSTAAHPSTHHV 297
                                                                                                     EMBL; M22056; AAA45738.1; -.

PIR; AJ0082; JUVLHH.

InterPro; IPR001462; DNApol_viral_N.

InterPro; IPR000477; RVTse.

Pfam; PP003042; DNA_pol_viral_N, 1.

Pfam; PP00342; DNA_pol_viral_N; 1.

Pfam; PP00378; rVt; 1.

ProDom; PD000814; DNApol_viral_N; 1.

ProDom; PD000814; DNApol_viral_C; 1.

ProDom; PNO00814; DNA-binding.

SEQUENCE 788 AA; 90070 MW; FB44F38F75EADF44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   65;
                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.7%; Score 85.5; DB 1; Length 788; Best Local Similarity 19.7%; Pred. No. 18; Matches 40; Conservative 32; Mismatches 66; Indels 65
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Search completed: June 21, 2004, 15:55:22 Job time: 7.55556 secs 

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June 21, 2004, 15:45:30 , Search time 30.6667 Seconds (without alignments) 2458.984 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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1: Sp_archea:*
2: Sp_bacteria:*
3: Sp_tungi:*
4: Sp_tungi:*
5: Sp_tungi:*
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Gapop 10.0 , Gapext 0.5
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sp_bacteriap:*
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1274
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seq length: 200000000
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Perfect score:
Sequence:
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			Description	2 azotobacter	25 aequorea vi	4 azomonas ag	3 azotobacter	)5 aequorea vi	o aequorea vi	se aednorea ma	35 aequorea ma	24 aequorea ma	10 aequorea ma	38 aequorea ma	39 aequorea ma	7 aequorea ma	:5 aequorea ma	17 montastraea	v5 montastraea
			Desc	Q8ghe2	093125	08ghe4	Q8ghe3	017105	017106	Q8wtc6	Q8wp95	Q8wtc4	Q8wtd0	Q8wtc8	Q8wtc9	08wtc7	Q8wtc5	Q95ua7	Q720w5
				32	25	34	33	35	90	36	35	74	00	80	60	72		47	45
			a	Q8GHE2	093125	Q8GHE	Q8GHE	1710	017106	Q8WT	QBWP95	Q8WTC4	OBWTD	OBWICE	QBWTC9	OBWIC	OBWTCS	· 095UA7	Q7Z0W5
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		Query	Match	97.6	97.3	97.2	97.1	94.6	93.4	85.2	84.9	84.5	84.4	84.3	84.3	84.1	84.0	19.8	19.8
			Score	1243	1240	1238	1237	1205	1190	1085	1081	1077	1075	1074	1074	1072	1070	252.5	252.5
		Result	No.	1	7	m	4	ß	9	7	<b>6</b> 0	6	10	11	12	13	14	15	16

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Gaps ; 0

Query Match 97.6%; Score 1243; DB 2; Length 238; Best Local Similarity 97.9%; Pred. No. 1.9e-96; Matches 233; Conservative 2; Mismatches 3; Indels

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62 VITLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERIFFKDDGNYKTRAEVKFEGDTLV 121

2 VSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL

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62 VITLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
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                                                                                                                                                                                                     Koranyi P., Berenyi M., Burg K.; "Occurrence of green fluorescence protein in diazotrophic bacteria Azonomas and Azotobacter"; Bubl/GenBank/DDBJ databases. Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 97.2%; Score 1238; DB 2; Length 238; Best Local Similarity 97.5%; Pred. No. 5e-96; Matches 232; Conservative 2; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                            EMBL; AF324405; AAN06137.1; -...
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR000917; GFP_like.
Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFU0078SCENT.
ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 26902 MW; 15FE989CSB4F6B89 CRC64;
  Last sequence update)
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01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25, Green fluorescence protein.
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                                                                             Azomonas agilis.
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                                       NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Yeast Enhanced Green Fluorescent Protein (yEGFP): a reporter of gene expression in Candida albicans.";
Microbiology 0:0-0(1996).
Missp: U73901; AAB18957.1; -.
HSSP; P42212; 1BFP.
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MEDLINE=96305137; PubWed=8707053;
Cormack B.P., Valdivia R.H., Falkow S.;
"FAGC-optimized mutants of the green fluorescent protein (GFP).";
Gene 173:33-38(1996).
                                                                                                                                                                                                                                                                                                                                                                                                  Aeguorea victoria (Jellyfish).
Eukaryota; Metazoa; Chidaría; Hydrozoa; Hydroida; Leptomedusae;
Aeguoreidae; Aeguorea.
NCBI_TaxID=6100;
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PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 26840 MW; A28622809A9DEA60 CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 97.5
Matches 232; Conservative
                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Koranyi P., Berenyi M., Burg K.;
"Occurrence of green fluorescence protein in diazotrophic bacteria Azomonas and Azotboacter."

Bubmitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF324406; AAN86138.1; -.

GO; GO:0006091; Preneryy pathways; IEA.

InterPro; IPR009017; GFP like.

InterPro; IPR009017; GFP like.

Pfam; PF01533; GFP; 1.

PRINTS; PR01229; GFLUORESCENT.

PRODOM; PD013756; Green fl protein; 1.

SEQUENCE 238 AA; 26887 NW; E0B1616BD2AF6188 CRC64;
                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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Last sequence update)
Last annotation update)
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RESULT 3
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Query Match
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                                                                                                                                                      2 VSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPMPTL
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Eukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Leptomedusae,
Aequoreidae, Aequorea.
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Pred. No. 6.1e-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Watkins J.N., Campbell A.K.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, X83959; GA559789.1; -.
PIR, JS0692; JQ1514.
HSSP, P42212; JGFL.
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                                                                         2; Mismatches
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InterPro; IRR009017; GFP like.
InterPro; IPR000186; Green_fl_protein.
Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLÜORESCENT.
ProDom; PD013756; Green_fl_protein; 1.
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                                97.5%;
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                                    Best Local Similarity 97.5
Matches 232, Conservative
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Q17105;
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RESULT 6 Q17106 ID Q1710

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Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
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                                                                                                                            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.4%; Score 1190; DB 5; Length 238; 93.3%; Pred. No. 5.4e-92; ive 7; Mismatches 9; Indels
                                                                                                                                                                                                                                    Watkins J.N., Campbell A.K.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
BMBL, X83960; CAR58790.1;
PIR, JS0692, JQJ514.
HSSP, P42212; IBFP.
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR00076; Green_fl_protein.
Pfam; PF01353; GFP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 AA; 26867 MW; BD4648262D8EABD4 CRC64;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl_protein; 1.
238 238 238 AA; 26867 MW; BD464828
                                                                   Green fluorescent protein (Fragment)
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                                                                                                            Aequorea victoria (Jellyfish)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 93.3%
Matches 222; Conservative
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                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=GFPxm19uv;
                                                                                                                                                                              NCBI_TaxID=6100;
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Query Match
Best Local Similarity
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                                                                                                                                                                            NCBI_TaxID=147615;
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           macrodactyla.";
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                                                                           01-MAR-2002
                                                 Q8WTC4
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OBWTD0
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STRAIN-GFPXm, and GFPdnaxm;
STRAIN-GFPXm, and GFPdnaxm;
Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Qin Y.X., Pang S.Q.,
Li S.J., Xia N.S.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
ENBL; AY013821, AAK020501;
EMBL; AY013821, AXK020501;
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR000786; Green_fl_protein.
                                                                                                                    VSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                      VSKGEELPTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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                                                     Length 238;
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                                                  85.2%; Score 1085; DB 5; Length 2
82.4%; Pred. No. 3.6e-83;
tive 20; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23; Indels
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ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 27049 MW; 8185D0E5E529012B CRC64;
PRINTS, PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 27015 MW; 6B8FD75E88926903 CRC64;
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Last sequence update)
Last annotation update)
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81.9%; Pred. No. 7.7e-83;
cive 20; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25, Green fluorescent protein.
                                                                           Matches 196; Conservative
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Matches 195; Conservative
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                                                               Local Similarity
                                                                                                                                                                                                                                                                                  181
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61 VITLGYGILCFARYPEHMKANDFPKSAMPEGYIQERTIFFQDDGKYKTRGEVKFEGDTLV 120
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                                                                                                                                                                                                                                                                                                                                          Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M., Li S.J., Xia N.S.; "Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                   Aequorea macrodactyla.
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
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Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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                                                                                                                                                                                                                                                                                                                                                                                                                                macrodactyla.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF4334318.1; -.
GO, GO:0006091; P:energy pathways; IEA.
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InterPro; IPR00786; Green_fl_protein.
Pfam; PF01353; GFP; li.
PRINTS; PR01229; GFLUORESCENT.
PRODOM; PD013756; Green_fl_protein; l.
SEQUENCE 238 AA; 26956 MW; 75521EAFOCEBA73A CRC64;
(TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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                                                                                         Green fluorescent protein.
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121 NRIELKGMDFKEDGNILGHKLEYNFNSHNVYIMPDKANNGLKVNFKIRHNIEGGGVQLAD 180
122 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
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Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
Li S.J., Xia N.S.,
"Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aequorea macrodactyla.
Bukaryota; Metazoa; Chidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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81.5%; Pred. No. 3e-82;
iive 20; Mismatches 24; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              macrodactyla.";
Submitted (OCT-201) to the EMBL/GenBank/DDBJ databases.
EMBL; AF453-428. AAL33913.1;
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR000901; GFP_like.
InterPro; IPR000796; Green_fl_protein.
PRINTS; PR01259; GFLUORESCENT.
ProDom; PD013756; Green fl_protein; 1.
SEQUENCE 218 AA; 27031 WW; 5F80A19C19DC584D CRC64;
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Last annotation update)
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Last annotation update)
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QBWTC7;
01-MRA-2002 (TrEMBLrel. 20,
01-MRA-2002 (TrEMBLrel. 20,
01-OCT-2003 (TrEMBLrel. 25,
Green fluorescent protein.
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01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2003 (TrEMBLrel. 25,
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Matches 194; Conservative
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Q8WTC9
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Luo W.X., Xia N.S.;

Li S.J., Xia N.S.;

Li S.J., Xia N.S.;

Li S.J., Xia N.S.;

Colorful mutants of green fluorescent protein from Aequorea macrodactyla.

The macrodactyla mutants of green fluorescent protein from Aequorea macrodactyla.

EMBL, AF435429; AAL33914.1; ---

EMBL, AF435429; AAL33914.1; ---

EMBL, AF435429; AAL33914.1; ---

EMBL, AF435429; AFLOWO0916; Green fl protein.

R InterPro; IPR000917; GFP like.

InterPro; IPR000917; GFP like.

R Pfam; PF01353; GFP; 1.

R PRINTS; PR01229; GFLUORESCENT.

R Problom; PD013756; Green fl protein; 1.

R PROBONCE 238 AA; 27047 MW; SF80A18FALE7C84D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aequorea macrodactyla.
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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81.5%; Pred. No. 3e-82;
.ive 20; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           24; Indels
(OCT-2001) to the EMBL/GenBank/DDBJ databases.
                  EMBL, AF435477, AAL33912.1; -...
GO: GO: 0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IRR000786; Green_fl_protein.
PF01383; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
PRODOM; P013756; Green_fl_protein; 1.
SEQUENCE 238 AA; 26997 MW; 5F80A192173CB84D CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                         5;
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                                                              Chen M.,
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Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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                                                            Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Li S.J., Xia N.S., "Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
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82.4%; Pred. No. 6.5e-82;
ive 17; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   macrodactyla..;
Submitted (OCT-2011) to the EMBL/GenBank/DDBJ databases.
EMBL; AF4458431; AAL3917.1; -...
GO, GO:0006091; P:energy pathways; IEA.
InterPro; IPR00917; GFP 11ke.
InterPro; IPR00786; Green_fl_protein.
                                                                                                                                                   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF435430, AAL33915.1;
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IRR00786; Green_fl_protein.
Pf01353; GFP; 1.
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ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 27018 MW; 75521EA5534E573A CRC64;
                                                                                                                                                                                                                                                                         Pfam, PF01353; GFP, 1.
PRINTS; PR01229; GFUDORSCENT
PPCDOM; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 27002 WW; BD5BA2982264C018 CRC64;
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Last sequence update)
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81.5%; Pred. No. 4.4e-82;
iive 20; Mismatches 24;
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Matches 196; Conservative
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Matches 194; Conservative
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                   SEQUENCE FROM N.A. STRAIN=GFPxm191uv;
                                                                                                                                  macrodactyla.";
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Best Local 8
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131 FKEDGNILGHK-LEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVQLADHYQQNTPI 189
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                                                                                                                                                                                                           NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Gaps
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cyan fluorescent protein (Fragment).
Montastraea cavernosa (great star coral).
Eukaryota; Metazoa; Conidaria; Anthozoa; Zoantharia; Scleractinia; Faviliae; Faviliae; Montastraea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Talkowski P. G., Sun Y.;

"Alkowski P. G., Sun Y.;

"Alkowski P. G., Sun Y.;

"Montastraca cavernosa fluorescent protein.";

"Montastraca Gararnosa fluorescent protein.";

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

REMEL, AVOS6460; ABL17995.1;

"InterPro; IPRO009017; GFP like.

"InterPro; IPRO009017; GFP like.

"InterPro; IPRO009018; Green_fl_protein.

"Pfan; PRO135; GFP.1.

"REMINTS; PRO1229; GFLUORESCENT.

"REMINTS; PRO1229; GFLUORESCENT.

"REMINTS; PRO1229; GFLUORESCENT.

"REMINTS; PRO1229; GFLUORESCENT.

"REMINTS; PRO1229; GFLUORESCENT.

"REMINTS; PRO1229; GFLUORESCENT.

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EGFP sign
Jellyfish
A. victor
Amino aci
A. victor
Protease
Aequorea
Aequorea
Green flu
Green flu
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Amino aci
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                                                   June 21, 2004, 15:41:49; Search time 47.1111 Seconds (without alignments) 1433.395 Million cell updates/sec
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                                                                                                         MVSKGEELFTGVVPILVELD........VLvGFVTAAGITLGMDELYK
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Abr83616 G
Abu63204 Abu63204
Adc18358 B
Abw00914 A
Adc28570 B
Abw79011 B
Aag68319 B
Aau99804 E
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Aae17517
Aay52882
Aay52349
Aay79584
Aab58804
Aab58900
Aab59900
Aab31171
Aag66198
Aae14599
Aae14599
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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                                    protein search, using sw model
                                                                                                                                                                                                                                      Listing first 45 summaries
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AAG65781
AAG65782
AAE17517
AAB22882
AAY54349
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AAG66198
ABG94444
AAE14599
AAE34958
AAG79829
ABR83616
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AAB85900
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Gapop 10.0 , Gapext 0.5
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geneseqp2003as;*
geneseqp2003bs;*
geneseqp2004s;*
                                                                                                                                                                                                                                             A Geneseq 29Jan04:*
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geneseqp2001s:*
                                                                                                                                                                                                                   Post-processing: Minimum Match 0% Maximum Match 100%
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geneseqp1990s:*
                                                                                        US-09-887-784-222V
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seq length: 200000000
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Match Length DB
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## ALIGNMENTS

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Novel fluorescent protein in in vitro assay for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution, has a green fluorescent protein with F64L and E222G
                                                                                                                                                                                                                            /note= "Wild type Phe substituted with Leu; This corresponds to position 64 in the wild type protein" 223 "note= "Wild type Glu substituted with Gly; This corresponds to position 222 in the wild type protein"
                                                                                                                            Jellyfish; green fluorescent protein, GFP; protein redistribution, cellular function; genetic reporter; mutant; Stoke's shift; mutein.
                                                                                                    Enhanced F64L-E222G jellyfish green fluorescent protein mutant.
                                                                                                                                                                                                Location/Qualifiers
65
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                          AAE17518 standard; protein; 239
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20-JUN-2000; 2000US-0212681P.
10-MAY-2001; 2001DK-00000739.
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                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAY-2001; 2001US-0290170P
                                                                            (first entry)
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N-PSDB; AAD28163.
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                                                                                                                                                               Aequorea victoria.
Synthetic.
                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                       Key
Misc-difference
                                                                                                                                                                                                                                                                                                           WO200198338-A2
                                                                            22-APR-2002
                                                                                                                                                                                                                                                                                                                                   27-DEC-2001
                                                   AAE17518;
RESULT 1
AAE17518
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Claim 9; Page 37; 41pp; English

mutation.

Enhanced Jellyfish Aequorea Enhanced

Biomembra

AAG68319 AAU99804 ADE28570 ABM79011

us-09-887-784-222v.rag

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The inversion protein (GPP) or its analogue. The GPP containing mutations at F44L and E222G has a bigger compared to other GPP's making it very guitable for high throughput screening due to better resolution. The fluorescent protein is useful in invitro assays for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution. The fluorescent protein is useful in studying cellular functions in living cells as protein tags in transgenic animals, living and fixed cells; organelle tags, secretion marker and genetic reporter. The fluorescent protein is also useful as a cell or organelle integrity marker, a marker for changes in cembination with fluorescence activated cell sorting (PACS). The novell proteins can also be used as reporters to monitor live or dead biomass of organisms, such as fungi. The fluorescent protein is also useful as markers in transcriptional and translational fusions for performing transposons encoding the fluorescent protein are useful for screening promoters and for tagging plasmids and chromosomes. The fluorescent protein engineered into the genome of a phage is useful for deadspaing diagnostic tool. The present sequence is a DNA encoding enhanced F64L-E222G jellyfish green fluorescent protein (GPP) mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLVGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 239;
              invention relates to a fluorescent protein derived from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.8%; Score 1271; DB 5; 99.6%; Pred. No. 1.1e-122; cive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human amino acid sequence SEQ ID NO: 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABR40352 standard; protein; 363 AA
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11-OCT-2001; 2001US-0328896P.
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Best Local Similarity 99.6
Matches 238; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BIOL-) BIOLMAGE AS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 239 AA;
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Novel cell for identifying modulators of protein interaction, contains a first conjugate comprising anchor protein, second conjugate having type B interactor protein and third conjugate with detectable group.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel cell, comprising three heterologous conjugates (HC), a first HC (HC1) comprising an anchor protein that specifically binds to an internal structure within the cell conjugated to an internal structure within the cell conjugated to an interactor protein (IP) of type A, a second HC (HC2) comprising IP of type B conjugated to a first protein of interest, and a third HC (HC3) comprising a second protein of interest conjugated to detectable group. The cell is useful for detecting if a compound disrupts or induces the interaction between two intracellular proteins. The cell is also useful for screening compounds that modulate the interaction between two exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LVTTLSYGVQCFSRXPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWVLGFVTAAGITLGMDELXK 239
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                                                                                                                                                                                                                                                                                                                                                                                                                             6; Length 363;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1271; DB 6;
Pred. No. 2e-122;
                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 112-113; 118pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG65781 standard; protein; 893 AA
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29-MAY-2000; 2000DK-00000849.
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Best Local Similarity 99.6
Matches 238; Conservative
              WPI; 2003-430211/40.
N-PSDB; ACC72604.
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The invention relates to determining, if a compound, is a dislocator of PDE4. The method comprises testing if the compound removes PDE4 spots, which may optionally be induced by a Rolipram-like reference compound, and testing if it inhibits the catalytic activity of the PDE4, where the compound is a dislocator of PDE4, if it removes PDE spots and if it does not inhibit the catalytic activity of PDE4. The method is useful for identifying compounds useful for the treatment of diseases of the central nervous system such as depression and for the treatment of inflammatory disease such as joint inflammation, Crohn's disease, inflammatory bowel disease, respiratory diseases, chronic obstructive pulmonary disease. COPD), including asthma, chronic bronchitis, pulmonary emphysema, endotoxic shock, toxic shock syndrome, systemic lupus erthematosis, psoriasis, bone resorption diseases, reperfusion injury, cancer and HIV including and are accompanied of a reagent that can minic or reverse the effect of the compound with affinity for the preparation of a medicament. The present sequence represents the amino acid sequence of a HSPDE4Al-E22G fusion
                                                                                                           Determining if a compound is a dislocator of PDE4 for identifying compounds for treating CNS and inflammatory disease comprises identifying compounds which remove PDE4 spots.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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Thastrup O, Almholt DC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of HSPDE4A4-E222G fusion protein
                                                                                                                                                                                       Example 1; Page 156-160; 160pp; English.
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 Bjorn SP,
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Matches 238; Conservative
 Scudder KM,
                                                    WPI: 2001-611727/70.
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                                                                           N-PSDB; AAI66852.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 893 AA;
                     Praestegaard M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fusion protein.
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The invention relates to determining, if a compound, is a dislocator of DDE4. The method comprises testing if the compound removes PDE4 spots, which may optionally be induced by a Rolipram-like reference compound, and testing if it inhibits the catalytic activity of the PDE4, where the compound is a dislocator of PDE4, if it removes PDE spots and if it does not inhibit the catalytic activity of PDE4. The method is useful for compound useful for the treatment of diseases of the central retreatment of morphy and if it does not inhibit the catalytic activity of PDE4. The method is useful for compounds useful for the treatment of inflammatory disease such as joint inflammation, Crohn's disease, inflammatory bowel disease, respiratory diseases, chronic obstructive pulmonary disease (COPD), including asthma, chronic bronchitis, pulmonary emphysema, endotoxic shock, toxic shock syndrome, systemic lupus erthematosis, psoriasis, bone resorption diseases, reperfusion injury, cancer and HIV infection. The use of a reagent that can mimic or reverse the effect of the compound with affinity for the catalytic site on intracellular distribution of the PDE for the preparation of a medicament. The present sequence represents the amino acid sequence of a HSPDE4A4-E222G fusion
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                                                                                                                                                                                                                                                                               Determining if a compound is a dislocator of PDE4 for identifying compounds for treating CNS and inflammatory disease comprises identifying compounds which remove PDE4 spots.
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                                                                                                                                                                     Almholt
                                                                                                                                                                     Thastrup O,
                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 162-167; 160pp; English.
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                                     11-APR-2001; 2001WO-DK000264.
                                                                        17-APR-2000; 2000DK-0000651.
29-MAY-2000; 2000DK-00000849.
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Matches 238; Conservative
                                                                                                                                                                       Scudder KM,
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N-PSDB; AAI66853.
                                                                                                                                (BIOI -) BIOIMAGE AS
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25-OCT-2001.
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XBXBXXXX
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The invention relates to a fluorescent protein derived from green fluorescent protein (GFP) or its analogue. The GFP containing mutations at F6L and E322G has a bigger compared to other GFP's making it very suitable for high throughput screening due to better resolution. The fluorescent protein is useful in invitro assays for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution. The fluorescent protein is useful in studying cellular curvitions in living cells as protein tags in transgenic animals, living and fixed cells; organelle tags, secretion marker and genetic reporter. The fluorescent protein is also useful as a cell or organelle integrity marker, a marker to be used in combination with fluorescence activated cell sorting (FACS). The novel proteins can also be used as resporters to monitor live or dead biomass of organisms, such as fungi. The fluorescent protein is also useful as markers in transcriptional and translational fusions for performing transposons encoding the fluorescent protein are useful for screening promoters and for tagging plasmids and chromosomes. The fluorescent protein engineered into the genome of a phage is useful contains for the present sequence is enhanced F64L contains the present sequence is enhanced F64L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel fluorescent protein in in vitro assay for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution, has a green fluorescent protein with F64L and B222G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MVSKGEELFTGVVPILVELDGDVNGHKKSVSGEGEGBDATYGKLTLKFICTTGKLPVPWPT
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                                                                                                                                                      /note= "Wild type Phe substituted with Leu; This corresponds to position 64 in the wild type protein"
Jellyfish; green fluorescent protein; GFP; protein redistribution; cellular function; genetic reporter; mutant; Stoke's shift; mutein.
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Pred. No. 7.4e-122;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     jellyfish green fluorescent protein (GFP) mutant
                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thastrup 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 35; 41pp; English.
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99.2%;
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20-JUN-2000; 2000US-0212681P.
10-MAY-2001; 2001DK-00000739.
10-MAY-2001; 2001US-0290170P.
                                                                                                                                                                                                                                                                                          18-JUN-2001; 2001WO-EP006848
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                                                                                                                    Key
Misc-difference 65
                                                          Aequorea victoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAD28162
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                                                                              Synthetic.
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The invention relates to systems, methods and reagents for cell-based screening or detection of compounds which affect particular biological functions. The methods of the invention utilize fluorescent biodetector collected on by a compound of interest, cause an allocation in the cellular distribution of at least the fluorescent alteration in the cellular distribution of at least the fluorescent conciety. In one embodiment, the biosensors comprise hear shock proteins (HSPS) fused to a fluorescent protein (e.g., jellyfish green fluorescent protein (e.g., jellyfish green fluorescent protein stress activation transboacate to the nucleus. In another embodiment biodetector proteins can be used to detect protease cativity. Such protease biodetector fusion proteins comprise one or more fluorescent proteins, a recognition signal which is cleaved by the protease, or may be from heterologue sources. Due to the nucleus components may be from heterologues sources. Due to the components of a single protein which is acted upon by the protease, or may be from heterologues sources. Due to the creations of more components of a single protein is localised to a particular region of the cell. Once acted on by the protease of interest, the region of the cell. Once acted on by the protease of interest, the fluorescent protein to be directed to a different cellular comparatment after cleavage of the protease recognition sequence. The compartment after cleavage of the protease recognition sequence. The magning methods with a high degree of spatial resolution. The methods and imaging methods with a high degree of spatial resolution.
                                                                                                                                                                                                                                                                                                                                                                                Biodetector protein; fusion protein; recognition site; cellular targetting sequence; cellular localisation; fluorescent protein; protease activity detection; toxin detection; cellular stress detection; drug discovery; cell based screening.
181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 239
                                                                   DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLVGFVTAAGITLGMDELYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Automated cell-based characterization of toxin by contacting cells containing luminescent reporter molecules with test substance and
                                                                                                                                                                                                                                                                                                                                           Enhanced green fluorescent protein (EGFP), SEQ ID NO:46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 11; Fig 29A; 336pp; English.
                                                                                                                                                                                                                       AAB22882 standard; protein; 239 AA
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99US-0123399P.
99US-00352171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-FEB-2000; 2000WO-US004794.
                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          analyzing optically.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-1999;
08-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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                                                                                                                                                                                                                                                                 AAB22882;
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cellular activities and to screen compounds which modulate these exactivities. Biosensors containing a recognition site for caspase, for example, may be used for the screening of compounds which modulate apoptosis, which biosensors containing other protease recognition sites may be used for the detection of proteolytic toxins (such as anthrax lethal factor). The method provides improved target validation and candidate compound optimisation by combining many cell screening formats with fluorescence-based molecular reagents and computer-based feature extraction, data analysis and automation, resulting in increased quantity and speed of data collection and faster evaluation of drug candidates. Sequences AAB22881-B22885 represent fluorescent proteins which may used as components of biosensor fusion proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                            LVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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 biosensors of the invention can be used to investigate a wide range of
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                                                                                                                                                                                                                                                                                                                                        1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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                                                                                                                                                                                                                                                                     Length 239;
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                                                                                                                                                                                                                                                                   Score 1260; DB 3;
Pred. No. 1.5e-121;
2; Mismatches 1;
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                                                                                                                                                                                                                                                                     98.9%;
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98US-00172063
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UNIV OREGON STATE
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Best Local Similarity 98.7
Matches 236; Conservative
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                                                                                                                                                                                                                                    Sequence 239 AA;
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(UYOR-) 1
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The present sequence represents a functional engineered fluorescent protein based on the Aequorea green fluorescent protein (GFP). The emission intensity changes as pH varies between 5 and 10 of the present protein are novel. The functional engineered fluorescent proteins show reversible changes in fluorescence over physiological pH ranges. They can be used for determining the pH of samples and cells. The polynucleotides can also be used to produce transgenic animals. The fluorescent protein pH sensors can be delivered to cells in the form of polynucleotides encoding the protein sensor fused to a targeting signal. The targeting signal directs the expression of the protein sensors to restricted cell locations. This makes it possible to measure the pH of a precisely defined cellular region or organelle
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                                                                                  New functional engineered green fluorescent proteins, used for measuring the pH in biological samples and cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLVGFVTAAGITLGMDELYK 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                    Disclosure; Page 9; 89pp; English
   Wachter RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY79584 standard; peptide; 239
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99US-0136078P.
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 Llopis J,
                               WPI; 2000-116540/10.
N-PSDB; AAZ45642.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                         Sequence 239 AA;
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Tsien RY,
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17-MAY-2000; 2000WO-US013684.

99US-00316919.

21-MAY-1999; 21-MAY-1999;

(REGC ) UNIV CALIFORNIA. Baird GA; 2001-032017/04.

Tsien RY,

N-PSDB; AAC90488.

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The present sequence is that of the EGFP signal domain, which can be included in novel recombinant protease biosensors (PBS) of the invention. The PBS (see AAY79538-54) comprise: a first domain (see AAY79579-87) comprising at least 1 detectable polypeptide signal such as the present sequence, a second domain (see AAY79589-622) comprising at least 1 protease recognition site; and a third domain (see AAY7953-37) comprising at least 1 reactant target sequence. A recombinant nucleic acid (see AAA2767-43) encoding the PB, an expression vector, and a genetically engineered host cell are also claimed. A claimed method for identifying compounds that modify protease activity in a cell involves contacting a host cell that possesses the recombinant PB with a test compound, and determining the PB distribution in the host cell, where compound, and determining the PB distribution in the host cell, where compounds that modify protease activity in a host cell include the recombinant nucleic acid, or the recombinant pB, or the vector, or the recombinant nucleic acid, or the recombinant screen to detect in vivo activation of enzymatic activity and to identify specific activity based on cleavage of a known recognition motif is a protease activity based
                                                                  Recombinant nucleic acid encoding a protease biosensor useful for fluorescence based cell and molecular biochemical assays for drug discovery comprising three operably linked nucleic acid sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB50804 standard; protein; 239 AA
                                                                                                                                            Claim 14; Fig 29A; 218pp; English
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es 236; Conservative
                                  N-PSDB; AAA27573
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The present sequence is a fluorescnet protein used in the construction of a fluorescent protein indicator. The indicator comprises a sensor polypeptide that is responsive to a chemical, biological, electrical or physiological parameter, and a fluorescence protein functional group. The sensor polypeptide is operatively inserted into the fluorescent moiety. The fluorescent indicator is useful for detecting the presence of a response inducing member in a sample. The method involves contacting the sample with the indicator and detecting a change in fluorescence, in which a change is indicative of the effect of the parameter on the sensor polypeptide. The novel fluorescent proteins are advantageous due to their transfer)-based sensors

Novel fluorescent proteins comprising a sensor protein inserted into them, useful for measuring the response of a sensor biological, chemical, electrical or physiological parameter in vivo or in vitro.

Disclosure; Page 24; 94pp; English.

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Gaps

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1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
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121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                  181 DHYQQNTPIGDGPVILLPDNHYLSTQSALSKDPNEKRDHMVLVGFVTAAGITLGMDELYK 239
                                                                                                                                  Melanin concentrating hormone receptor; MCHR; MCH; chimeric; fusion; fluorescent polypeptide; orexigenic; anabolic; food intake; GFP; green fluorescent protein.
                                                                                                                                                                                                                                                                                                       A. victoria green fluorescent protein (GFP) and linker sequence.
                                                                                                                                                                                                                       AAB85900 standard; protein; 239 AA
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                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
Aequorea victoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200168706-A1
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WO200071565-A2

30-NOV-2000

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The invention provides melanin concentrating hormone (MCH) receptor (MCHR) chimeric and fusion proteins. The MCHR chimeric proteins comprise MCHR polypeptide regions from different species. The MCHR fusion protein comprise MCHR polypeptide region and a fluorescent polypeptide region protein joined directly, or via a linker, to the carboxy side of the MCHR polypeptide region. The MCHR fusion proteins can be expressed by standard recombinant methodology. MCH action promotes feeding (orexigenic) and up regulation of MCH activity stimulates food intake. The present sequence represents a A. victoria green fluorescent protein (GFP) and a linker
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                                                                                                                                                                                                               Fusion proteins comprising melanin concentrating hormone receptor peptides and fluorescent proteins, useful for identifying appetite
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                                                                                                                                                                                                                                                                               2; Page 14; 71pp; English.
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                              14-MAR-2001; 2001WO-US008071
                                                               15-MAR-2000; 2000US-0189698P
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death rate of a micro-organism within a predetermined time period in a desired environment. The method comprises introducing at least two reporter genes encoding luminescent and/or fluorescent products into the micro-organisms, incubating the micro-organism within the desired environment, and detecting luminescence and/or fluorescence after a predetermined time period. Use of two different markers within a micro-organism enables the differentiation between growth and death rates. The method is used to assess the growth rate and death rate of a micro-organism within a predetermined time period in a desired environment. The present sequence represents a green fluorescent protein (GFP), and is encoded by a plasmid which encodes luminescent and fluorescent proteins, and is and is used in the method of the invention
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                                                                                                                                                                                           Assessing growth and death rates of a micro-organism in a desired environment, by introducing 2 reporter genes encoding luminescent and fluorescent products and detecting luminescent fluorescence.
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                                                                                                                                                                                                                                                                                                      specification describes a method for assessing the growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 98.9%; Score 1260; DB 4; Length 239; Best Local Similarity 98.7%; Pred. No. 1.5e-121; Matches 236; Conservative 2; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A. victoria green fluorescent protein (EGFP).
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                                                                                                                                                                                                                                                                   Disclosure; Page 27; 32pp; English
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               99FI-00001296
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                                                                                                     Virta M;
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                                              (LILI/) LILIUS E. (VIRT/) VIRTA M.
                                                                                                                                                           N-PSDB; AAC86954
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X B X B X S X X X X B X B X B X Y X P
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29-OCT-1999;
01-DEC-1999;
17-SEP-1999;
                                                                       Giuliano K,
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                                        GIUL/)
                                                 (KAPU/)
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AAE14599
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                                                                                                                                                                                                                                                                                                                                                                                             VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                                                                                                                   The invention relates to a gene encoding proteins having cyan-green fluorescence characteristic and having a function of showing stable fluorescence characteristic in acid region. A method for the preparation of a cyan-green fluorescent protein is provided which involves a transformant transformed by a recombinant vector comprising the gene, where the transformed by a recombinant vector comprising the gene, culture. The present sequence represents the A. victoria green fluorescent protein (EGFP)
                                                                                                                                                                                                                                                                                                                                       LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                           61 LVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                                                                                                                                                                                                                                                                  1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                               1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
                                                                                                                                                                                                                                                                                                                                                                                                                                   Detection; classification; identification; toxin detection, protease;
ADP-ribosylating toxin; cytotoxic phospholipase; exfoliative toxin;
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                          .
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                                                                                                                                                                                                                                                        Length 239;
                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                    Query Match 98.9%; Score 1260; DB 5; Best Local Similarity 98.7%; Pred. No. 1.5e-121; Matches 236; Conservative 2; Mismatches 1;
                                                                                            gene encoding cyan-green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protease biosensor signal sequence #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG94444 standard; protein; 239 AA
                                                                                                                  Example; Page 14; 20pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-00031271.
99US-0122152P.
99US-0123399P.
99US-00352171.
 04-AUG-2000; 2000JP-00237165
                     04-AUG-2000; 2000JP-00237165
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                                          (RIKA ) RIKAGAKU KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                              WPI; 2002-299190/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        toxic threat agent
                                                                          N-PSDB; ABL40628
                                                                                                                                                                                                                                   Sequence 239 AA;
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12-JUL-1999;
31-AUG-1999;
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The invention describes methods of automated detection, classification
and identification comprising treating cells containing luminescent
creporter molecules (I) in array of locations with a test substance, where
(I) are detectors, classifiers or identifiers, imaging cells in each
location to obtain luminescent signals and converting optical information
into digital data to interpret presence of toxins in the test substance.
The method are useful for detection of toxins in the test substance.
Three classes of cell-based luminescent reporter molecules such as
reporters of toxic threat agents. The first two levels of
characterisation ensure a rapid readout of toxin class without
carrier maintain or dissect
characterisation ensure a rapid readout of toxin class without
several complex mixtures of known toxins. This is the amino acid sequence
of a protease biosensor related signal sequence used in the cell-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mutagenesis; enhanced green fluorescent protein; EGFP; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGGEGDATYGKLTLKFICTTGKLPVPMPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MVSKGERLFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPMPT
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or
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0
                                                                                                                                                                                                                                                                                                                                                                  Automated cell-based toxin detection, classification, and/or identification by treating cells involves use of three classes luminescent reporter molecules such as detectors, classifiers o identifiers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1260; DB 5;
Pred. No. 1.5e-121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 10; Fig 29A; 214pp; English
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99US-00398965.
99US-00430656.
99US-0168408P.
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                                                                                                                                                                                                                                    Kapur R;
                                                                                                                                                                                                                                                                                                2002-634730/68.
                                                                                                                                    GIULIANO K.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   screening system
                                                                                                                                                                                                                                                                                                                             N-PSDB; ABS71491
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The invention relates to a method for mutagenesis that comprises synthesising a mutated strand and a complementary strand by use of synthesising a mutated strand and a complementary strand by use of complemers. The method basically comprises a DNA synthesis in which one or more primers that have a nucleotide sequence containing at least one mutation and a phosphorylated 5'-terminus are annealed to a template DNA and then subjected to an elongation reaction using a thermostable bNA ligase the elongated terminus are ligated by means of a thermostable DNA ligase the step of DNA synthesis is repeated several times to amplify the DNA containing the primers and them, a least DNAs other than the amplified circular DNA are digested into several fragments; and a double-stranded circular DNA are digested into several fragments; and a double-stranded circular DNA synthesis in which, with the several fragments obtained in the step of digestion as megaprimers, the megaparimers are annealed to the circular DNA synthesis and which by an elongation reaction performed using the thermostable high-fidelity DNA polymerase. The method is useful for mutagenesis, particularly for introducing cratain mutations at certain sites of the nucleotide sequence. The present method is simple, speedy, economical and widely applicable. The present method is simple, speedy, economical and widely applicable. The present method is simple, a Aequorea victoria enhanced green fluorescent protein (GFP) used for withering the green fluorescent protein (GFP) sequence of Aequorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Method for mutagenesis, e.g. for introducing certain or random mutations at certain sites of the nucleotide sequence, comprises synthesizing a mutated strand and a complementary strand by use of megaprimers.
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note= "Wild-type GFP Met-Ser are replaced with Met-Val-
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                                                                                                                        "GFP Phe64 is replaced by Leu"
                                                                                                                                                                  /note= "GFP Ser65 is replaced by Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 13-14; 31pp; English.
                     Location/Qualifiers
                                                                                                                                                                                                                                                                                             03-AUG-2001; 2001EP-00306650
                                                                                                                                                                                                                                                                                                                                         04-AUG-2000; 2000JP-00237166
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nes 236; Conservative
                                                                                                                             'note=
                                                                                                                                                                                                                                                                                                                                                                                                                           Miyawaki A, Sawano A;
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                                                                                                                                                                                                                                                                                                                                                                                   (RIKE ) RIKEN KK.
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                                       Misc-difference
                                                                                                                                              Misc-difference
                                                                                                     Misc-difference
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Matches
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comprising a phosphorylation polypeptide and a fluorescent protein or in operative linkage, a donor molecule, a phosphorylatable domain, a phosphorylation domain (PAABD) and an acceptor molecule. The phosphorylation indicators of the invention are useful for detecting kinases or phosphatases in a biological sample. They are also useful in this throughput analysis e.g. for detecting a kinase inhibitor or phosphatase inhibitor. The present sequence is Aequorea victoria enhanced green fluorescent protein (EGFP) used in the invention
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                    181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 239
DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLVGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                     Phosphorylation indicator; fluorescent protein; detection; phosphatase; kinase; enhanced green fluorescent protein; EGFP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to chimeric phosphorylation indicators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kinase/phosphatase in samples, has donor molecule, phosphorylatable domain, phosphoaminoacid binding domain, and acceptor molecule, in operative linkage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel chimeric phosphorylation indicators, useful for detecting
                                                                                                                                                                                                                                 Aequorea victoria enhanced green fluorescent protein (EGFP).
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                                                                                                                            AAE34958 standard; protein; 239
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                                                                                                                                                                                                (first entry)
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Best Local Similarity 98.7
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ting AY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-148474/14
                                                                                                                                                                                                                                                                                                                           Aequorea victoria.
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                                                                                                                                                              AAE34958;
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                                                                                         RESULT 15
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Length 239; Indels 9

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181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 239

Search completed: June 21, 2004, 15:54:12 Job time: 48.1111 secs

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Sequence 46, Appli
Sequence 3, Appli
Sequence 2, Appli
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                                                               June 21, 2004, 15:46:55 ; Search time 12.7778 Seconds (without alignments) 965.630 Million cell updates/sec
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Sequence 125,
Sequence 2, Apj
Sequence 6, Apj
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Sequence
Sequence
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-513-783A-46

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US-09-62-102-1

US-09-62-102-1

US-09-172-063-21

US-09-172-063-21

US-09-617-197-129

US-09-417-197-129

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US-08-818-253-6
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Maximum Match 100%
Listing first 45 summaries
                                            - protein search, using sw model
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1274
1 MVSKGEELFTGVVPILV
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Perfect score:
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Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 75, Appli Sequence 71, Appl Sequence 11, Appl Sequence 114, Appl Sequence 114, Appl Sequence 114, Appl Sequence 1176, Appl Sequence 1178, Appl Sequence 1178, Appl Sequence 61, Appl Sequence 61, Appl Sequence 61, Appl Sequence 61, Appl Sequence 61, Appl Sequence 1178, Appl Sequence 1178, Appl Sequence 1178, Appl Sequence 1178, Appl Sequence 1178, Appl Sequence 1178, Appl Sequence 1178, Appl Sequence 1178, Appl Sequence 1178, Appl	SAMPLE	Length 239;  Indels 0; Gaps 0;  GKLTLKFICTTGKLPVPWPT 60  GKLTLKFICTTGKLPVPWPT 60  GKLTLKFICTTGKLPVPWPT 60  GKLTLKFICTTGKLPVPWPT 60  GKLTLKFICTTGKLPVPWPT 60  GKLTLKFICTTGKLPVPWPT 60  GKLTLKFICTTGKLPVPWPT 60  GKLTLKFICTTGKLPVPWPT 60  GKLTLKFICTTGKLPVPWPT 60  GIKVNFKIRHNIEDGSVQLA 180  GIKVNFKIRHNIEDGSVQLA 180  GIKVNFKIRHNIEDGSVQLA 180  GIKVNFKIRHNIEDGSVQLA 180  LVGFVTAAGITLGMDELYK 239  LLEFVTAAGITLGMDELYK 239
US-08-818-252-2 US-08-818-253-4 US-08-818-253-4 US-08-818-253-4 US-09-417-197-75 US-09-417-197-71 US-09-417-197-11 US-09-417-197-11 US-09-417-197-141 US-09-417-197-141 US-09-417-197-143 US-09-417-197-141 US-09-417-197-17 US-09-417-197-61 US-09-417-197-61 US-09-417-197-61 US-09-417-197-61 US-09-417-197-61	ALIGNMENTS  BESULT 1  18-09-172-063-3  Sequence 3, Application US/09172063  Sequence 3, Application US/09172063  Sequence 1, Application US/09172063  Patent No. 6150176  APPLICANT: Tsien, Roger Y. APPLICANT: Miyawaki, Atsushi APPLICANT: Miyawaki, Atsushi APPLICANT: Miyawaki, Atsushi APPLICANT: Menter, Rebekka M. APPLICANT: Mennington, S. James  TITLE OF INVENTION: FUNDESCENT PROTEIN SENSORS FOR  TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL FILE REFERENCE: 0725/7071001  FILE REFERENCE: 0725/7071001  FILE REFERENCE: 0998-10-13  EARLIER APPLICATION NUMBER: 09/094,359  EARLIER APPLICATION NUMBER: 09/094,359  EARLIER PELING DATE: 1998-06-09  NUMBER OF SEQ ID NOS: 38  SOFTWARE: FastSEQ for Windows Version 4.0  ELENGTH: 239  TYPE: PRT  FEATURE: NAME/KEY: VARIANT  LOCATION: (0)(0)  COTHER INFORMATION: EGFP	Score 1260; DB 3;   Pred. No. 1.5e.127;   2;   Mismatches
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	SULT 1 -09-172-063-3 Sequence 3, Application US/0917206 Batent No. 6150176 GENERAL INFORMATION: APPLICANT: Tsien, Roger Y APPLICANT: Michart, Rebekka M. APPLICANT: Michart, Rebekka M. APPLICANT: Michart, Rebekka M. APPLICANT: Machter, Rebekka M. APPLICANT: Michart, Rebekka M. APPLICANT: Michart, Rebekka M. APPLICANT: Michart, Rebekka M. APPLICANT: Michart, Rebekka M. APPLICANT: Michart, Rebekka M. APPLICANT: Michart, Rebekka M. APPLICANT: Michart, Rebekka M. APPLICANT: Michart, Nores Jane CURRENT FILING DATE: 1998-10-13 EARLIER APPLICATION UNMER: 09/09 EARLIER FILING DATE: 1998-10-13 SOFTWARE: FABLICANTON UNMER: 09/09 EARLIER FILING DATE: 1998-06-09 NUMBER OF SEQ ID NOS: 38 SOFTWARE: FABLICANT FEATURE: NAME/KEY: VARIANT LOCATION: (0)(0) CTHER INFORMATION: EGFP	98.98, y 98.78, reative   Frative   Frigvypilyi   Frigvypilyi   VQCFSRYPDi   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI    VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI    VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCFSRYPDI   VQCF
	LT 1 9-172-063-3 quence 3, Applicati quence 3, Applicati tent No. 615010. PPLICANT: Fisin, Ro PPLICANT: Tsien, Ro PPLICANT: Myawaki, PPLICANT: Myawaki, PPLICANT: Remington ITLE OF INVENTION: ITLE REFERENCE: 0725 URENT APPLICATION OFTWARE: FILING DATE: ARLIER APPLICATION OFTWARE: FILING DATE: CO ID NO 3 LENGTH: 239 UNDER OF SEQ 1D NOS Q ID NO 3 LENGTH: 239 TYPE: PRT NAME/KEY: VARIANT NAME/KEY: VARIANT NAME/KEY: VARIANT OCCATION: (0)(0) CHERR INFORMATION: 0-172-063-3	Similarity 98.  Similarity 98.  Conservative 98.  WVSKGEELFTGVVPI
00000000000000000000000000000000000000	SULT 1 -09-172-063- Sequence 3, Patent No. 6 GENERAL INFO APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE OF IN TITLE TITLE OF IN TITLE TITLE OF IN TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TITLE TI	itch 336 236 1 1 .61 .61 .121 121 181
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NUMBER OF SEQ ID NOS: 9
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                                                                                                                                                                                                                                                                                                                                       , OTHER INFORMATION: Description of Artificial Sequence: EGFP US-09-513-783A-46
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                             Sequence 46, Application US/09513783A

Patent No. 6416959

GENERAL INFORMATION;
APPLICANT: Galuliano, Kenneth A.

TILLE OF INVENTION: A System for Cell Based Screening;
FILE REPRENCE: 97-022-L1;
CURRENT APPLICATION NUMBER: US/09/513,783A;
CURRENT FILING DATE: 2000-02-25

NUMBER: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09316919;
Sequence 4, Application US/09316919;
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Baird, Geoffrey;
TITLE OF INVENTION: FLUCRESCENT PROTEIN INDICATORS;
FILE REFERENCE: 07257/073001;
CURRENT APPLICATION NUMBER: US/09/316,919;
CURRENT FILING DATE: 1999-05-21;
NUMBER OF SEQ ID NOS: 63;
SOFTWARE: FastSEQ for Windows Version 4.0;
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1260; DB 4;
Pred. No. 1.5e-127;
2; Mismatches 1;
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98.9%; Score 1260; DB 4;
Best Local Similarity 98.7%; Pred. No. 1.5e-127;
Matches 236; Conservative 2; Mismatches 1;
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Best Local Similarity 98.7
Matches 236; Conservative
RESULT 2
US-09-513-783A-46
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LENGTH: 239
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US-09-316-919-4
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121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
                                            121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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APPLICANT: Miyawaki, Atsushi
APPLICANT: Miyawaki, Atsushi
APPLICANT: Miyawaki, Atsushi
APPLICANT: Mochter, Rebekka M.
APPLICANT: Remington, S. James
ITILE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
ITILE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
ITILE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/071001
CURRENT APPLICATION NUMBER: US/09/602,641
CURRENT APPLICATION NUMBER: 09/172,063
PRIOR APPLICATION NUMBER: 09/172,063
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 239
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98.9%; Score 1260; DB 4;
Best Local Similarity 98.7%; Pred. No. 1.5e-127;
Matches 236; Conservative 2; Mismatches 1;
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APPLICANT: Sawano, Asako
TITLE OF INVENTION: METHOD FOR MUTAGENESIS
FILE REPERBUGE: 11283-01201
CURRENT APPLICATION NUMBER: US/09/920,922
CURRENT FILING DATE: 2010-08-02
PRIOR APPLICATION NUMBER: JP 2000-237166
PRIOR FILING DATE: 2000-08-04
                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09602641 Patent No. 6608189
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ORGANISM: Aequorea victoria
FEATURE:
NAME/KEY: VARIANT
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CTHER INFORMATION: EGFP
US-09-602-641-3
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Query Match
Best Local Similarity
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US-09-513-783A-2
                   JS-09-364-946-1
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LENGTH: 281
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Factor No. 613013

GENERAL INFORMATION:
APPLICANT: Kain, Steve
APPLICANT: Li, Xianqiang
TITLE OF INVENTION: Rapidly Degrading GFP-Fusion Proteins and Methods
TITLE OF INVENTION: of Use
FILE REFERENCE: D6100
CURRENT APPLICATION NUMBER: US/09/062,102
CURRENT FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: US 60/060,855
EARLIER FILING DATE: 1997-10-02
NUMBER FILING DATE: 1997-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Sequence of the EGFP-MODC422-461 fusion protein.; Patent No. 6130313
US-09-062-102-1
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Pred. No. 1.9e-127;
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                     ORGANISM: Aequorea victoria
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Best Local Similarity 98.7
Matches 236; Conservative
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LENGTH: 239
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LENGTH: 281
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                                                                                        US-09-920-922-2
                                                     TYPE: PRT
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Sequence 1, Application US/09364946

Sequence 1, Application US/09364946

Sequence 1, Application US/09364946

GENERAL INFORMATION:
APPLICANT: Kain, Steve
APPLICANT: Li, Xianqiang
TITLE OF INVENTION: Rapidly Degrading GFP-Fusion Proteins and Methods
TITLE OF INVENTION: OF USE
FILE REFERENCE: D6.00CIP/D2
CURRENT APPLICATION NUMBER: US/09/364,946
CURRENT APPLICATION NUMBER: US 09/191,233
EARLIER APPLICATION NUMBER: US 09/191,233
EARLIER FILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 14
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COTHER INFORMATION: GFP-DEVD-Annexin II construct
US-09-513-781A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1260; DB 4;
Pred. No. 1.9e-127;
2; Mismatches 1;
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Best Local Similarity 98.7%;
Matches 236; Conservative
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1 MVSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT 60
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Patent No. 6150176

GENERAL INFORMATION:
APPLICANT: Miyawaki, Ataushi
APPLICANT: Miyawaki, Ataushi
APPLICANT: Llopis, Juan
APPLICANT: Llopis, Juan
APPLICANT: Remington, S. James
ITTLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
ITTLE OF INVENTION: MEAGURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/071001
CURRENT APPLICATION NUMBER: US/09/172,063
CURRENT FILING DATE: 1998-10-13
BARLIER APPLICATION NUMBER: 09/094,359
BARLIER FILING DATE: 1998-06-09
NUMBER OF SEQ ID NOS: 38
SOFTWARE FEASTSEQ for Windows Version 4.0
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98.9%; Score 1260; DB 3; Length 323;
Best Local Similarity 98.7%; Pred. No. 2.4e-127;
Matches 236; Conservative 2; Mismatches 1; Indels (
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ORGANISM: Aequorea victoria
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OTHER INFORMATION: GT-EGFP
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US-09-602-641-21
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Sequence 21, Application US/09602641; Patent No. 6608189; GENERAL INFORMATION:

APPLICANT: Tsien, Roger Y. APPLICANT: Miyawaki, Atsushi APPLICANT: Llopis, Juan

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Patent No. 6191269
GENERAL INFORMATION:
APPLICANT: Pollock, Allan
APPLICANT: Lovett, David H.
APPLICANT: Truck, Johanna
TITLE OF INVENTION: Malignant Cancer Cells by Delivery of N.Terminal
TITLE OF INVENTION: Interleukin-1-Alpha Pro-Piece Polypeptide
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
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APPLICANT: Remington, S. James, TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE FILE REFERENCE: 0725/071001
CURRENT APPLICATION NUMBER: US/09/602,641
CURRENT FILING DATE: 2000-06-22
PRIOR PAPLICATION NUMBER: 09/172,063
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 223
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APPLICATION NUMBER: US/09/085,305
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CIASSIFICATION:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Aequorea victoria FEATURE:
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OTHER INFORMATION: GT-EGFP
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APPLICATION NUMBER:
FILING DATE:
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US-09-085-305-6
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Sequence 127, Application US/09417197

Sequence 127, Application US/09417197

Parent No. 65180121

GENERAL INFORMATION:

APPLICANT: Ole THASTRUP, et al.

TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An Ir.

TITLE OF INVENTION: On A Cellular Response

FILE REPERENCE: 3759-0110P

CURRENT PILING DATE: 1999-10-07

NUMBER OF SEQ ID NOS: 143

SOFTWARE: PatentIn version 3.0

SOFTWARE: PatentIn version 3.0
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                   181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLVGFVTAAGITLGMDELYK 239
                                            321 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 379
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Patent No. 6481667
GENERAL INFORMATION:
PAPLICANT: Kinsella, Todd
TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES
FILE REFRENCE: A-68614-1/DJB/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/800,170
CURRENT FILING DATE: 2001-08-28
PRIOR PILING DATE: 2000-03-06
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin version 3.1
SEQ ID NO 48
LENGTH: 434
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98.7%; Pred. No. 3.8e-127;
tive 2; Mismatches 1;
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Pred. No. 3.7e-127;
2; Mismatches 1;
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US-09-800-170-48
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Best Local Similarity 98.7%;
Matches 236; Conservative
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ORGANISM: Artificial Seguence
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Best Local Similarity
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Patent No. 6518021
GENERAL INFORMATION:
APPLICANT: Ole THASTRUP, et al.
TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An TILE OF INVENTION: On A Cellular Response
FILE REPERENCE: 3759-0110P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                                                                                                                                                                                                                                         Length 364;
                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
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                                                                                                                                                                                                                                                                                                                                     Score 1260; DB 3;
Pred. No. 2.8e-127;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SSOFTWARE: PatentIn version 3.0
LENGTH: 379
                                                           6510/102US1
             NAME: Francis, Carol L
REGISTRATION NUMBER: 36,513
REFERENCE/DOCKET NUMBER: 6510,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
                                                                                                                                INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 364 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                         98.9%;
98.7%;
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ORGANISM: Artificial Sequence
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               Matches 236; Conservative
                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
US-09-085-305-6
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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US-09-417-197-129
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61 LVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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                                                                   61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT 60
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US-09-513-783A-170
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                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-09-513-783A-170

Sequence 170, Application US/09513783A

Patent No. 6416599

GENERAL INFORMATION:
APPLICANT: Giuliano, Kenneth A.
TILLE OF INVENTION:
FILE REFERENCE: 97-022-L1

CURRENT APPLICANION NUMBER: US/09/513,783A

CURRENT FILING DATE: 2000-02-25

NUMBER OF, SEQ ID NOS: 180

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 170
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ORGANISM: Artificial Sequence
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Search completed: June 21, 2004, 16:04:04 Job time: 13.7778 secs

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June 21, 2004, 15:54:20 ; Search time 34.7778 Seconds (without alignments) 1940.117 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                   - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 4, Appli	Sequence 4, Appli	Sequence 6, Appli	Sequence 30, Appl	Sequence 32, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli		Sequence 4, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 4, Appli	'n	Sequence 13, Appl
SUMMARIES	LU TU	US-09-887-784-4	US-10-296-953-4	US-10-270-223-6	US-10-257-909A-30	US-10-257-909A-32	US-09-887-784-2	US-10-296-953-2	US-09-920-922-2	US-09-999-745-4	US-09-866-538-4	US-09-797-496B-2	US-09-794-308-4	US-09-865-291-4	US-10-457-982-3	US-10-121-258-13
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ns-o	US-09-887-784-4
, Se	guence 4, Application US/09887784
, Pa	Patent No. US20020177189A1
	GENERAL INFORMATION:
α.	APPLICANT: BJORN, Sara et al
Ţ.	TITLE OF INVENTION: NOVEL FLUORESCENT PROT
	FILE REFERENCE: 3759-0115P
٠.	CURRENT APPLICATION NUMBER: US/09/887,784
٠.	CURRENT FILING DATE: 2001-06-19
~	NUMBER OF SEQ ID NOS: 24
·.	SOFTWARE: PatentIn version 3.0

PROTEINS

ALIGNMENTS

; ORGANISM: Aequoria Victoria US-09-887-784-4 SEQ ID NO 4 LENGTH: 239 TYPE: PRT

ö 9 1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT Gaps ö Length 239; Indels Query Match 99.8%; Score 1271; DB 9; Best Local Similarity 99.6%; Pred. No. 2.2e-124; Matches 238; Conservative 1; Mismatches 0; ઠે

61 LVTTLSYGVQCFSRYPDHMKQHDFPKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120 61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120 121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180 121 VNRIELKGIDFKEDGNILGHKLEYNYNSHNYYIMADKQKNGIKVNPKIRHNIEDGSVQLA 180 1 MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT 60 g ò 요 ઠે 요

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WS-10-257-909A-30

| Sequence 30, Application US/10257909A
| Publication No. US20030187056A1
| Publication No. US20030187056A1
| Publication No. US20030187056A1
| GENERAL INFORMATION:
| APPLICANT: Bernard R. TERRY et al.
| TITLE OF INVENTION: distribution of phosphodiesterase (PDE) enzymes
| TITLE OF INVENTION: distribution of phosphodiesterase (PDE) enzymes
| TITLE OF INVENTION: distribution of phosphodiesterase (PDE) enzymes
| CURRENT PELICATION NUMBER: US/10/257,909A
| CURRENT PILING DATE: 2002-10-17
| NUMBER OF SEQ ID NOS: 36
| SEQ ID NO 30
| SEQ ID NO 30
| LENGTH: 893
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US-10-257-903A-32
Squence 32, Application US/10257909A
Squence 32, Application US/10257909A
Squence 32, Application US/20030187056A1
GENERAL INFORMATION:
THIS OF INVENTION:
TITLE OF INVENTION: distribution of phosphodiesterase (PDE) enzymes
TITLE OF INVENTION: distribution of phosphodiesterase (PDE) enzymes
TITLE OF INVENTION: 40157
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US-10-257-909A-30
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Publication No. US20030143634A1
GENERAL INFORMATION:
APPLICANT: Bioimage A/S
TITLE OF INVENTION: AN IMPROVED METHOD TO DETECT INTERACTIONS BETWEEN CELLULAR COMPON
TITLE OF INVENTION: INTERACTIONS BY FLUORESCENCE REDISTRIBUTION.
TITLE OF INVENTION: INTERACTIONS BY FLUORESCENCE REDISTRIBUTION.
FILE REFERENCE: 3759-0126P
CURRENT APPLICATION NUMBER: US/10/270,223
CURRENT PILLING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
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Pred. No. 2.2e-124;
1; Mismatches 0;
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99.6%; Pred. No. 4.1e-124;
iive 1; Mismatches 0;
                                                                                                                                                                 APPLICANT: BACKLARO, LEN
APPLICANT: BAGLIARO, LEN
APPLICANT: PAGLIARO, LEN
APPLICANT: THASTRUP, OLE
TITLE COF INVENTION: NOVEL FLUORESCENT PROTEINS
FILE REFERENCE: PL0095
CURRENT APPLICATION NUMBER: US/10/296,953
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: 60/212,681
PRIOR APPLICATION NUMBER: 60/212,681
PRIOR PILING DATE: 2000-06-20
PRIOR FILING DATE: 2001-05-10
PRIOR PILING DATE: 2001-05-10
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: PA 2001 00739
PRIOR FILING DATE: 2001-05-10
PRIOR PILING DATE: 2001-05-10
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; ORGANISM: Aequoria Victoria and Human
US-10-270-223-6
                                                               Sequence 4, Application US/10296953
Publication No. US20040072995A1
GENERAL INFORMATION:
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ORGANISM: Aequorea victoria
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Best Local Similarity 99.6%
Matches 238, Conservative
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Best Local Similarity 99.6
Matches 238; Conservative
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Pred. No. 1.5e-123;
1; Mismatches 1;
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                               APPLICANT: PACLIARO, LEN
APPLICANT: THASTRUP, OLE
TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS
FILE REFERENCE: PLOO95
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Fatent No. US20020083488A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Miyawaki, Atsushi
APPLICANT: Sawano, Asako
ITLE OF INVENTYON: METHOD FOR MUTAGENESIS
FILE REFERENCE: 11283-012001
CURRENT APPLICATION NUMBER: US/09/920,922
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: UP 2000-237166
PRIOR PETLING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 239
                                                                                                                      CURRENT APPLICATION NUMBER: US/10/296,953
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: PA 2000 00953
PRIOR FILING DATE: 2000-06-19
PRIOR PILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2001-05-10
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PRIOR PILING DATE: 2001-05-10
PRIOR PILING DATE: 2001-05-10
PRIOR PILING DATE: 2001-05-10
SEQID NO 2: SEQID NOS: 24
SOFTWARE: PALENTIN Ver: 2.1
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; ORGANISM: Aequorea victoria
US-10-296-953-2
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; ORGANISM: Aequorea victoria
US-09-920-922-2
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Best Local Similarity 99.29
Matches 237; Conservative
       APPLICANT: BJORN, SARA P.
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Best Local Simi
Matches 236;
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US-09-920-922-2
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                                                                                                                           ; OTHER INFORMATION: Fusion between Aequorea victoria and human US-10-257-909A-32
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                                                                                                                                                                                                     Query Match 99.8%; Score 1271; DB 14; Best Local Similarity 99.6%; Pred. No. 2.1e-123; Matches 238; Conservative 1; Mismatches 0;
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Patent No. US20020177189A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS
FILE REFERENCE: 3759-0115P
CURRENT APPLICATION NUMBER: US/09/887,784
CURRENT FILING DATE: 2001-06-19
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 239
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                                            TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-887-784-2
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US-09-887-784-2
SEQ ID NO 32
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APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
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APPLICANT: Tsien, Roger Y.
APPLICANT: Baird, Geoffrey
TILE OF INSURANCION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
FILE REFERENCE: RECENIATO-1
CURRENT APPLICATION NUMBER: US/09/999,745
CURRENT PILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 09/316,920
PRIOR PILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 4
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; Publication No. US20030032088A1
; Publication No. US20030032088A1
; GENERAL INFORMATION:
; APPLICANT: REGENT OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: Campbell, Robert
; TILE COF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
; FILE REFERENCE: REGENIS30-2
; CURRENT APPLICATION NUMBER: US/09/866,538
; CURRENT FILING DATE: 2010-05-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.0
; SEQ ID NOS: 29
; LENGTH: 239
; TYPE: PRI
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Pred. No. 3.1e-123;
2; Mismatches 1;
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Best Local Similarity 98.7%;
Matches 236; Conservative
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ORGANISM: Aequorea victoria
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OTHER INFORMATION: Aequorea victoria green fluorescent protein modified as described OTHER INFORMATION: in specification
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Publication No. US20030049597A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Simon, Sanford M.
APPLICANT: Chen, Yu
TITLE OF INVENTION: Chimeric Fluorescent Enzymes and Uses Thereof
FILE REFERENCE: 600-1-267
CURRENT APPLICANTE: 2002-05-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
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                                                                    Score 1260; DB 10;
Pred. No. 3.1e-123;
2; Mismatches 1;
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                                                                    Query Match
Best Local Similarity 98.7%;
Matches 236; Conservative
; ORGANISM: Aequorea victoria
US-09-866-538-4
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TYPE: PRT
ORGANISM: Aequorea victoria
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NAME/KEY: VARIANT

LOCATION: (0)...(0)

OTHER INFORMATION: EGFP

US-10-457-982-3
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Publication No. US2003018622941
GENERAL INFORMATION:
APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TSIEN, ROGET
APPLICANT: TING, Alice
APPLICANT: ZHANG, Jin
FILLE REFERENCE: REGENISON RATIOMETRIC INDICATORS OF PHOSPHORYLATION
FILLE REFERENCE: REGENISO
CURRENT APPLICATION NUMBER: US/09/865,291
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                APPLICANT: ZACHARIAS, David
APPLICANT: BAIRD, Geoffrey
TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
FILE REFERENCE: REGEN1530
CURRENT PEPLICATION UNBER: US/09/794,308
CURRENT FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.0
LENGTH: 239
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SOFTWARE: Patentin version 3.0
SEQ ID NO L
LENGTH: 239
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ORGANISM: Aequorea victoria
                                                                                                                                                                                                                                        ; ORGANISM: Aequorea victoria
US-09-794-308-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 98.77
Matches 236; Conservative
  TSIEN, Roger
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                                                        181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK 239
181 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLVGFVTAAGITLGMDELYK 239
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Fublication No. US20030059835A1
GENERAL INFORMATION:
APPLICANT: Teien, Roger

APPLICANT: Campbell, Robert

TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT

TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME

TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME

TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME

TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME

CURRENT APPLICATION NUMBER: 09/794,308

PRIOR APPLICATION NUMBER: 09/794,308

PRIOR APPLICATION NUMBER: 09/866,538

PRIOR FILING DATE: 2001-02-26

PRIOR FILING DATE: 2001-05-24.
                                                                                                                                                                                                                                                             Sequence 3 Application US/10457982

Publication No. US20030212265A1

GENERAL INFORMATION:
APPLICANT: Taien, Roger Y.
APPLICANT: Miyawaki, Atsushi
APPLICANT: Miyawaki, Atsushi
APPLICANT: Machter, Rebeka M.
APPLICANT: Machter, Rebeka M.
APPLICANT: Wachter, Rebeka M.
APPLICANT: Wachter, Remindron, S. James
ITILE OF INVENTION: FUORESCENT PROTEIN SENSORS FOR
ITILE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/071001
CURRENT APPLICATION NUMBER: US/09/602,641
FRICH FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/172,063
PRIOR FILING DATE: 1200-06-22
PRIOR PLING DATE: 2000-06-22
PRIOR PLING DATE: 2000-06-22
PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 2000-06-22
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PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 1000-06-22
PRIOR FILING DATE: 1000-06-22
PRIOR FILING DATE: 1000-06-22
PRIOR FILING DATE: 1000-13
NUMBER OF SEQ ID NOS: 38
SOFTWARE PESTSEQ for Windows Version 4.0
SEQ ID NO 3
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VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA 180
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                                                                                                                                                                                                 Query Match 98.9%; Score 1260; DB 14; Length 239; Best Local Similarity 98.7%; Pred. No. 3.1e-123; Matches 236; Conservative 2; Mismatches 1; Indels 0
) NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 2.39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Enhanced Green Fluorescent Protein (EGFP)
US-10-121-258-13
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Search completed: June 21, 2004, 16:09:29 Job time : 35.7778 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein June 21, 2004, 15:46:00 ; Search time 10.3333 Seconds Run on:

(without alignments) 2224.817 Million cell updates/sec

1 MVSKGEELFTGVVPILVELD.......VLvGFVTAAGITLGMDELYK 239 US-09-887-784-222V 1274 Title: Perfect score: Sequence:

283366 segs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		* Query			SUMMARIES	
No.	Score	Match	Length	8	ΠD	Description
-	1238	97.2	238	-	JQ1514	green-fluorescent
7	104	8.2	785	~	H72228	hypothetical prote
m	91.5	7.2	861	~	H64102	Ø
4	90	7.1	632	~	T06586	- 14
Ŋ	89.5	7.0	797	~	JC4078	
9	89.5	7.0	808	~	F64102	protective surface
7	89.5	7.0	887	~	E82590	leucyl-tRNA synthe
æ	88.5	6.9	655	~	D83917	DNA topoisomerase
σ	88.5	6.9	941	~	S29043	cellulase (EC 3.2.
10	88	6.9	578	-	I40794	dihydrolipoamide d
11	87.5	6.9	370	~	E70390	iron-sulfur cofact
12	87.5	6.9	860	~	AC0582	leucyl-tRNA synthe
13	87.5	6.9	2222	~	A36028	DNA-directed DNA p
14	87.5	6.9	2573	~	D71614	hypothetical prote
15	98	6.8	357	~	G81355	•
16	85.5	6.7	613	~	A99552	oligoendopeptidase
17	85.5	6.7	788		ЗВУГНН	DNA-directed DNA p
18	85.5		889	~	JC5576	inter-alpha-trypsi
19	82	6.7	281	~	AD2052	hypothetical prote
	84.5	9.9	425	N	C97354	
21	84	9.9	353	~	E84941	eglyc
	84	9.9	874	~	JC4930	S-layer protein pr
	83.5	9.9	836		JDAFD	DNA-directed DNA p
	83.5	9.9	1134	~	A60234	IgA Fc receptor pr
25		•	1164	-	FCSOAG	н
56	83	6.5	461	7	T06936	photosystem II chl
27	ä	6.5	263	~	S53488	water-stress-induc
28	ς.	6.5	534	-	NICLMA	nitrogenase (EC 1.
59	•	6.5	740	~	G95153	neuraminidase, pro

hypothetical prote	synaptogamin o-p65	hypothetical prote	hypothetical prote	carboxy-terminal p	hypothetical prote	hypothetical prote	proprotein convert	alpha-amylase homo	lipoxygenase (EC 1	synergohymenotropi	hypothetical prote	hypothetical prote	hypothetical prote	conserved hypothet	leucine-tRNA ligas
S76940	JH0414	D90946	H85794	A41798	T13674	T13673	KXRTC1	T39539	T11852	S68225	G86643	C64468	S76853	C64613	SYECL
~	~	N	N	~	~	N	H	N	~	N	N	N	~	N	-
355	439	682	682	682	734	743	752	774	865	310	1983	336	1290	393	860
6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.3	6.3
82	82	82	82	82	82	82	82	82	82	81.5	81.5	81	81	80.5	80.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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0	S
S	1514

green-fluorescent protein [validated] - hydromedusa (Aequorea victoria)
C;Species: Aequorea victoria
C;Date: 03-Dec-1999 #text_change 23-Mar-2001
C;Accession: US0692; UQ1514; FQ0315; S48693; S31330; S51331
R;Prasher, D.C.; Eckenrode, V.K.; Ward, W.W.; Prendergast, F.G.; Cormier, M.J. 66ne 11, 229-233, 1992
A;Tile: Primary Structure of the Aequorea victoria green-fluorescent protein. A;Reference number: UQ1514; MUID:92175527; PMID:1347277

A,Accession: JS0692
A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Cross.references: GB:M62654; NID:g155662; PIDN:AAA27722.1; PID:g155663
A,Accession: JQ1514
A,Molecule type: mRNA
A,Residues: 1-99, F',101-140, L',142-218, V',220-238 <PRA2>
A,Cross.references: GB:M62653; NID:g155660; PIDN:AAA27721.1; PID:g155661
A,Accession: PQ0335

A, Molecule type: protein
A, Residues: 46-6477-122,132-151;154-183;185-200 <PRA3>
A, Residues: 46-6477-122,132-151;154-183;185-200 <PRA3>
R. Inouye, S.; Tsuji, F.I.
FBS Lett. 351, 211-214, 1994
A, Title: Evidence for redox forms of the Aequorea green fluorescent protein.
A, Reference number: 548693; MUID:94364470; PMID:8082767
A, Accession: 548693
A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-24, 70', 26-156, 'P', 158-171,'K', 173-238 <INO>
A, Cross-references: GB:L29345; NID:9606383; PIDN:AAA58246.1; PID:9606384
R, Watkins, J. N.; Campbell, A.K.
submitted to the BMBL Data Library, January 1995
A, Reference number: 551330

A,Accession: S51330 A,Molecule type: mRNA A,Rosidues: 1-13, 'V,15-24,'Q',26-44,'N',46-153,'G',155-156,'P',158-171,'K',173-227,'R',; A,Crose-references: EMBL:X83959; NID:g634008; PIDN:CAAS8789.1; PID:g634009 A,Experimental source: clone gfpl

A,Accession: S51331
A,Molecule type: mRNA
A,Residues: 1-24, (0',26-29,'R',31-83,'L',85-153,'G',155-156,'P',158-171,'K',173-208,'Q',';
A,Residues: 1-24, (0',26-29,'R',31-83,'L',85-153,'G',155-156,'P',158-171,'K',173-208,'Q',';
A,Cross-references: EMBL:X83360; NID:g634010; PIDN:CAA58790.1; PID:g634011
A,Cross-references: EMBL:X83360; NID:g634010; PIDN:CAA58790.1; PID:g634011
A,Rang, F.; Moss L.G.; Phillips Jr., G.N.
A,Reference number: A65692; PDB:1GFL
A,Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 'A',2-79,'R', 81-95
A,Note: engineered sequence based on JQ1514, cloned and expressed in Escherichia coli
R,Yang, F.; Moss, L.G.; Phillips Jr., G.N.
Nat: Biotechnol. 14, 124, 1296
A,Title: The molecular structure of green fluorescent protein.
A,Title: The molecular structure of green fluorescent protein.
A,Reference number: A58953; MUID:98294543; PMID:9631087

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16 LVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLSYGVQCFSRY
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A;Contents: annotation; X-ray crystallography, 1.9 angstroms
C;Comment: This protein is excited by the photoprotein aequorin (see PIR:AQJFNV) emittin
C;Comment: The chromophore of this protein is formed by modification of Ser-dehydro-Tyr-
C;Gene: GFP
A;Gene: GFP
A;Introns: 69/3; 167/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 399, 323-329, 1999
Aritle: Evidence for lateral gene transfer between Archaea and Bacteria from genome seg A,Fitle: Evidence for lateral gene transfer between Areference number: A72200; MUID:99287316; PMID:10360571
A,Accession: H72228
A,Statuer: preliminary
A,Molecule type: DNA
A,Residues: 1-785 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein TM1624 - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: H72228
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE001806; GB:AE000512; NID:g4982196; PIDN:AAD36691.1; PID:g498219
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1624
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                                                                                                                                                                                                                                                                                                                                                                 1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLILKFICTTGKLPVPMPTL 60
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                                                                                                                               C;Superfamily: green-fluorescent protein
C;Keywords: chromoprotein; luminescence
F;65-67/Cross-link: 5-imidazolinone (Ser-Gly) #status experimental
F;66/Modified site: dehydrotyrosine (Tyr) #status experimental
                                                                                                                                                                                                                                               Score 1238; DB 1; Length 238;
Pred. No. 4.3e-96;
5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.2%; Score 104; DB 2; Length 785; 19.7%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71; Indels
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                                                                                                                                                                                                                                               97.2%;
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Best Local Similarity
Matches 46; Conservat
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                                                                                                                                                                                                                                                                                           230;
                                                                                                                                                                                                                                               Query Match
Best Local S:
Matches 230
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A;Cross-references: GB:U32774; GB:L42023; NID:g1573942; PIDN:AAC22581.1; PID:g1573943; T]
C;Genetics:
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                  N.Alternate names: leucyl-tRNA synthetase
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Accession: H64102
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, P. R;Fleischmann, R.D.; Scoti, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J. M.; Weidman, J. D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Grehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Accession: H64102
A;Accession: H64102
A;Accession: H64102
A;Acsession: H6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 DGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADK-QKNGI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         365 DEEIDLTKOAFVEHGKLVNSDEFDGKNF--DGAFNG------IADKLEKLGV 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 ---KVNFKIRH--------NIEDGSVQLADHYQQNTPIGDGPVLLPDNHYL- 202
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DNA-binding protein PD2 - garden pea

C;Species: Pisum sativum (garden pea)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999

C;Accession: T06586

R;Sato, N.; Kazuno, A.A.; Ohta, N.; Ohshima, K.
submitted to the EMBL Data Library, June 1996

A;Description: Identification of a novel family of DNA-binding proteins witl

A;Reference number: Z15774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        409 GKRQVNYRLRDWGVSRQRYWGAPIPMLTLENGDVVPA-----PMEDLPILLPEDVVMD
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-632 - SATA
A,FResidues: 1-632 - SATA
A,Cross-references: EMBL:X98740; NID:e995229; PIDN:CAA67292.1; PID:e275185
A,Experimental source: cv. Alaska
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 TIGKLPVPWPTLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKD----
- Haemophilus influenzae (strain Rd KW20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.1%; Score 90; DB 2; Length 632; Best Local Similarity 23.3%; Pred. No. 12; Matches 49; Conservative 26; Mismatches 79; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.2%; Score 91.5; L
Best Local Similarity 24.1%; Pred. No. 14;
Matches 46; Conservative 26; Mismatches
            Leucine-tRNA ligase (EC 6.1.1.4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVKSPINADPN 472
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---QERTIFFKDDGNYKTRAEVKFEGDTLVNRIE 125

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	### SCORE ### 1.00
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, P. Godayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J. B.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Glodek, A.; Kelley, J.M.; Weidman, J. Science 269, 496-512, 1995 Science 269, 496-512, 1995 A;Authors: Ganehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Authors: Ganehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Reference number: A64000; MUID:95350630; PMID:7542800 A;Reference number: A64000; MUID:95350630; PMID:7542800 A;Retaus: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-808 4TIGR> A;Cross-references: GB:L42023; TIGR:HI0917 C;Superfamily: protective surface antigen D-15 C;Keywords: surface antigen	Matches

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240 LVELNG----QLTLAGE---DGT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192 GPVLLPDNHYLSTQSALSKDPN
                                                                                                                                                                                                                                                                                                      Local Similarity 20.74
les 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-578 < KRU>
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Matches
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$229043
cellulase (EC 3.2.1.4) - Bacillus sp.
NyAlternate names: endo-1,4-beta-glucanase
(Species: Bacillus sp.
C;Species: Bacillus sp.
C;Accession: $29043; PC4404
S;Ozaki, K.; Shikata, S.; Kawai, S.; Ito, S.; Okamoto, K.
J. Gen. Microbiol: 136, 1327-1334, 1990
A;Title: Molecular cloning and nucleotide sequence of a gene for alkaline cellulase from A;Reference number: $29043; MUD:91037937; PMID:2230718
A;Reference possible: $29043; MUD:91037937; PMID:2230718
A;Residues: 1-941 <0ZAA
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R;Shirai, T.; Yamane, T.; Hidaka, T.; Kuyama, K.; Suzuki, A.; Ashida, T.; Ozaki, K.; Itc
J. Blochem. 122, 683-685, 1997
J. Blochem. 122, 683-685, 1997
A.Title: Crystallization and preliminary X-ray analysis of a truncated family A alkaline
A,Recession: PC4404
A.Accession: PC4404
A.Accession: PC4404
A,Residues: 228-584 <SHI.>
A,Experimental source: strain KSM-635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB05859.1; GSPDB:GN00
A;Experimental source: strain C-125
G;Genetics:
A;Gene: BH2140
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B
                                                                                                                                                                                                                                                                                                         F.; Hira
                                                                                                                                                                                           DNA topoisomerase IV subunit B BH2140 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                               C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: D83917
S;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; INucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans ak;Reference number: A83650; MUID:20512582; PMID:11058132
A;Reference number: A8350; MUID:20512582; PMID:11058132
A;Reference number: A8350; MUID:20512582; PMID:11058132
A;Reference number: A8350; MUID:20512582; PMID:11058132
A;Reference number: A8350; MUID:20512582; PMID:11058132
A;Reference number: A8350; MUID:20512582; PMID:11058132
A;Reference number: A8350; MUID:20512582; PMID:11058132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : ||::| : | : | : | 242 VFFNGESNGIEIEFAFQFN---DGYTENVLSFVNNVRTKDG-----GTHELGAKTAMTRAV 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --NYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADK----
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Best Local Similarity 21.9%; Pred. No. 17;
Matches 53; Conservative 37; Mismatches
-HYLSTQSALSKDPNEKR 216
                                     483 VAFSGTGSPIKTDPEWRK 500
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A; Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as cell A; Pathway: cellulose degradation cyapperfamily: Bacillus sp. KSM-615 alkaline cellulase; S-layer repeat homology; Thermot(C; Keywords: glycosidase; hydrolase; polysaccharide degradation F;41-95/Domain: S-layer repeat homology <SLR1>F;101-153/Domain: S-layer repeat homology <SLR2>F;161-153/Domain: S-layer repeat homology <SLR2>F;164-219/Domain: S-layer repeat homology <SLR3>F;164-219/Domain: Thermotoga xylanase A amino-terminal repeat homology <TXA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Description: catalyzes the oxidation of dihydrolipoamide to lipoamide using NAD A; Description: catalyzes the oxidation of dihydrolipoamide to lipoamide using NAD A; Pathway: acetoin dehydrogenase enzyme system C; Superfamily: Alcaligenes dihydrolipoamide dehydrogenase; dihydrolipoamide dehydrogenase; C; Keywords: FAD; flavoprotein; lipoamide; NAD; oxidoreductase; redox-active disulfide F; 5-77/Domain: lipoyl/biotin-binding homology <LPB.
F;117-145/Region: beta-alpha-beta FAD nucleotide-binding fold F;189-561/Domain: dihydrolipoamide dehydrogenase homology <DLD>
F;187-315/Region: beta-alpha-beta NAD nucleotide-binding fold F;189-158/Disulfide bonds: redox-active #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dihydrolipoamide dehydrogenase (EC 1.8.1.4) [validated] - Clostridium magnum
N/Alternate names: 2-oxoglutarate dehydrogenase complex chain E3; acetoin dehydrogenase c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Kruger, N.; Oppermann, F.B.; Lorenzl, H.; Steinbuchel, A.
J. Bacteriol. 176, 3614-3630, 1994
A;Title: Biochemical and molecular characterization of the Clostridium magnum acetoin del
A;Reference number: 140789; MUID:94266715; PMID:8206840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 TLSYGVQCF6RYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 ----PKNHYIIWELANEPSPNNNGGPGLTNDEKGWEAVKEYAEPIVEMLREKGDNMILV 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Clostridium magnum
.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 LVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLSYGVQCFSRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------PVQLRGMST---HGLQWFG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 PDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 NILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSV----QLADHYQQNTPIGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 TGVVPILVELDGDVNGHKFSVSGBGGBGDATYGKLTLK-----FICTTGKLPVPWPTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GB:L31844; NID:g472324; PIDN:AAA21748.1; PID:g472330 C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      272 -EIVNENAFVALSNDWGSNMIRLAMYIGENGYATNPEVK---DLVYEGIELA----
                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nydrogenase complex chain E3; S-complex 50K chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.9%; Score 88; DB 1
Best Local Similarity 22.9%; Pred. No. 16;
Matches 57; Conservative 43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         20.7%; Preα. ως. tive 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                6.9%; Score 88.5; 1
10.7%; Pred. No. 28;
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A,Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serova A,Reference number: AB0502, MUD:21534947; PMID:11677608
A,Accession. AC0582
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-860 <PAR>
A,Cross-references: GB:AL513382; PIDN:CAD05125.1; PID:g16501899; GSPDB:GN00176
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ashouse
Ashouse
Ashouse
DAN-directed DNA polymerase (EC 2.7.7.7) II catalytic chain - yeast (Saccharomyces cerev)
Nalternate names: DNA-directed DNA polymerase II chain A; protein N0825; protein YNL262v
C;Species: Saccharomyces cerevision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: AsiO289; B36028; S6019; S63235; S63121
R;Mocrison, A.; Araki, H.; Clark, A.B.; Hamatake, R.K.; Sugino, A.
A;Hitle: A third essential DNA polymerase in Saccharomyces cerevisiae.
A;Hates A third essential DNA polymerase in Saccharomyces cerevisiae.
A;Hatesidues: 1-222 cMOR>
A;Hocession: A36028; MUD:90381771; PMID:2169349
A;Rocession: A36028
A;Holecule type: DNA
A;Residues: 12-222 cMOR>
A;Residues: 12-222 cMOR>
A;Residues: 12-222 cMOR>
A;Residues: 12-221 cMOR>
A;Residues: 12-221 cMOR>
A;Residues type: DNA
A;Residues to the Rawl Data Library, October 1995
A;Holecule type: Drovein
A;Residues: 12-221 cMOR>
A;Residues: 12-221 cMOR>
A;Residues: 12-221 cMOR>
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A,Title: The sequence of a 24 152 bp segment from the left arm of chromosome XIV from Sac
A,Reference number: S65111, MUID:96310631, PMID:8740425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-2221 - SEF>
A;Residues: 1-2221 - SEF>
A;Cross-references: EMBL:X92494; NID:g1045236; PIDN:CAA63235.1; PID:g1045247
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | | ::|| | : | | | | 314 TGEEIPV-WAANFVLMAYGGH-DQRD-YEFASKYGLTIKPVILAADGSEPDL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 RAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 TTGKLPVPWPTLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQBRTIFFKDDGNYKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371 SEQALTEKGVLFNSGEFDGLAFEAAFNAIADKL------AEKGVGERKVNYRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 H------NIEDGSVQLADHYQQNTPIGDGPVLLPDNHYL-STQSALSKDP
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R, Sen-Gupta, M.; Lyck, R.; Fleig, U.; Niedenthal, R.K.; Hegemann, J.H.
Yeast 12, 505-514, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39;
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 860;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78;
                                                                                                                                                                                                                                                                                                                                                                                                         ch 6.9%; Score 87.5; DB 2; 1 Similarity 23.3%; Pred. No. 30; 42; Conservative 21; Mismatches 78;
                                                                                                                                                                                                                                                                                                       A;Gene: STY0699
C;Superfamily: leucine-tRNA ligase
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
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A,Residues: 1-370 <AQF>
A,Residues: 1-370 <AQF>
A,Residues: 1-370 <AQF>
A,Cross-references: GB.AE000720; NID:g2983529; PIDN:AAC07111.1; PID:g2983536; GB.AE00065
A,Experimental source: strain VF5
C,Genetics:
A,Gene: nifs1
C,Superfamily: nitrogen fixation protein nifs
C,Reywords: phosphoprotein; pyridoxal phosphate; sulfurtransferase
F,195/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
F,195/Binding site: Cys (cysteine persulfide intermediate) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A,Reference number: A70300; MUID:9819666; PMID:9537320
A,Accession: E70390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                  --- AKAKLIRDGININNN 346
                                                                                      124 IELKGIDFKEDG----NILGHKLEYNYNSHNVYIMADKQKN--GIKVNFKIRHNIEDGSVQ 178
                                                                                                                               :: |: || :: | || | :: | || |: 347 CKVTRIEQGEDGLKVSFIGDKGESIDVEKVLIAVGRRSNIEGLDVE-KIGVKTEGGSII 405
                                                                                                                                                                                                                                    179 LADHYQQNT----PIGD--GPVLLPDNHYLSTQSALSKD----PNEKRDHMVLVGFV--- 225
                                                                                                                                                                                                                                                                             164 KGVPLLTDAVQAIGKIPIELKNISYATFSGHKFHAIKGSGFLYISDEANYEPLIVGGGOE 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 TGKLP-----VPWPTLVTTLSYGVQCFSRYPDHMKQ-HDFFKSAMPEGYVQERTIFFKDD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 NGKRSGTENVVGILSLAKALEIIVSNFSRYQEQLKKCLRDLFENLLLEA-LPDAQIVGKDA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 GNYKTRAEV---KFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283 ERSPSISSVIMPKFFGAEIVNKLSEKGIYCSTGSACLSGEYEPNKHMLKMGFSQEKALRM 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              iron-sulfur cofactor synthesis protein nifS - Aquifex aeolicus
N;Contains: L-cysteine sulfurtransferase (EC 2.8.1..)
C;Species: Aquifex aeolicus
C;Date: 08-May_1998 #sequence_revision 08-May-1998 #text_change 07-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KGEELFTGVV----PILVELD----GDVNGHKF-SVSGEG----EGDATYGKLTLKFICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match
Local Similarity 25.4%; Pred. No. 9.9;
les 49; Conservative 30; Mismatches
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(981355
tRNA (uracil-5-)-methyltransferase (EC 2.1.1.35) Cj0831c [imported] - Campylobacter jejuu
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: G81355
C;Accession: G8135
R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C;W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp.
A;Heference number: A81250; MUID:20150912; PMID:10688204
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
hypothetical protein PFB0460c - malaria parasite (Plasmodium falciparum)
c;Species: Plasmodium falciparum
c;Species: Plasmodium falciparum
c;Species: Dlasmodium falciparum
c;Species: Plasmodium falciparum
c;Species: Dlate: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
c;Accession: D71614
R;Gardner, M.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
s; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O. Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-2573 <GAR>
A;Cross-references: GB:AE001396; GB:AE001362; NID:g3845188; PIDN:AAC71881.1; PID:g384515
A;Experimental source: clone 3D7
C;Genetics:
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                          983 LPKSFPETYFFTLENGKKLYLSYPCSMLNYRVHQKFTNHQYQELKDPLNYIYETHSENTI
                                                                                                                                                                                                                                                                                                   54 LPVPWP-TLVTTLSYGVQCFSRYPDHM------KQHDFFKSAMPEGYV----QERTI
                                                                                                                                                                                                                                         Gaps
                           A;Cross-references: SGD:S0005206; MIPS:YNL262w
A;Map position: 1d.
C;Superfamily: DNA-directed DNA polymerase II
C;Keywords: DNA binding; nucleotidyltransferase; nucleus; zinc finger
                                                                                                                                                                        Query Match 6.9%; Score 87.5; DB 1; Length 2222; Best Local Similarity 28.2%; Pred. No. 1e+02; Matches 37; Conservative 14; Mismatches 49; Indels 31;
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A; Gene: SGD: POL2; DUN2; MIPS: YNL262w
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237 TYLKRERDYM 246
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A; Molecule type: DNA
A; Residues: 1-37 < PAR>
A; Residues: 1-37 < PAR>
A; Residues: 1-37 < PAR>
A; Residues: 1-37 < PAR>
A; Residues: 1-37 < PAR>
A; Cross-references: GB:AL139076; GB:AL111168; NID:GG688128; PIDN:CAB73096.1; PID:G696877.
A; Experimental source: serotype O2, strain NCTC 11168
C; Genetics:
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336	682	737	393	658	860	860	860	461	312	468	546
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81	81	81	80.5	80.5	80.5	80.5	80.5	80	79.5	79.5	79.5
34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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                                                                                                                                                                                                                                                          Aequorea victoria (Jellyfish).
Eukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Leptomedusae,
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"Primary structure of the Aequorea victoria green-fluorescent
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=92175527; PubMed=1347277;
Prasher D.C., Eckenrode V.K., Ward W.W., Prendergast F.G.,
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"Aequorea green fluorescent protein. Expression of the gen fluorescence characteristics of the recombinant protein."
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GFP AEQVI STANDARD; PRT; 238 AA. P42212; Q17104; Q27903; 01-NOV-1995 (Rel. 32, Greated) 01-NOV-1995 (Rel. 32, Last sequence update) 01-NOV-2093 (Rel. 42, Last annotation update) Green fluorescent protein.
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RAY MEDLINE=99238303; PubMed=10220315;

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RAY SELLIGERAPHY (2.10 ANGSTROMS).

RAY "Structural and spectral response of green fluorescent protein

ratiants to changes in PH.";

ratiants to changes in PH.";

ratiants to changes in PH.";

LISTINGTION: Energy-transfer acceptor. Its role is to transduce the blochemiluminescence of the protein aequorin into green

fluorescent light by energy transfer. Fluorescence in vivo upon receiving energy from the Ca(2+)-activated photoprotein aequorin.

CC Absorbs light maximally at 395 nm and exhibits a smaller absorbance peak at 470 nm. The fluorescence emission spectrum

CC ABBOATH NORMORE.

CI TISSUE SPECIFICITY: Photocytes.

CI CONTINUE SPECIFICITY: Photocytes.

CI CONTINUE AND ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF MONITORIA ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTANCE OF ACCEPTA
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EMBL; M62654; AAA27722.1; -. EMBL; M62653; AAA27721.1; -. EMBL; L29345; AAA58246.1; -. EMBL; X96418; CAA65278.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-JUN-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1B9C; 17-NOV-00
1BFP; 07-JUL-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0-AUG-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7-NOV-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS0692; JQ1514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1BFP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1C4F;
1EMA;
1EMB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1EME;
1EMF;
1EMG;
1EMK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEMM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1EMC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LF09;
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07-JAN-03. 28-AUG-02. 10-APR-02.

1-JAN-97

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VITESYGVQCESRYPDHWKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HXQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLVGFVTAAGITLGMDELYK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                 5-imidazolinone (Ser-Gly). 2,3-DIDEHYDROTYROSINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26886 MW; EASA6F21FBFB6E05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1244; DB 1;
Pred. No. 3.1e-95;
2; Mismatches 3;
                                 PDB; 2EMO; 20-AUG-97.
InterPro; IPR009017; GPP_like.
InterPro; IPR000786; Green_fl_protein.
Pfam; PP01353; GPP; 1.
                                                                                PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl_protein; 1.
Luminescence; 3D-structure.
                                                                                                                                           MOOEW CEHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 97.9
Matches 233; Conservative
                                                                                                                                66
100
108
141
219
25
25
80
80
157
                                                                                                                                                                                                                                                                                                              28-OCT-98.
20-AUG-97.
                       20-AUG-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 ;
238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
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                                                                                                                                              163 ---KVNFKIRH------NIEDGSVQLADHYQQNTPIGDGPVLLPDNHYL- 202
                                                                                                                                                                                       100 FFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNI---LGH------KLEYNYNS 148
   104 DGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADK-QKNGI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 LSYGVQCFSRYPDHMKQHDF-------RTSAMPEGYVQE------RTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAINERG / KWZO / ATCC 51907;

STRAINERG / KWZO / ATCC 51907;

MEDLINE-95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F.,

Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Goczyne J.D.,

Soctt J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Protective surface antigen D15 precursor (80 kDa D15 antigen)
(D-15-Ag) (Outer membrane protein D15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 19 POTENTIÂL.
20 795 PROTECTIVE SURFACE ANTIGEN D15.
795 AA; 87478 MW; B85691FC22E6ED44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SIMILARITY: Belongs to the surface antigen D15 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR; HI0917; -.
InterPro; IPR000184; Bac_surfAg_D15.
Pfam; PF01103; Bac_surface_Ag; I.
Antigen; Outer membrane; Signal; Complete proteome.
                                                                           365 DEEIDLTKOAFVEHGKLVNSDEFDGKNF--DGAFNG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.0%; Score 89.5; DE Best Local Similarity 22.4%; Pred. No. 9.2; Matches 49; Conservative 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 795 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U32773; AAC22575.1; -.
                                                                                                                                                                                                                                                                                             203 STQSALSKDPN 213
                                                                                                                                                                                                                                                                                                                                      :| :: |||
462 GVKSPINADPN 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter J.C.; "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAMAP, ME 00049; -; 1.

InterPro; IPR002302; Leu-tRNAsyntla.

InterPro; IPR0014012; tRNA-synt 1a.

InterPro; IPR001412; tRNA-synt 1a.

InterPro; IPR009008; Valks IleR_edit.

PRINTS; PR00985; TRNASYNTHILD.

PRINTS; PR00985; TRNASYNTHILD.

PRINTS; PS00178; AA TRNA_LIGASE 1; 1.

PROSITE; PS00178; AA TRNA_LIGASE 1; 1.

Aminoacy1-tRNA synthetase; Protein biosynthesis; Ligase, ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 TTGKLPVPWPTLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i - CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP +
diphosphate + L-leucyl-tRNA(Leu).
-i - SUBUNIT: Monomer (By similarity).
-i - SUBCELLULAR LOCATION: Cytoplasmic.
-i - SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAINER ( KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 41, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.2%; Score 91.5; DB 1; Length 861; 24.1%; Pred. No. 6.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       861 AA; 97750 MW; EB93304F6B4C8FB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60;
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ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U32774; AAC22581.1; -.
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                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Haemophilus influenzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                      OR HI0921
                                                                                                                                                                                SYL HAEIN
P43827;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                          HNVYIMADKQK-NGIKVNFKIRHNIEDGSVQLADHYQQ-------NTPIGDGPVLL 196
                                                                                                                                                                                                                                                                                                                                                                                                                   543 RNLYIQSMKFKGNGIKTN-----DFDFSFGWNYNSLNRGYFPTKGVKASLG-GRVTI
                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS).
LEUCY OR XF2176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                   P--DNHYLSTQSALSKDPNEKRDHMVLVGFVTAAGITLG 233
                                                                                                                                  594 PGSDNKYYKLSADVQGFYPLDRDHLWVVSAKASAGYANG 632
                                                                                                                                                                                                       879 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE004031; AAF84975.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; MF_00049; -; 1.
Interpro; IPR002302; Leu-tRNAsyntla.
                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=985C;
MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                                                                                                                                                                                      Xanthomonadaceae; Xylella.
                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=2371;
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Q9PBG8;
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   187 FFENYDNSKSDTSSNYKRTTYGSNVTL-GFPVNENNSYYVGLGHTYNKISNFALEYN--- 542
                                 --NTPIGDGPVLL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : | | : | | : | | : | IGYGTESGISYQASVKQDNFLGTGAAVSIAGTKNDYGTSVNLGYTEPYFTKDGVSLGGNV
                                                            543 RNLYIQSMKFKGNGIKTN-----DFDFSFGWNYNSLNRGYFPTKGVKASLG-GRVTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Outer membrane protein D15 is conserved among Haemophilus influenzae species and may represent a universal protective antigen against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Minna / Serotype B, and Eagan / Serotype B;
MEDLINE=97427952; PubMed=9284140;
Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                          Flack F.S., Loosmore S., Chong P., Thomas W.R.; "The sequencing of the 80-kDa D15 protective surface antigen of Haemophilus influenzae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63;
                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protective surface antigen D15 precursor (80 kDa D15 antigen)
(D-15-Ag) (Outer membrane protein D15).
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----FKSAMPEGYVQE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.0%; Score 89.5; DB 1; Length 797; 22.4%; Pred. No. 9.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTECTIVE SURFACE ANTIGEN D15.
2F93DE538696AF1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Infect. Immun. 65:3701-3707(1997).
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SIMILARITY: Belongs to the surface antigen D15 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78; Indels
                                                                                                                    594 PGSDNKYYKLSADVQGFYPLDRDHLWVVSAKASAGYANG 632
                                 149 HNVYIMADKQK-NGIKVNFKIRHNIEDGSVQLADHYQQ--
                                                                                         197 P--DNHYLSTQSALSKDPNEKRDHMVLVGFVTAAGITLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29; Mismatches
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-Serotype B;
MEDLINE-95255676; PubMed=7737523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam, PF01103, Bac_surface_Ag; 1
Antigen; Outer membrane; Signal.
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                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene 156:97-99(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                797 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invasive disease."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            species and may
                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=727;
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                                                                                                                                                                                              HAEIN
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                                                                                                                                                                                                                                                                                                        50 TIGKLPVPWPILVTILSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNY-- 107
                                                                                                                                                                                                                                                                                                                                321 TNEQLPV-WVANFVLMAYGTGAVMAVPGHDQRDQEF--ANKYGLPIRQVIALKEPKNQDE 377
                                                                                                                                                                                                                                                                                                                                                                             --KTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                154 MADKQKNG-IKVNFKIRHNIEDGSVQLADHYQQNTPI------GDGPVLLPDN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              422 ---ROGRGORRVNYRLR----DWGVSRORYWGCPIPVIYCPTCGAVPVPEDQLPVILPEN 474
               InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR00908, valR2_IleRc_edit.
Pram; PF0013; tRNA-synt_I.i.
PRINTS; PR00985; TRNASYNTHLEU.
TIGRRAMS; TIGR00396; leuS_bact; 1.
FRRFAMS; TIGR00396; leuS_bact; 1.
Aminoacyl-tRNA synthētase; ProteIn biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                378 STWEPDVWRDWYADKTR---EFE---LINSAEFDGLDYQDAFEVLAERFE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Outer membrane protein D15 is conserved among Haemophilus influenzae species and may represent a universal protective antigen against invasive disease.";
                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protective surface antigen D15 precursor (80 kDa D15 antigen)
(P-15-Ag) (Outer membrane protein D15).
Haemophilus influenzae.
                                                                                                                                                                                                                                      7.0%; Score 89.5; DB 1; Length 879; 22.2%; Pred. No. 10;
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-i- SIMILARITY: Belongs to the surface antigen D15 family.
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                    879 AA; 99796 MW; 9FDCCB992092919E CRC64;
                                                                                                                                                                   "KMSKS" REGION.
ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     793 AA.
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                                                                                                                                                   "HIGH" REGION
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MEDLINE=97427952; PubMed=9284140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 -HYLSTQSALSKDPNEKR 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  475 VAFSGTGSPIKTDPEWRK 492
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032629;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               487 FFENYDNSKSDTSSNYKRTTYGSNVTL-GFPVNENNSYYVGLGHTYNKISNFALEYN--- 542
                                                                                                                                                                                                                                                                                                                                                                                                          486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 FFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNI---LGH------KLEYNYNS 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 HNVYIMADKQK-NGIKVNFKIRHNIEDGSVQLADHYQQ------NTPIGDGPVLL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         543 RNLYIQSMKFKGNGIKTN-----DFDFSFGWNYNSLNRGYFPTKGVKASLG-GRVTI 593
                                                                                                                                                                                                                                                                                                                                                                             : || : || : || :| | 427 IGYGTESGISYQTSIKQDNFLGTGAAVSIAGTKNDYGTSVNLGYTEPYFTKDGVSLGGNI
                                                                                                                                                                                                                                                Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDILINE 91037937; PubMed=2230718; MEDILINE 91037937; PubMed=2220718; Ozaki K., Shikata S., Kawai S., Ito S., Okamoto K.; Ozaki K., Shikata S., Kawai S., Ito S., Okamoto K.; Molecular cloning and nucleotide sequence of a gene for alkaline cellulase from Bacillus 8p. KSM-635."; J. Gen. Microbiol. 136:1327-1334(1990).
-!- CATALYTICA CATIVITY: Endohydrolysis of 1,4-beta-D-glucosidic linkages in cellulose, lichenin and cereal beta-D-glucosic.
-!- SIMILARITY: Belongs to cellulase family A (family 5 of glycosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF03424; CBM 17_28; 2.
Pfam; PF00150; cellulase; 1.
Pfam; PF00155; SLH; 3.
PROSITE; PS00659; GLYCOSYL_HYDROL_F5; 1.
PROSITE; PS01072; SLH DOMAIN; 2.
Cellulose degradation; Hydrolase; Glycosidase; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
10-CCT-2003 (Rel. 42, Last sentotation update)
Endoglucanase precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)
                                                                                                                                                         6.9%; Score 88.5; DB 1; Length 793; 22.8%; Pred. No. 11; tive 27; Mismatches 79; Indels 6:
19 POTENTIAL.
793 PROTECTIVE SURFACE ANTICEN DIS.
87511 MW; 51BFDB2036801A14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hydrolases).
-!- SIMILARITY: Contains 3 S-layer homology (SLH) domains.
                                                                                                                                                                                                                                                                                                                               -----FKSAMPEGYVQE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus sp. (strain KSM-635).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 P--DNHYLSTQSALSKDPNEKRDHMVLVGFVTAAGITLG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       594 PGSDNKYYKLSADVQGFYPLDRDHRWVVSAKASAGYANG 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 941 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDB; 1G01; 31-DEC-02.
PDB; 1G0C; 31-DEC-02.
INTERPO; IPR005086; CBM 17 28.
INTERPO; IPR008979; Gal_bind like.
INTERPO; IPR001547; Glyco_hydro_5.
INTERPO; IPR001119; SLH.
                                                                                                                                                                                                                                                                                                                               65 LSYGVQCFSRYPDHMKQHDF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M27420; AAA22304.1; -. PIR; S29043; S29043.
                                                                                                                                                                                                   Best_Local Similarity 22.8
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Alkaline cellulase).
        1
20
793 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Firmic
NCBI_TaxID=1415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3D-structure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 TIGKLPVPWPTLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      419 DWGVSRQRYWGAPIPMVTLEDGTV-----LPTPEDQLPVILPEDVVMDGITSPIKADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 RAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 SEQALTEKGVLFNSGEFDGLAFEAAFNAIADKL------AEKGVGERKVNYRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 H-------NIEDGSVQLADHYQQNTPIGDGPVLLPDNHYL-STQSALSKDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=LTZ / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCCICLILand M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvaney E., Ryan B., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00178; AA TRNA_LIGASE I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-OcT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leucyl-ERNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
LEUS OR STM0648.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.9%; Score 87.5; DB 1; Length 860; 3.3%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP diphosphate + L-leucyl-tRNA(Leu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             523 "KWSKS" REGION.
522 ATP (BY SIMILARITY).
96940 MW; 2F95E480BBABE33C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "HIGH" REGION
                                                                                                                                                                                                                                                                                                           HAMAP; MF_00049; -; 1.
InterPro; IPR002302; Leu-tRNAsyntla.
InterPro; IPR001412; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR009008; ValRs_IERS_edit.
Pf00133; tRNA-synt_l; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0985; TRNASYNTHLEU.
TIGRFAMS; TIGR00396; leuS bact; 1.
PROSITE; PS00178; AA TRNA_LIGASE I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                           EMBL; AL627267; CAD05125.1; -.
                                                                                                                                                                                                                                                                                    EMBL; AE016841; AA069822.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 23.3%
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52
623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               860 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYL SALTY
Q8ZQZ6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ::||: | :: | :: | :: | :: | 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 -----PKNHYIIWELANEPSPNNNGGPGLTNDEKGWEAVKEYAEPIVEMLREKGDNMILV 415
                                                                                                                                                                                                                                                                                                                                                                                                         76 PDHMKQHDFFKSAMPEGYVQBRTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----- 222
                                                                                                                                                                                                                                                                                                                                           136 NILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGSV----QLADHYQQNTPIGD 191
                                                                                                                                                                                                                                                                                                                16 LVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLSYGVQCFSRY 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
                                                                                                                                                                                                                                                                                                                                                                                                                                          10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-UCT-2003 (Rel. 42, Last annotation u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain of Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Mitchead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant Salmonella enterica servovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                              97;
                                                                                                                                                                                                              6.9%; Score 88.5; DB 1; Length 941; 20.7%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Bacteriol. 185:2330-2337(2003). -!- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP diphosphate + L-leucyl-tRNA(Leu).
                                                                                            225 SLH 3.
373 PROTON DONOR (BY SIMILARITY)
485 NUCLEOPHILE (BY SIMILARITY).
104628 MW; BEA2AC3B169BFADA CRC64;
                                                                                                                                                                                                                                                                62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 GPVLLPDNHYLSTQSALSKDPN------
                        ENDOGLUCANASE.
                                                                                                                                                                                                                                                              32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 413:848-852(2001)
29
941
151
2225
485
                                                                                                                                                                    941 AA;
                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 G 223
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                                                                                                                                                                                                                                                              50;
                                                                                                                ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         272
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                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                            Local
                        CHAIN
DOMAIN
                                                                        DOMAIN
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  SIGNAL
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Matches
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471

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cerevisiae."
EMBO J. 11:7
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셤
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                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 TTGKLPVPWPTLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | ::|| | : | | | : | | 314 TGEEIPV-WAANFVLMEYGTGAVMAVPGH-DQRD-YEFASKYGLTIKPVILAADGSEPDL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 RAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           371 SEQALTEKGVLFNSGEFDGLAFEAAFNAIADKL------AEKGVGERKVNYRLR 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 H------NIEDGSVQLADHYQQNTPIGDGPVLLPDNHYL-STQSALSKDP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      419 DWGVSRQRYWGAPIPMVTLEDGTV-----LPTPEDQLPVILPEDVVMDGITSPIKADP 471
                                                                                                                                                                                                                                             Pfam; PF00133; tRNA-synt_1; 1. PRINTS; PR00985; TRNA-SYNTHLEU.
TIGRFAMs; TIGROO396; leus, bact; 1. PROSITE; PS00178; AA TRNA_LIGASE_I; 1. Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96310631; PubMed=8740425; Sen-Gupta M., Lyck R., Fleig U., Niedenthal R.K., Hegemann J.H.; Sen-Gupta M., Lyck R., Fleig U., Niedenthal R.K., Hegemann J.H.; The sequence of a 24,152 bp segment from the left arm of chromosome "The sequence Saccharomyces cerevisiae between the BNI1 and the POL2
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Bukarycta; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                  39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 1214-1221.
MEDLINE=90381771; PubMed=2169349;
Morrison A., Araki H., Clark A.B., Hamatake R.K., Sugino A.;
"A third essential DNA polymerase in S. cerevisiae.";
Cell 62:1143-1151(1990).
                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
DNA polymerase egsilon, catalytic subunit A (EC 2.7.7.7)
POLZ OR DUNZ OR YNLZ62W OR N0825.
                                                                                                                                                                                                                                                                                                                                                                                                                               78; Indels
                                                                                                                                                                                                                                                                                                                                                                         860 AA; 96985 MW; D5003584DFBCCAB6 CRC64;
                                                                                                                                                                                                                                                                                                                                               "KMSKS" REGION.
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                               21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                  "HIGH" REGION
                                                                                                                                                                                                                                                                                                                                                                                                     6.9%; Score 87.5;
                                                                                                                                                                    Stycene, MC 00049; -; 1.
HAMAP, MF 00049; -; 1.
InterPro; IPR002300; Leu-tRNAsyntla.
InterPro; IPR002300; tRNA-syntla.
InterPro; IPR001412; tRNA-syntl.
InterPro; IPR009008; ValRS lleRS edit.
                                                                                                                                                 EMBL; AE008725; AAL19599.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-2221 FROM N.A. STRAIN=S288c / FY1679;
                                                                                                                                                                                                                                                                                                                                                                                                                 23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                 StyGene; SG????; leus.
                                                                                                                                                                                                                                                                                                                                  52
623
622
                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                     Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPOE YEAST
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 LPVPWP-TLVTTLSYGVQCFSRYPDHM-----KQHDFFKSAMPEGYV----QERTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBUNIT: CONSISTS OF FIVE SUBUNITS (200 kDa, 80 kDa, 34 kDa, 30 kDa, AND 29 kDa).
-1- SUBCELLULAR LOCATION: Nuclear.
-1- DOMAIN: THE DNA POLYMERASE ACTIVITY DOMAIN RESIDES IN THE N-TERMINAL HALF OF THE PROTEIN, WHILE THE C-TERMINUS IS NECESSARY FOR COMPLEXING SUBUNITS B AND C.
-1- MISCELLANEOUS: In eukaryotes there are five DNA polymerases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.9%; Score 87.5; DB 1; Length 2222;
28.2%; Pred. No. 46;
ive 14; Mismatches 49; Indels 31; Gaps
                                                                                                                                                                                                                         "DNA polymerase II, the probable homolog of mammalian DNA polymerase epsilon, replicates chromosomal DNA in the yeast Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alpha, beta, gamma, delta, and epsilon which are responsible for different reactions of DNA synthesis. SIMILARITY: Belongs to the DNA polymerase type-B family.
                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: DNA POLYMERASE II PARTICIPATES IN CHROMOSOMAL DNA
                                                                                                            MEDLINE-92164663; PubMed=1537345;
Araki H., Ropp P.A., Johnson A.L., Johnston L.H., Morrison A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M60416; AAA88711.1; -.

R EMBL; X29494; CAA62235.1; -.

R EMBL; X29494; CAA62235.1; -.

R EMBL; X36028; A36028

R Germonline: 143268; -.

Germonline: 143268; -.

R SGD; SO005206; POLZ.

R GO; GO:0000731; P:DNA repair synthesis; IMP.

R InterPro; IPR006134; DNA_Pol_B = Comp.

R InterPro; IPR006134; DNA_Pol_B = Comp.

R InterPro; IPR006134; DNA_Pol_B = Comp.

R Pfam; PF00114; DNA_Pol_B = Comp.

R Pfam; PF00116; DNA_POLYMERASE B; PALSE NEG.

R PARSITE; PS00116; DNA_POLYMERASE B; PALSE NEG.

R PROSITE; PS00116; DNA_POLYMERASE B; PALSE NEG.

R NATAMETER = Comp. POLYMERASE B; PALSE NEG.

W Transferase; DNA-directed DNA_DIYMERASE; DNA replication;

T VARLANT 644 644 M -> I (IN POL2-9 TS MUTANT).

T VARLANT 710 P -> S (IN POL2-18 TS MUTANT).

SEQUENCE 2222 AA; 255669 MM; CBCDDE2AB147D65B CRC64;
                                                                            TEMPERATURE SENSITIVE MUTANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 28.2%
nes 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1000 SDIFKVFLEGD 1010
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Keast 12:505-514(1996).
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TISSUB-Brain, and Testis;

MEDLINE-22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.E., Zeeberg B., Barcow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buclow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altschul S.F., Zeeberg B., Buclow K.H., Schaefer C.F., Bhat N.K.,

A stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21638749; PubMed=11780052;

MEDLINE=21638749; PubMed=11780052;

MEDLINE=21638749; PubMed=11780052;

MEDLINE=21638749; PubMed=11780052;

MEDLINE=21638749; PubMed=11780052;

MEDLINE=21638749; PubMed=11780052;

MEDLINE=21638749; PubMed=11780052;

MEDLINE=21638749; PubMed=11780052;

MEDLINES A., Barlow K.F., Bardgeman A.W., Brown A.J.,

Basaley O.P., Bird C.P., Blakey S.E., Bridgeman D.M., Brown A.J.,

MEDLING D. M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,

Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.R.,

Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.R.,

MEDLINGCON A.G., Fraser A., Fraser P.,

Ammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

MARCH E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,

Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

Lehvacelaino M.H., Leversha M.A., Lloyd C., Lloyd C., Loyd D.M., Lovell J.D.,

Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,

MILNE S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,

Nich C.M., Ross M.T., Scott C.E., Sehra H.K., Showhkeen R., Sins S.,

Skuce C.D., Smith M.L., Soderlund C., Sreward C.A., Sulston J.E.,

Skuce C.D., Smith M.L., Soderlund C., Sreward C.A., Sulston J.E.,

Skuce C.D., Smith M.L., Soderlund C., Sreward C.A., Sulston J.E.,

Skuce C.D., Smith M.L., Soderlund C., Sreward C.A., Sulston J.E.,

Skuce C.D., Waray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,

Whitehead S.L., Whiteker P., Willey D.L., Williams L., Williams S.A.,

Whitehead S.L., Whiteker P., Willey D.L., Williams L., Williams S.A.,

Whitehead S.L., Whitehead S.L., Whitehead S.L., Whomes D. W.,

Whitehead S.L., Whitehead S.L., Whitehead S.L., Whitehead S.L., Whitehead S.L., Whitehead S.L., Whitehead S.L., Whitehead S.L., Whitehead S.L., Whitehead S.L., Whitehead S.L., Whitehead S.L., Whitehead S.L., Whitehead S.L., Whitehead S.L., Whitehead S.L., Whitehead S.L., Whitehead S.L., Whitehead S.L., White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414:865-871(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Placenta, and Tongue;
Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
Ratsuta N., Sato K., Tanikawa M., Yamazaki M., Irie R., Sato H.,
                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                             Q9NUB1; QBIV99; Q8N234; Q96J11; Q96JX6; Q9NU28; 10-OCT-2003 (Rel. 42, Created) 10-OCT-2003 (Rel. 42, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Acetyl-coenzyme A synthetase 2-like, mitochondrial precursor (EC 6.2.1.1) (Acetate--CoA ligase 2) (Acetyl-CoA synthetase 2-ACAS21 OR KIAA1846.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                           689 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
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                           STANDARD;
                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rogers J.;
                              AC2L HUMAN
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DT 10-OCT
DT 10-OCT
DE (EC 6.
GN ACAS21_L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ç
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for oxidation through the tricarboxylic cycle to produce ATP and CO(2) (By similarity).
-!- CATALYTIC ACTIVITY: ATP + acetate + CoA = AMP + diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                       Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XX. The complete sequences of 100 new cDNA clones from brain which code
Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Ota T., Hayashi K., Sugiyama T., Otsuki T., Ishibashi J. Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y., Wakamatsu A., Kanahori K., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Sugano S., Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for large proteins in vitro.";
DNA Res. 8:85-95(2001).
-!- FUNCTION: Converts acetate to acetyl-CoA so that it can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CAUTION: Ref.1 (CABB1884) sequence differs from that shown due erroneous gene model prediction.
-!- CAUTION: Ref.3 sequence differs from that shown due to a frameshift in position 250 and numerous sequencing errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACETYL-COENZYME A SYNTHETASE 2-LIKE.
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCÉLLULAR LOCATION: Mitochondrial matrix (By similarity).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isoid=Q9NUB1-2; Sequence=VSP 007249;
Note=No experimental confirmation available;
SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              splicing.
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/FIId=VSP 007249.
V -> M (IN REF. 2; AAH39261).
GEB4E39302AD08B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.8%; Score 87; DB 1; Length 689; 84.1%; Pred. No. 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transit peptide; Alternative sp
MITOCHONDRION (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 336-689 FROM N.A. (ISOFORM 1).
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EMBL, AK0270817; BABS2390.1; ALT_INIT.
EMBL, AK092295; BAC03853.1; ALT_SEQ.
EMBL, AB0S8749; BAB47475.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21245130; PubMed=11347906;
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Pfam; PF00501; AMP-binding; 1.
PROSITE; PS00455; AMP_BINDING; 1.
Ligase; Mitochondrion; Transit pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74856 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:16091; ACAS2L.
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689
53
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689 AA;
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446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acetyl-CoA.
                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family
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SYL XYLFT
Q87<u>C</u>65;
    CONFLICT
                                                                                         SEQUENCE
                                                                                                                                                                             Query Match
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        FT
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473 FFGIVPVLMDEKGSV------VEGSNVSGALCIS------QAWPGMARTI--- 510
                                                                                    69 VQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRA---EVKFEGDTLVNRIE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Geber A., Hitchcock C.A., Swartz J.E., Pullen F.S., Marsden K.E., Kwon-Chung K.J., Bennett J.E.;
Kwon-Chung K.J., Bennett J.E.;
"Deletion of the Candida glabrata ERG3 and ERG11 genes: effect on cell viability, cell growth, sterol composition, and antifungal susceptibility.";
                                                                                                                                     IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             methyl-5-alpha-ergosta-8,14,24(28)-trien-3-beta-ol + formate + 3 NADP(+) + 3 H(2)0.
PATHWAY: Ergosterol biosynthesis.
SIMILARITY: Belonge to the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the significance of the s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P50859; 002312; 002312; 013022; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 01-0CT-2003 (Rel. 42, Last annotation update) Cytochrome P450 51 (EC 1.14.13.70) (CYPLI) (P450-LIAI) (Sterol 14-alpha-demethylase) (Lanosterol 14-alpha demethylase) (P450-14DM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Catalyzes C14-demethylation of lanosterol which is critical for ergosterol biosynthesis. It transforms lanosterol into 4,4'-dimethyl cholesta-8,14,24-triene-3-beta-ol (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITÉ; PS00086; CYTOCHROME_P450; 1.
Electron transport; Oxidoreductase; Monooxygenase; Membrane; Heme; Sterol biosynthesis; NADP. IRON (HEME AXIAL LIGAND) (BY SIMILARI; METAL 472 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-ATCC 2001;
MEDLINE-95081364; PubMed-7989540;
Burgener-Kairuz P., Zuber J.P., Jaunin P., Buchman T.G., Bille J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rossier M.;

"Rapid detection and identification of Candida albicans and
Torulopsis (Candida) glabrata in clinical specimens by
species-specific nested PCR amplification of a cytochrome P-450
lanosterol-alpha-demethylase (LIA1) gene fragment.";

J. Clin. Microbiol. 32:1902-1907(11994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Candida glabrata (Yeast) (Torulopsis glabrata).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharom
Saccharomycetales, mitosporic Saccharomycetales, Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -! - SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antimicrob. Agents Chemother. 39:2708-2717(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               533 AA
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Pfam; PF00067; p450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96161286; PubMed=8593007;
                                                                                                                                                                                                                                                     126 LKGIDFKEDGNILGHKL 142
                                                                                                                                                                                                                                                                                                                                              ------NISGHRL 560
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SEQUENCE OF 60-473 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L40389; AAB02329.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=5478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CANGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WEDLINE-2242131; PubMed=12533478;
Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Mon D.H.,
A Takita M.A., Lemos B.G.M., Machado M.A., Ferro M.T.T., da Silva F.R.,
A Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M.,
A Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
A Carrer H., Carraro D.B.T., Ferro B.S., Harakava R., Kuramae B.E.,
A Marino C.L., Giglioti B., Abreu I.L., Alves L.M.C., do Amaral A.M.,
Baia G.S., Blanco S.R., Barto M.S., Cannavan F.S., Celestino A.W.,
A de Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sassaki F.T., Sena J.A.D.,
A civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
A Kitajima J.P.,
                                                                                                                                                                                                                                                         109 GHEFIFNAKLADVSAEAAYSHL-------TTPVFGKGVIYDCPNHRLM 149
                                                                                                                                                                                                                                                                                                                                                              207
                                                                                                                                                                                                                                                                                                                                                                                                                                                208 TASRSLIGKEMRDKLDTDFAYLYSDLDKGFTPINF-VFPNLPLEHYRKRDHAQQAIS--- 263
                                                                                                                                                                                                                                                                                                            80 KQHDFFKSAM-PEGYV-----QERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDF 131
                                                                                                                                                                                                                                                                                                                                                                                                                132 KEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGD 191
                                                                                                                                                                                                            79
                                                                                                                                                                                                         25 GHKFSVS---GEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLSYGVQCFSRYPDH--M
                                                                                                                                                                                                                                                                                                                                                           150 EQKKFVKGALTKEAFVRYVPLIABEIYKYFRNSKNFKINENNSGIVDVMVSQPEM--TIF
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol. 185:1018-1026(2003).
-!- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP +
diphosphate + L-leucyl-tRNA(Leu).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leucyl-ERNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)
LEUS OR PD1230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Comparative analyses of the complete genome sequences of Pierce's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xylella fastidiosa (strain Temecula1 / ATCC 700964).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                         49;
                                                                                                    6.8%; Score 86.5; DB 1; Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease and citrus variegated chlorosis strains of Xylella
                                                                                                                                                       Indels
64 I -> M (IN REF. 2).
473 I -> T (IN REF. 2).
61305 MW; A0506C17507EGEF7 CRC64;
                                                                                                                                                       81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     879 AA
                                                                                                                            Local Similarity 21.4%; Pred. No. 10; es 44; Conservative 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 -----GTYMSLIKERREKND 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 GPVLLPDNHYLSTQSALSKDPNEKRD 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xanthomonadaceae; Xylella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAMAP; MF 00049; -; 1.
                                                     533 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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POTENTIAL.
VITELLOGENIN 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                  23.4%; Pred. ...
tive 32; Mismatches
                                                                                                                                                                                                                                                     Storage protein; Multigene family; Signal. SignAL 1 15
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                                                                                                                                                                                                                                                                                                         WFD.
                                                                                                                                                                          WormPep; FSSDB.2; CE26817.
InterPro; IPR001747; Lipid_transp:
InterPro; IPR001846; WWF D.
Edan; PF01347; Vitellogenin_N; 1.
SMART; SM00638; LPD N; 1.
                                                                                                                        EMBL; AC024137; AAK09074.1; -.
                                                                                                                                     EMBL; M11498; AAA28163.1; -. EMBL; X02754; CAA26531.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 23.4
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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169
187
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169 16
183 18
275 27
1603 AA;
                                                                                                                                                                  PIR; A43084; A43084
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MEDLINE=8526964); PubMed=4022780;
MEDLINE=8526964); PubMed=4022780;
MEDLINE=8526964); PubMed=4022780;
MITTE C. elegans vitellogenin genes: short sequence repeats in the promoter regions and homology to the vertebrate genes.";
MITTE C. elegans vitellogenin genes: short sequence repeats in the promoter regions and homology to the vertebrate genes.";
MITTE C. elegans vitellogenin genes: short sequence repeats in the nutrients during embryonic development (Potential).

C. elegans vitellogenin secreted.

TISSUE SPECIFICITY: Synthesized in Caenorhabditis only by 32 cells building the intestine of adult hermaphroditic individuals; they are cortranslationally secreted into the body cavity and subsequently taken up by the gonad.

C. elegans vitellogenin secreted.

SEQUENCE OF TISSUE SPECIFICITY Synthesized in the body cavity and subsequently taken up by the gonad.

C. elegans vitellogenin secreted.

SEQUENCE OF TISSUE SPECIFICITY Secreted into the body cavity and subsequently taken up by the gonad.
                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                            154 MADKÖKNG-IKVNFKIRHNIEDGSVQLADHYQQNTPI-------GDGPVLLPDN 199
                                                                                                                                                                                                                                                               50 TTGKLPVPWPTLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNY-- 107
                                                                                                                                                                                                                                                                                              321 TNEQLPV-WVANFVLMAYGTGAVMAVPGHDQRDQEF--ANKYGLPIRQVIALKEPKNQDE 377
                                                                                                                                                                                                                                                                                                                        108 ------KTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYI 153
                                                                                                                                                                                                                                                                                                                                                                                               : | ::||:||:|
---ROGREGORRVNYRLR----DMGVSRQRYWGCPIPVIYCPTCGAVPVPENQLPVILPEN 474
                                                                                                                                                                                                                                                                                                                                        378 STWEPDVWRDWYADKTR---EFE---LINSAEFDGLDYQGAFEVLAERFE------
                                                     Pfam; PF00133; tRNA-synt_1; 1.
PRINTS; PR00985; TRNASYNTHLEU.
TIGRPAMS; TIGR00396; leug. Dect; 1.
PROSITE; PS00178; AA TRNA_LIGASE I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda, Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                        57;
                                                                                                                                                                                                            DB 1; Length 879;
                                                                                                                                                                                                          ; Score 86.5; DB 1; Length 8; Pred. No. 18; 28; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blumenthal T., Spieth J., Zucker E.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                  4C2EE01B8FDC497E CRC64;
                                                                                                                                                     "KMSKS" REGION.
ATP (BY SIMILARITY)
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                                                                                                                                          "HIGH" REGION
InterPro; IPR002302; Leu-tRNAsyntla.
InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR009008; ValRS_IleRS_edit.
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                                                                                                                                                                                  99823 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vitellogenin 4 precursor.
VIT-4 OR F59D8.2.
Caenorhabditis elegans.
                                                                                                                                                                                                                                          44; Conservative
                                                                                                                                          55
641
640
                                                                                                                                                                  640 6
879 AA;
                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                    Complete proteome. SITE
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                                                                                                                                                                                  SEQUENCE
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BINDING
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VIT4 CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 -----NYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMAD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 LINVNGQEVVKSETRAKVTFVEESKINR-EIK-----KVSGPKEEIVYSMENEKLIEQ 308
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Campylobacteraceae; Campylobacter.
NCBI_TaxID=197;
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SEQUENCE FROM N.A.
MEDLINE=2015.0912. PubMed=10688204;
MEDLINE=2015.0912. PubMed=10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Qagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
methyltransferse) (RUMT)
TRMA OR CJ0831C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 Y -> V (IN REF. 3).

69 L -> V (IN REF. 2).

87 EVAYT -> RSRLH (IN REF. 2).

75 T -> S (IN REF. 2).

186307 MW; B303170325BC99BB CRC64;
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us-09-887-784-222v.rsp

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or send an email to ...

or send an email to ...

Dr send an email to ...

Sensol send an email to ...

Dr send an email to ...

BR BHI, AL13076; CAB73096.1; ...

BR HAMAP; MF 01011; .; 1.

DR HAMAP; MF 01011; .; 1.

DR InterPro; IPR001566; TrmA.

DR InterPro; IPR001566; TrmA.

DR ROSITE; PS01230; TRMA.1; 1.

DR PROSITE; PS01231; TRMA.2; FALSE NEG.

METHORIE PROSITE; PS01231; TRMA.2; FALSE NEG.

SIMILARITY.

SADENOSYLMETHIONINE BINDING (BY SIMILARITY.

SIMILARITY.

315 BY SIMILARITY.

""" My; CEC5328347CEE4497 CRC64;

""" My; CEC5328347CEE4497 CRC64;
                                       genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                       subfamily.
RRAH BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARA
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80 KQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKF--EGDTLV------NRIELKG 128

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Search completed: June 21, 2004, 15:55:23 Job time : 6.55556 secs

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Koranyi P., Berenyi M., Burg K.;
"Occurrence of green fluorescence protein in diazotrophic bacteria Azomonas and Azotobacter.";
Bubmitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF324408; AAN86140.1; -.
GO; GO:0006091; Prenergy pathways; IEA.
InterPro; IPR009017; GFP-like.
InterPro; IPR009017; GFP-like.
Pfam; PF01153; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
Prodom; PD013756; Green fl_protein; 1.
SEQUENCE 238 AA; 26914 WW; F84840FIF9064018 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azotobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Green fluorescence protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=DSM2289;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8GHE2
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2458.984 Million cell updates/sec
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                                                                                                                                                                                                1274
1 MVSKGEELFTGVVPILVELD......VLvGFVTAAGITLGMDELYK 239
                                                                                                        June 21, 2004, 15:45:30 ; Search time 30.6667 Seconds
                                                                                                                                                                                                                                                                                                                                              1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                          1017041 segs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_fungi:*
sp_human:*
sp_mammal:*
sp_mammal:*
sp_organelle:*
sp_bhage:*
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sp_vertebrate:*
sp_unclassified:*
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sp_bacteriap:*
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Maximum DB seq length: 200000000
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Database

238 AA.

	Description	OROBE CARREST			Q8ghe3 azotobacter	Q17105 aequorea vi	Q17106 aequorea vi	Q8wtc6 aequorea ma	Q8wp95 aequorea ma	Q8wtc4 aequorea ma	Q8wtd0 aequorea ma	Q8wtc8 aequorea ma	Q8wtc9 aequorea ma	Q8wtc7 aequorea ma	Q8wtc5 aequorea ma	Q95ua7 montastraea	Q7z0w5 montastraea
SUMMARIES	ID	ORGHE2	093125	Q8GHE4	Q8GHE3	Q17105	Q17106	QBWTC6	Q8WP95	Q8WTC4	Q8WTD0	QBWTCB	Q8WTC9	Q8WTC7	Q8WTC5	Q95UA7	Q7Z0W5
	DB	10	ហ	~	~	S	S	ഹ	Ŋ	വ	S	ß	ហ	Ŋ	Ŋ	ഹ	Ŋ
م	* Query Match Length DB	238	238	238	238	238	238	238	238	238	238	238	238	238	238	225	225
	Query Match	97.3	97.1	96.9	96.9	94.3	93.2	84.9	84.6	84.3	84.1	84.1	84.1	83.9	83.8	19.8	19.8
	Score	1240	1237	1235	1234	1202	1187	1082	1078	1074	1072	101	101	1069	1067	252.5	252.5
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61

62 VTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERIFFKDDGNYKTRAEVKFEGDTLV 121

1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 60

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2 VSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTIGKLPVPWPTL

Query Match 97.3%; Score 1240; DB 2; Length 238; Best Local Similarity 97.5%; Pred. No. 4.8e-96; Matches 232; Conservative 3; Mismatches 3; Indels (

Q963f5 montastraea Q8t6u0 dendronepht Q7z0w9 montastraea Q8i6j8 trachyphyll		Q720%6 montastraea Q720%7 montastraea Q8mmal agaricia ag Q8mmal agaricia fr Q8m572 montastraea	1 - 10 00 00		Q95vtO montabradea Q9u6y8 discosoma s Q9gz28 anemonia su Q7z168 cerianthus Q8t6t9 radianthus Q9u6y7 discosoma Q8t5f0 scolymia cu
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61 VTTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
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"Occurrence of green fluorescence protein in diazotrophic bacteria Azomonas and Azotbacter.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF324406; AAN86138.1;
                                                                                                                                                                                                                                                                                               Koranyi P., Berenyi M., Burg K.; "Occurrence of green fluorescence protein in diazotrophic bacteria Azomonas and Azotobacter.";
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                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azomonas.
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EMBL, AF324405; AAN86137.1; -...
EMBL, AF324405; AAN86137.1; -...
EQ, GO.1006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IPR000786; Green_fl_protein.
Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green_fl_protein; 1.
SEQUENCE 218 AA; 26902 MW; ISFE9B9C5B4F6B89 CRC64;
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26887 MW; EOE1616BD2AF6188 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Green fluorescence protein.
      Last sequence update)
Last annotation update)
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NCBI_TaxID=354;
01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25, Green fluorescence protein.
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Azotobacter vinelandii.
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                                                                                                                                 Azomonas agilis.
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            61 VTTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                        NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
                                                                                                                        121 NRIBLKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
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Brown A.J.P.;

"Yeast Enhanced Green Fluorescent Protein (yEGFP): a reporter of gene
expression in Candida albicans.";

Microbiology 0:0-0(1996).

BiNBL; U73901; AAB18957.1; -.

HSSP; P42212; IBFP.

GO; GO:0006091; P:energy pathways; IEA.

InterPro; IPR009017; GFP like.

InterPro; IPR009018; Green fl_protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aequorea victoria (Jellyfish).
Eukaryota; Metazoa; Chidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
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ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 26840 MW; A28622809A9DEA60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Green fluorescent protein mutant 3.
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Pred. No. 8.7e-96;
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01-MAR-2003 (TrEMBLrel. 23, Created)
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Best Local Similarity 97.13
Matches 231; Conservative
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Q93125;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Green fluorescent protein (Fragment).
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                                                                                                                                    61 VITESYGVQCFSRYPDHMXRHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDILV 120
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Eukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Leptomedusae,
Aequoreidae, Aequorea.
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 Pred. No. 1.5e-95;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watkins J.N., Campbell A.K.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; X83599; CAA58789.1; -.
PIR; JS0692; JQ1514.
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GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IPR000786; Green_fl_protein.
Pfam; PF01353; GFP; 1.
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ProDom; PD013756; Green fl protein; 1.
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97.18;
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                 Matches 231; Conservative
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 Best Local Similarity
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Best Local Similarity
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121 61 VITFSYGVQCFSRYPDHMKQHDFLKSAMPEGYVQERIIFYKDDGNYKTRAEVKFEGDILV 120 122 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVQLAD 181 9 61 182 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLVGFVTAAGITLGMDELYK 239 181 HYQQNTPIGDGPVLLPDNHYLSTQSALSQDPHGKRDHMVLLEFVTSAGITHGMDELYK 238 2 VSKGEBLPTGVVPILVELDGDVNGHKPSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 62 VITLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV STRAIN=GFDxml9uv;
Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea Gaps Aequorea victoria (Jellyfish). Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae; Aequoreidae; Aequorea. ö Aequorea macrodactyla. Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae; Aequoreidae; Aequorea. NCBI_TaxID=147615; Query Match 93.2%; Score 1187; DB 5; Length 238; Best Local Similarity 92.9%; Pred. No. 1.3e-91; Matches 221; Conservative 8; Mismatches 9; Indels ( Matkins J.N., Cambbell A.K.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
R EMBL; X83960; CAA58790.1; -.
R HSSP; P42212; JBFP.
R HSSP; P42212; JBFP.
R GO; GO:0006091; P:energy pathways; JBA.
R InterPro; JFR009017; GFP_like.
R InterPro; JFR009076; Green_fl_protein.
R Pfam; PF01353; GFP; 1.
R PRINTS; RR01229; GFLUORESCENT.
R ProDom; PD013756; Green_fl_protein; 1.
R ProDom; PD013756; Green_fl_protein; 1.
R NON TER 238 AA; 26867 MW; BD4648262D8EABD4 CRC64; macrodactyla."; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF43431; AAL33916.1; -. GO; GO:0006091; P:enercyp pathways; IEA. InterPro; IPR009017; GFP like. InterPro; IPR0090786; Green_fl_protein. Last sequence update) Last annotation update) ACC OCC OCT RAP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP BE REP

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STRAIN=GFPAM, and GFPdnaxm;
STRAIN=GFPAM, and GFPdnaxm;
Liuo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Qin Y.X., Pang S.Q.,
Lii S.J., Xia N.S.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
BMBL, AN013821, AR02062.1;
GO, GO:0006091; P:energy pathways; IEA.
InterPro; IPR00918; GFP_like.
InterPro; IPR00918; Gref_ilprotein.
PF01353; GFP; 1.
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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                                                                                                                                Length 238;
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3 238 AA; 27015 MW; 6B8FD75E88926903 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                         Query Match

84.9%; Score 1082; DB 5;
Best Local Similarity 81.9%; Pred. No. 8.6e-83;
Matches 195; Conservative 21; Mismatches 22;
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PRINTS; PR01229; GFLUORESCENT.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VSKGEELFTGVVPILVELDGDVNGHKFSVSGEGGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                       Lio W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M., Li S.J., Xia N.S.; "Colorful mutants of green fluorescent protein from Aequorea
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                    Aequorea macrodactyla.
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
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STRAIN=GFPxm161;
Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q.,
Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea macrodactyla.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.3%; Score 1074; DB 5; Length 238; 82.4%; Pred. No. 4e-82; rive 18; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   macrodactyla.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0006091; P:energy pathways; IEA.

InterPro; IPR000076; GFen_fl.protein.

PRINTS; PR01353; GFP; 1.

PRINTS; PR01259; GFUORESCENT.

PRODOM; P013756; Green fl.protein; 1.

SEQUENCE 238 AA; 26956 WW; 75521EAF0CEBA73A CRC64;
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01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2003 (TrEMBLrel. 25,
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NCBI_TaxID=147615;
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122 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, AF435428; AAL333913.1;
GO; GO:0006691; P:energy pathways; IEA.
InterPro; IPR000917; GFP_like.
InterPro; IPR010966; Green_fl_protein.
Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green_fl_protein; 1.
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Matches 193; Conservative
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
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Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q.,
Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                                                                                                  84.1%; Score 1072; DB 5; Length 238; 81.1%; Pred. No. 6e-82; ive 21; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.1%; Score 1071; DB 5; Length 238; 81.1%; Pred. No. 7.2e-82; ive 21; Mismatches 24; Indels
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF415427; AAL33912.1; -
GO; GO:0006091; Penergy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR0090786; Green_fl_protein.
Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
PRODOM; PD013756; Green fl_protein; 1.
SEQUENCE 238 AA; 26997 MW; 5F80A192173CB84D CRC64;
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 27047 MW; 5F80A18FA1E7C84D CRC64;
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Last annotation update)
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GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR0009017; GFP_like.
InterPro; IPR00786; Green_fl_protein.
Pfam; PF01353; GFP; 1.
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Matches 193; Conservative
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Matches 193; Conservative
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62 VTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
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                                                          182 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLVGFVTAAGITLGMDELYK 239
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Colorful mutants of green fluorescent protein from Aeguorea
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QBWTC7
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AC QBWTC
DT 01-MA
DT 01-MA
DT 01-OC
DB Green
GN GFP.
OS Aequo
OC BUKAZ
OC BUKAZ
OC BUKAZ
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SEQUENCE
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                                 Chen M.,
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.8%; Score 1067; DB 5; Length 238; 81.9%; Pred. No. 1.6e-81; ive 18; Mismatches 25; Indels (
                              Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Li S.J., Xia N.S., "Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                           Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   macrodactyla.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF435432; AAL33917.1; -.
GO, GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR00786; Green_fl_protein.
PF01353; GFP; 1.
                                                                 macrodactyla.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF453-9103 AAL33915.1;
GO, GO:0006091; P:energy pathways; IEA.
InterPro; IPR000901; GFP_like.
InterPro; IPR000786; Green_fl_protein.
PRINTS; PR01353; GFP; 1
ProDom; PR013756; Green_fl_protein.
ProDom; P013756; Green_fl_protein; 1.
SEQUENCE 238 AA; 27002 MW; BD5BA2982264C018 CRC64;
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ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 27018 MW; 75521EA5534E573A CRC64;
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Last sequence update)
Last annotation update)
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Pred. No. 1.1e-81;
                                                                                                                                                                                                                 21; Mismatches
                                                                                                                                                                                            83.9%; Score 1069;
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                                                                                                                                                                                                        81.18;
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Matches 193; Conservative
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SEQUENCE FROM N.A.
STRAIN-GFPXm191uv;
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Best Local 8
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71 CFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGID 130
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                                                                                                NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 VVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKF-ICTTGKLPVPWPTLVTTLSYGVQ 70
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                                                                                                                                                                                                                                                         HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLVGFVTAAGITLGMDELYK 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cyan fluorescent protein (Fragment).

Montastraea caetr protein (great star coral).

Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia; Faviina; Faviidae; Montastraea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | SEQUENCE FROM N.A. | SEQUENCE FROM N.A. | SEQUENCE FROM N.A. | SEQUENCE FROM N.A. | SEQUENCE FROM N.A. | SEQUENCE FROM N.A. | Montastraea cavernosa fluorescent protein."; | Montastraea cavernosa fluorescent protein."; | Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. | EMBL, AVOS6460; AAL17905.1; | EMBL, AVOS6460; AAL17905.1; | RG), GO; GO; GOGO6091; PP: energy pathways; IEA. | InterPro; IPR000786; Green_fl_protein. | RFF01353; GRF; 1. | PRINTS; PR01229; GFLUORESCENT. | PRINTS; PR01229; GFLUORESCENT. | PRODOM; PD013756; Green_fl_protein; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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Job time : 30.7778 secs
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es 64; Conservative 4
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